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(54) **GENE SIGNATURE.**

(57) A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomoly or discriminating cells. The cloned gene can produce porteins utilizable as a medicine or the like.

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## Fields of the Invention

The present invention relates to purified single-stranded DNA molecules, purified single-stranded DNA molecules complementary thereto or purified double-stranded DNA molecules consisting of said single-stranded DNA molecules, which can specifically hybridize to human genomic DNA, human cDNA or human mRNA at particular sites. The DNA molecules of the present invention can be used for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting and diagnosing cellular abnormalities due to disease and viral infection, or distinguishing and identifying the cell type, and efficiently cloning genes expressed in a tissue-specific manner. The present invention further includes cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products or the like.

## Related Arts

Recognizing the importance of the most fundamental attribute of mRNA, that is, "the nature of the cell is determined by the expression pattern of genes as reflected in the population of mRNA", the inventors of the present invention have proposed "body mapping" as a unique approach to their objective. This is an entirely novel attempt to prepare "the information on gene expression" for presumably about 200 different kinds of cells and tissues present in the human body and elucidate when, where and to what extent a certain gene is expressed, and map genes to the respective organ or cell type in which they are expressed.

While a variety of cells in the living body express various proteins depending on their respective biological functions, the intracellular concentrations of these proteins vary according to the cell type, stage of development and differentiation, environment, etc.

In general, genes are classified into "genes encoding proteins essential for the life of the cell" and "genes encoding proteins responsible for functions specific to the cell". Of these two, "genes encoding proteins essential for the life of the cell" are expressed constantly in all types of cells and also called "housekeeping genes", while "genes encoding proteins responsible for functions specific to the cell" are often expressed specifically in a particular type of cells or a particular group of cells, and also may be specifically expressed at a particular stage of cellular development and differentiation. Furthermore, they are often "inducible genes" and the amount of their expression varies depending upon the environment to which cells are exposed. In other words, cells may grow as a result of the expression of "genes encoding proteins essential for the life of the cell" and display their specific functions as a result of the expression of "genes encoding proteins responsible for functions specific to the cell".

However, under abnormal cellular conditions due to disease or infection, the expression of genes within individual cells is altered as compared with that under the normal conditions. Especially, during viral infection, RNAs encoding virus-specific proteins are synthesized in large amounts within the cell, leading to the production of said protein in large amounts. In other words, the alteration in the expression level of genes within the cell, especially as reflected in the concentration of intracellular mRNA, can lead to such abnormal cellular conditions as seen in diseases.

Thus, the function of each cell in the living body is closely related to the expression status of genes within the cell. Accordingly, in order to elucidate the function of each cell at molecular level or to investigate the pathogenesis of a disease at molecular level, it becomes necessary to comprehend the expression status of cellular genes, especially the intracellular concentration of each mRNA.

A theoretically possible approach to this objective is the extraction and analysis of all cellular proteins for determination of expression status. However, although it may be possible to isolate a specific protein, in most cases it is almost impossible to completely isolate all of these proteins, because a great variety of proteins are expressed within the cell.

Another approach is to directly estimate the concentrations of cellular mRNAs corresponding to all intracellular proteins. However, although it may be possible to isolate a specific mRNA, it is practically impossible to completely isolate all of these mRNAs and directly estimate their amounts, because a great variety of mRNAs are synthesized simultaneously within the cell and furthermore they may be unstable and susceptible to enzymatic degradation during their extraction.

This invention aims to provide DNA molecules which can be used as probes or primers required for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting or diagnosing cellular abnormalities due to disease or virus infection, recognizing and identifying various cell types, and efficiently cloning genes expressed in a tissue-specific manner. Moreover, the present invention aims to provide cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products.



## Summary of the invention

In general, the genetic information flows in order from DNA to mRNA and to protein (F. H. C. Crick, 1958). That is, "the information for the amino acid sequence of a protein" is first transcribed into mRNA and then translated into protein.

To explain this in further detail mammalian genes commonly comprise a region encoding a protein and a region regulating the expression of said gene. The regions of a gene encoding protein (called "exons") are often separated by intervening sequences (called "introns"). When a gene is transcribed into RNA, the introns of the precursor RNA (pre-mRNA) are excised and exons are connected in tandem to form a contiguous structure coding for a particular protein (this process is called "splicing"). On the other hand, the region regulating the expression of gene comprises, in addition to the regions directly regulating transcription such as a promoter and operator which are present upstream of the transcription region, untranslated regions are located both upstream (5') and downstream (3') of the coding region. In particular, 3' untranslated region (3' UTR) is important for regulating expression, since it contributes to the transport and stability of mRNA. During the processing of pre-mRNA, a methylated cap is added at its 5' end, the 3' untranslated region is cleaved at a specific site, a poly(A) tail is attached by adding 100 - 200 adenylate residues to the cleaved end, and the coding regions are spliced together to form mRNA. The protein is then synthesized after attachment of ribosomes to the mRNA.

The inventors of the present invention have elucidated that, in general, when the intracellular level of a particular mRNA is high, the expressed amount of the corresponding protein is also elevated, and also that it is possible to estimate the relative concentration of each intracellular protein by estimating relative intracellular concentration of the corresponding mRNA [DNA sequence 2, 137-144 (1991); Nature genetics, 2, 173-179 (1992)].

Basically in the present invention, mRNA is extracted from a particular cell and cDNA is synthesized by conventional methods using reverse transcriptase. However, in the present invention, cDNA is synthesized using a method developed by the inventors of the present invention so as to reflect the relative intracellular concentration of mRNA. A cDNA library is constructed and a group of cDNAs representing the population of total mRNA are cloned and sequenced.

An approach which appears to be similar to the one used by the inventors of the present invention but is entirely different, is the method of cloning of a cDNA library constructed by the random priming by Venter et al.

Venter's group randomly cloned cDNAs from commercially available cDNA libraries derived from brain cells (catalog No. 936206, 936205 or 935, Stratagene, California) and determined their base sequences [Science 252, 1651-1656 (1991); Nature 355, 632-634 (1992)].

While the method used by Venter et al. involves sequencing of cDNAs obtained by random priming, this method has the following drawbacks:

- 1) Since random cloning of various regions of a single-stranded mRNA may often lead to the formation of many cDNA fragments without any mutual overlapping portions, it is difficult to determine whether these cDNA fragments are derived from the same mRNA or a different one,

- 2) The longer a mRNA strand, the higher the chance for said mRNA to be reverse-transcribed into cDNA, and

- 3) Since the availability of each primer to be used among random primers differs depending on their base sequences, the relative frequency of cDNA synthesis is variable.

From aforementioned reasons, the relative frequency of appearance of cDNA does not reflect the relative concentration of cellular mRNA. Consequently, it is impossible to determine the relative concentration of each mRNA and the actual population of intracellular proteins by using the method of Venter et al.

However, with the method developed by the inventor of the present invention, it is possible to construct a cDNA library which precisely reflects the relative concentration of mRNA without any of the aforementioned complications. Since, in the present invention, cDNA is synthesized using only "poly-T" as the primer, the 3' ends of the cDNA have "a poly A tail". Therefore, the synthesis of cDNA with "poly-T" as the sole primer is initiated from the 3' end resulting in the formation of 3'-oriented cDNA. Since the 3' untranslated sequence is unique to a particular mRNA species and not present in other mRNA species [Birnstiel, M. L., et al., Cell 41, 349-359 (1985)], almost all the 3' end-oriented cDNAs hybridize with specific mRNAs. Digestion of the resulting cDNA with a restriction enzyme MboI which recognizes the specific four-base sequence GATC results in the formation of cDNA extending from the 3'-terminus to the first MboI restriction site. In the present invention, each cDNA thus cloned and included in "a cDNA library faithfully reflecting the relative intracellular concentration of mRNA" is called a "gene signature" (abbreviated as GS hereinafter). A GS includes not only the double-stranded DNA but also each single-stranded DNA thereof.

The present invention relates to a purified single-stranded DNA, purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under the sequence identification number (SEQ ID NO) 1 - 7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA. The present invention also relates to a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) or any portion thereof at its 3' region and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA.

The present invention is explained further in detail as follows.

The DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1 - 7837 but also includes a single-stranded DNA containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

Furthermore, the DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) or any portion thereof at its 3' region but also includes a single-stranded DNA (or a single-stranded DNA complementary thereto) containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

In addition, the DNA of the present invention not only includes a single-stranded DNA or a single-stranded DNA complementary thereto but also includes a double-stranded DNA consisting of said single strands.

Obviously, the term "contain" as used herein does not necessarily mean that the DNA of the present invention contains at a single site without interruption (1) "a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1-7837 or a portion thereof" or (2) "a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any or any portion of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) at its 3' region or a portion of said single-stranded DNA." In other words, the term "contain" is applicable also to the case where one or more exogenous bases are inserted in the base sequence of the DNA (1) or (2).

The hybridization to a particular site of human genomic DNA, human cDNA or human mRNA can be achieved under standard conditions (see e.g., Molecular Cloning: A Laboratory Manual, Sambrook, J., et al., Cold Spring Harbor Laboratory Press, 1989). In the following preferred embodiment, there will be described methods for constructing a cDNA library which reflects precisely the relative intracellular concentration of mRNA, cloning cDNA groups which correspond to total mRNA, and determining the base sequence of each cDNA.

First, cells from specific tissues, for example, cells from organs, for example, cells derived from human liver (HepG2) are grown, and the total mRNA is extracted by standard procedures. mRNA thus obtained is attached to a vector to construct a cDNA library.

For example, mRNA is attached to the vector plasmid pUC19, which has the M13 sequences flanking the cloning site, as follows.

pUC19 is cleaved by HincII and PstI and poly-T of 20 bp - 30 bp is added to the PstI-digested end to which the 3'-end poly-A tail of the mRNA is hybridized (Fig. 1a). After the DNA strand is extended with conventional methods using reverse transcriptase, a double stranded DNA is formed with DNA polymerase (Fig. 1b). The double stranded DNA thus obtained is cleaved with the restriction enzyme MboI which recognizes a specific four base sequence (Fig. 1c).

MboI, which recognizes a four base sequence (GATC), cleaves the DNA within a few hundred bases from the poly-A tail. Since MboI is found to digest, without exception, about 300 human cDNAs which were randomly selected from the GenBank data base by the inventor of the present invention, this enzyme cleaves the cDNA to be cloned at a specific site. In addition, as pUC19 is prepared in dam<sup>+</sup> E. coli, e.g., E. coli JM109 and since its adenine at the MboI recognition site is methylated (G<sup>m</sup>ATC), it is not cleaved by MboI.

Subsequently, in order to prepare a vector containing the double-stranded DNA which has previously been attached to pUC19 and has the MboI-cleaved end, the pUC19 DNA is digested with BamHI to make termini cohesive with the MboI-cleaved end. Since the recognition sequence of BamHI (GGATCC) contains that of MboI (GATC), the extended portion of the double-stranded DNA is not cleaved with BamHI.

5 The resulting double-stranded DNA is then circularized by standard ligation methods, and the recombinant vector plasmid thus prepared is introduced into *E. coli*, e.g., *E. coli* DH5 in order to make a cDNA library.

With this method, only a clone containing the base sequence upstream of the poly-A tail of the mRNA is obtained.

10 Since the average size of the inserted cDNA fragment is relatively small, 270 bp, it is free from biased cloning resulting from variations in the efficiency of cDNA synthesis and transformation that occur in the case of larger sized DNAs. Furthermore, because instability due to repeated base sequences and the like is eliminated, the cDNA library of the present invention faithfully represents the relative concentration of mRNA in the cell.

15 Furthermore, when the cDNA inserted into the vector is relatively short, it is possible to accurately amplify the cDNA fragment using the sequence of the vector flanking it as a primer. It is also possible to determine the base sequence from the 5' end directly by the PCR without interference from the 3' poly-A tail which will reduce the accuracy of sequence determination.

Amplification of the GS, i.e., the cDNA fragment inserted into the vector, is performed as follows.

20 The *E. coli* cells in which the cDNA library is introduced are grown using standard methods and lysed. Debris contained in the bacterial lysate are removed by centrifugation and the supernatant containing the vector DNA is recovered. The vector DNA thus obtained is used as the DNA template for amplification by the PCR (Fig. 1d, amplification with PCR primers 1 and 2).

Base sequences flanking both ends of the GS is properly selected for use as primers and the PCR is 25 performed under standard conditions. PCR products thus obtained are subjected to the elongation reaction using fluorescence primers complementary to the vector sequence flanking the 5' end of the GS, and the sequence is determined with an autosequencer (Fig. 1d, sequence determination with dye primer).

Based on the results of the sequence determination of each GS, the species and the frequency of appearance of the GS in each tissue or cell type are analyzed.

30 As to each cell type not only normal cells but also cells under pathogenic conditions (such as tumor cells, virus infected cells, etc.) can be used without any restriction. For example, liver cells (from fetus, neonate or adult), various hematopoietic cells (granulocytic, monocytic, etc.), lung cells, adipocytes, endothelial cells, osteoblasts, colon mucosa cells, retinal cells and hepatoma cells (HepG2, etc.), and promyelocytic leukemia cells (HL60, etc.) will be used. The appearance frequency for each GS is described for each cell type in Tables 1 through 219. There, patent number represents "SEQ ID NO for each GS", size represents the "length of each GS", and F represents the "sum of appearance frequencies in the cells studied". In addition, hepG2 stands for "hepG2 (a liver cancer cell line)", HL60 stands for "HL60 promyelocytic leukemia cell line", granulo stands for "granulocytoid, HL60 stimulated by DMSO", mono stands for "monocytoids, HL60 stimulated by TPA", 40 w liver stands for "40 w neonatal liver", 19 w liver stands for "liver of a 19 weeks old fetus, adult liver is "adult liver ", lung stands for "adult lung", adipose stands for "subcutaneous adipose tissue", endothel stands for "primary cultured aortic endothelium", osteoblast stands for "primary cultured osteoblast", colon mucosa is "colon mucosa", small cell carci stands for "small cell carcinoma of lung", retina is "retina", cerebral cortex is "cerebral cortex", adenocarci (lung) stands for "adenocarcinoma of lung", squamous cell ca (lung) stands for "squamous cell carcinoma of lung", keratinocyte stands for "primary cultured keratinocyte", fibroblast stands for "primary cultured fibroblast", Alzheimer stands for "Alzheimer temporal lobe", cerebellum stands for "cerebellum", visceral fat is "visceral fat", corneal epithelium is "corneal epithelium", peripheral granulocyte is "peripheral granulocyte", neuroblastoma is "neuroblastoma" and taste bud of tongue is "taste bud of tongue".

"Accession number of target mRNA" represents the accession number of the entry in GenBank 50 Release 79 whose base sequence has homology with that of each GS, "match %" represents the percent homology of the GS sequence relative to that of said homologous sequence, "match starts at (GS)" represents the base position counted from the 5'-end of the GS at which the region for homology calculation starts, "match starts at (GenBank)" represents the base position counted from the 5'-end of the GenBank sequence at which the region for homology calculation starts, and "GenBank target size" 55 represents the whole length of the GenBank sequence corresponding to the GS. The columns in Tables 1 - 219 represent the same items as in Table 1.

Based on the data in Tables 1 - 219, each GS can be classified into several groups. A GS, which is expressed at high frequency in a specific cell or groups of cells with similar property, for example,

promyelocytic leukemia cell, granulocyte and monocyte and not expressed entirely or expressed very little in other cells (groups), is a likely GS corresponding to the gene encoding "the protein responsible for functions specific to the cell" (e.g., GS0001553, GS0002047, GS004895, etc.). On the other hand, a GS, which is expressed commonly in every kind of cell, most likely corresponds to the gene encoding "the protein essential for the life of the cell" (e.g., GS0000019, GS0000155, GS000861, etc.). In addition, some GSs are expressed at low frequency (e.g., GS0000013, GS0002399, GS0003155, etc.).

Since the GS with the sequence determined as described above will reflect the population of mRNA expressed in a particular cell, it must be possible to find the relative concentration of mRNA in each cell by determining the appearance frequency for each GS in a cDNA library derived from that cell. Therefore, to confirm the correlation between the appearance frequency for each GS in a cDNA library and the relative concentration of cellular mRNA, the GS thus obtained was labeled with  $^{32}\text{P}$  by standard methods and used as the probe in the following hybridization test. mRNA isolated from a specific cell is hybridized to said  $^{32}\text{P}$ -labeled probe under standard conditions. The results of this Northern hybridization test were such that, when a GS found with high appearance frequency in a cDNA library was used as a probe, a dense band was formed, confirming the correlation of the frequency of appearance of the GS with the relative concentration of mRNA in the cell (see Example 5).

Similarly, the colony hybridization test of the cDNA library constructed as described above with a  $^{32}\text{P}$ -labeled probe prepared as described above showed a close correlation between the frequency of appearance of the GS and the number of colonies hybridized with said GS (see Example 6), confirming the correspondence of the frequency of appearance of the GS and relative concentration of the GS in a cDNA library.

From the above results, by determining the appearance frequency of each GS in a cDNA library derived from a variety of cells, it has become possible to determine the expression status of the gene (or mRNA) corresponding to each GS. This fact implies conversely that each GS may be useful for industrial purposes as a specific probe or primer encoding information about the expression status of its corresponding gene (or mRNA) for each cell. For example, when it is proven that "a certain GS appears at high frequency only in a cDNA library derived from tissue A, that is, the gene corresponding to said GS is specifically expressed only in tissue A", by conventional cloning of the corresponding full-length cDNA using said GS as a probe or primer, it is possible to clone a full-length gene which is expressed in a tissue-specific manner.

Furthermore, for example, when it is proven that "the frequency of appearance of a certain GS is low in a cDNA library derived from tissue B, that is, the appearance frequency of the gene corresponding to said GS is low in tissue B", by examining the expression frequency of the gene corresponding to said GS in a test sample of tissue B from a patient using said GS as a probe or primer, it may be possible to identify the pathogenic gene, wherein an unusually high expression frequency of said gene being a strong indication that said GS may be the gene involved in the pathogenesis. Furthermore, by conventional methods for cloning said full-length cDNA using said GS as a probe or primer, it is possible to isolate said pathogenic gene and elucidate its characteristics.

In practice, the DNA of the present invention may be used as a probe or primer for detecting and diagnosing disease, cloning a pathogenic gene or related gene, cloning a viral gene, identifying and recognizing cell types, cloning a species-specific promoter and gene mapping.

One GS corresponds to one mRNA. It is therefore obvious that any portion of cDNA complementary to each mRNA carry the same "information for expression" as the GS. Accordingly, the DNA of the present invention is not restricted to "the DNA comprising the GS itself or portion thereof", but also includes the DNA comprising, for example, "a full-length cDNA complementary to each mRNA" and "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". They can be used as a probe or primer comprising the same "expression information" as that of the GS and can be used as a probe or primer in a similar manner as a GS. For example, by using a GS or a portion thereof as a probe or primer, it is obviously possible for those skilled in the art to readily isolate "a full-length cDNA corresponding to each mRNA" or "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". For example, as described hereinafter, conventional techniques such as "5' RACE", "nesting" and "inverse PCR" can be used.

An example of the method for detecting disease using the GS of the present invention will be described. As shown in Tables 1 - 219, with the method described above it is possible to detect a GS present specifically in a cDNA library constructed from each tissue by detecting and comparing the frequency of appearance of GS in each tissue. It is also possible to identify a GS corresponding to a protein which is expressed commonly in various tissues or which is expressed at low frequency. These GSs are denatured and then fixed on an appropriate filter, for example, nylon filter or nitrocellulose filter. It is

convenient to use a single filter with many GSs fixed on it. Usage of a single filter on which many denatured DNAs are fixed is well known. An example may be "the Escherichia coli Gene Mapping Membrane" (Takarashuzo, code No. 9035). It is a single nylon filter on which the cosmid contigs of genomic DNA of E. coli are fixed. It is possible to prepare a filter comprising a group of specific GSs corresponding to proteins expressed in a particular tissue, a filter comprising a group of GSs corresponding to proteins commonly expressed in various tissues, or a filter comprising a group of GSs corresponding to proteins expressed at low frequency. The single-stranded GSs fixed on these filters are then hybridized to labeled complementary DNA fragments synthesized using "random primers" prepared from template mRNA extracted from a test tissue, using four labeled nucleotides and reverse transcriptase (labeled mRNA can also be hybridized to the filters). Similarly, labeled complementary fragments synthesized using mRNA extracted from normal tissue as the template are hybridized (labeled mRNA can also be hybridized to the filters). If the profile of hybridization to a group of GSs has been categorized beforehand by comparing the hybridization profile of various pathogenic tissues to that of corresponding normal tissues, it is possible to diagnose the pathogenic condition of a particular test tissue by comparing the hybridization profile of the test tissue with that of the corresponding normal tissue and assigning that profile to a certain category. Virus infection can be detected in the same manner as in the case of other diseases.

Next, an example of the method for cloning pathogenic genes or their related genes using the GS of the present invention is described. As described above, using the filter on which denatured GSs are fixed, the GS-hybridization profile of various pathogenic tissues and that of corresponding normal tissues are compared. A considerable difference in the hybridization intensity between normal and pathogenic tissues will be an indication that the particular GS corresponds to a pathogenic gene. If a filter comprising only GSs specific for a particular tissue is applied to a sample from that particular tissue, the probability for detecting the GS with a great difference in hybridization intensity is elevated. Also a filter comprising GSs corresponding to proteins whose expression is low will facilitate the identification of the GS corresponding to the pathogenic gene by detecting an intense signal, because the hybridization signal for these GSs is usually weak. Once a GS corresponding to a pathogenic gene is found, said pathogenic gene can be cloned by established methods such as genomic Southern hybridization using said GS as a probe and/or a primer.

Furthermore, a method for cloning a full-length gene using a GS as a probe or primer is described in detail. Cloned genes isolated in the present invention are also appropriate for use in the production of proteins useful as pharmaceutical products. mRNA is extracted from tissues by conventional methods and cDNA libraries are then prepared (See Molecular Cloning, 2nd ed. Vol. 2, Section 8 New York; Cold Spring Harbor Laboratory). In this case, it is desirable to extract mRNA from tissues in which the target gene is highly expressed. One method to detect a specific gene in libraries thus prepared is, for example, to select positive clones via hybridization using a whole or partial GS as a probe. In general, since a GS is specific for a particular mRNA, hybridization can be carried out under certain stringent conditions. Probes used are at least more than 25 bases long, preferably more than 50 bases long, and more preferably more than 100 bases long.

Furthermore, if cDNA libraries, in which the cDNA for a specific gene is concentrated, are prepared, they will be preferable for selecting said specific gene. One method useful for this purpose is carried out as follows: 1) preparation of an affinity chromatographic column of resin on which the denatured GS corresponding to the specific gene is fixed; 2) application of mRNA extracted from a tissue to said column and retention of the mRNA species corresponding to the specific gene on said column; 3) elution and concentration of said retained mRNA; and finally 4) preparation of cDNA libraries using said concentrated mRNA species as the template. Another method is the selective amplification of cDNA corresponding to the specific gene by the PCR. Selective amplification of a specific gene is carried out as follows: using a partial sequence of a GS localized toward the 3' end of the specific gene as primer, cDNA is synthesized from mRNA with reverse transcriptase and 4 NTPs. To the 3' end of a single-stranded cDNA thus obtained a homopolymer such as poly-T is attached by the action of "terminal deoxyribonucleotide transferase (TdT)". In addition, using "a primer complementary to the homopolymer" and "a primer used in said reverse transcriptase reaction, or a primer whose sequence is included in the same GS but is located proximal to the 5' end", cDNA corresponding to the specific gene may be selectively amplified by the PCR [see 5'RACE (5' Rapid Amplification of cDNA ends): PNAS, Vol. 85, pp. 8998 - 9002 (1988); Nucleic Acids Res., Vol. 17, pp. 2919-2932 (1989)]. In addition, instead of the attachment of a homopolymer, there is another method comprising the following steps: 1) a single stranded anchor DNA is linked to the 3' end of a single stranded cDNA using "T4 DNA ligase"; and 2) said cDNA is amplified by the PCR using a primer complementary to said anchor DNA [Nucleic Acids Res., Vol. 19, pp. 5227-5232 (1991)]. Said primer is desirably more than 13 bases long, preferably more than 15 bases long, and more preferably more than 18

bases long. Furthermore, in order to enhance the efficiency of heat denaturation in the cycling reaction, said primer is preferably less than 50 bases long and more preferably less than 30 bases long. By linking said amplified DNA to a vector, a cDNA library concentrated with respect to the target gene is prepared.

In addition, it may be also possible to isolate a cDNA clone corresponding to the specific gene directly from the PCR products. Specifically, the PCR products are first separated by gel electrophoresis, subjected to Southern blotting analysis using the denatured GS as a probe, and examined for the presence of a band which specifically hybridizes to said GS. If a GS-hybridized band is detected, it is highly possible to isolate the cDNA clone corresponding to the specific gene by excising said band from the gel and subjecting it to direct cloning.

As described above, in order to further amplify the specific gene previously amplified by the PCR, it may be possible to perform the second PCR of the primary PCR products by replacing either or both primers previously used with a primer having the base sequence internal to said two primers (nesting) (Journal of Virology, Vol. 64, p. 864 (1990)). Nesting may be performed directly upon the products of the primary PCR. Alternatively, if a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of the primary PCR products, nesting may be performed for the DNA obtained by excision of the band followed by extraction. In the case where a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of nested products using the denatured GS as a probe, it is highly possible to successfully isolate the cDNA clone corresponding to the target gene by excising said band from the gel and subjecting it to direct cloning.

The isolated cDNA clone corresponding to the target gene may often correspond to the full-length mRNA, but it may be a cDNA with the 5' end deleted. In the case where the 5' end is deleted it is possible to isolate the full-length cDNA clone by conventional methods. For example, by screening a cDNA library using a probe comprising the base sequence in the 5' end region of the cloned cDNA, since the target position of said probe is shifted further toward the 5' end of the full-length cDNA than in the case of using a GS as a probe, it is possible to isolate only longer cDNA clones as the positive clone. Also by synthesizing cDNA using "a primer comprising the base sequence in the 5' end region of the cloned cDNA" with mRNA as the template followed by PCR amplification of "a single stranded cDNA having a homopolymer or anchor DNA sequence at the 5' end" and using "the primer used for previous cDNA synthesis or a primer having the sequence internal to that of said primer" and "a homopolymer or a primer complementary to anchor primer" as described above for the 5' RACE method, only the sequence toward the 5' side of the cDNA may be selectively amplified since the position of said primer is shifted further toward the 5' side of the full-length cDNA. Even if the cDNA thus obtained has a deletion at the 5' end, the population of cDNA fragments covering the full-length of the long cDNA may be obtained by repeating this procedure. It may be easy for those skilled in the art to obtain a full-length cDNA by suitably linking said cDNA fragments having overlap segments together.

Alternatively, by performing the inverse PCR (Inverse PCR: Genetics, Vol. 120, p. 621 (1988); Molecular Cloning, 2nd ed., Vol. 2, 14.12-14.13 (New York; Cold Spring Harbor Laboratory)), it may be possible to isolate a cDNA clone extending externally from the GS, that is, in the genomic DNA region. Specifically, the target DNA (genomic DNA or cDNA) is digested with restriction enzymes into fragments of about 2-3 kb and then circularized by ligating the cleaved ends. By performing the PCR for said DNA using "a set of primers which are complementary to the cDNA clone isolated using the GS or the GS as a probe or primer, and thereby making the direction of DNA synthesis mutually opposite (outward), it may be possible to amplify the DNA region extending externally from the GS. There is known a method to isolate a full-length genomic DNA of a specific gene by repeating this procedure (Nucleic Acids Res., Vol. 16, p. 8186 (1988)).

In addition, although "Taq polymerase" is conventionally used in the PCR described above, the cloning procedure may be more efficiently performed using the "LAPCR (long and accurate PCR" technique (Nature Genet., Vol. 7, p. 350-351 (1994), Nature., Vol.369, p.684-685(1994)).

Furthermore, needless to say that by linking said full-length gene thus obtained to a suitable expression vector followed by its expression in an appropriate host, it is possible to obtain the corresponding gene product (Molecular Cloning, 2nd ed.).

Next, there will be described an example of the method for identifying and recognizing cell types using the GS of the present invention. As shown in Tables 1 - 219, based on the appearance frequency of GS in each tissue and its comparison among tissues, it is possible to identify those GSs specifically present in a cDNA library constructed for each tissue. These "tissue-specific GSs" are fixed on a filter. It will be more convenient if GSs specific to each tissue are collected and fixed on a filter as a whole (e.g., a GS block specific for hepatocytes or cerebral cortex cells). As described above, to this filter are hybridized labeled complementary fragments synthesized using "random primers" prepared from mRNA extracted from test tissues or cells, "nucleotide containing 4 labeled nucleotides", and "reverse transcriptase". (Directly labeled

mRNA can also be hybridized to the filters.) Depending on the type of tissues or cells, intense hybridization signals will be observed with the GS groups specific to said tissue or cell. Furthermore, a tissue-specific promoter can be cloned by structure analysis of the 5' upstream sequence through the cloning of the corresponding gene using established methods such as genomic Southern hybridization with the "tissue-specific GS" as the probe and/or primer.

These tissue-specific promoters thus obtained are useful for gene therapy in the future.

Gene therapy in a narrow sense aims to supplement the defective protein of patients using gene technology, and in this case it is necessary to express the exogenous gene in a desired tissue in a desired quantity. For this purpose, a promoter which is known to be expressed in a specific tissue in a desired quantity (in most cases a large quantity is desired) is highly useful. Although, at present, a virus promoter is often used, it can be inactivated by endogenous modification such as methylation. Promoters provided by tissue-specific GSs will be ideal substitutes for viral promoters.

There will be described the method for chromosomal assignment of DNA corresponding to the GS of the present invention using the probe derived from the GS obtained as described above.

First, the Southern blotting method will be described.

According to this method, for example, chromosomes are isolated from a lymphoblast cell line of human normal karyotype (e.g., GM0130b), and then a monochromosomal hybrid cell is prepared by introducing each human chromosome into non-human cells, such as rodent cells, and cultured on a large scale by standard methods. Then the DNAs extracted from said hybrid cells are digested with various restriction enzymes and subjected to agarose gel electrophoresis. Then, the electrophoresed DNAs are hybridized to <sup>32</sup>P-labeled GS prepared as described above and used as the probe. By identifying the hybrid cell the DNA of which is hybridized to said probe, it is possible to identify the chromosome in which the DNA corresponding to the GS of the present invention is present. Southern hybridization test of the total human genomic DNA using each labeled GS as a probe formed a single band corresponding to the GS, indicating that the DNA of the present invention can be used as a desirable probe for human genomic DNA. It is obvious that a desirable probe for human genomic DNA can be used also as a desirable probe for human cDNA and human mRNA.

A method similarly using the PCR to determine chromosomal localization of the GS of the present invention will be described.

To prepare most appropriate primers, base sequences are selected from the sequence of the GS in question by conventional methods, for example, by using the computer software OLIGO4.0 (National Biosciences) and the oligonucleotides (20-24mer) having the selected sequences are synthesized. The preferred size of the sequence to be amplified by the PCR is from 50mer to 100mer.

Using the primers thus synthesized and the chromosomal DNA extracted from the monochromosomal hybrid cell as such as the template, amplification by the PCR is performed in a conventional manner. Resulting PCR products are subjected to non-denatured acrylamide gel electrophoresis and stained with ethidium bromide for fluorescent detection. The sizes of these PCR products are then determined.

Chromosomal assignment is confirmed when the presence of a PCR product of correct size is confirmed.

It is evident that a chromosome or chromosomes in which the DNA corresponding to a GS is localized can be identified by using these procedures. It has also become evident that the DNA of the present invention can be used as desirable primers for human genomic DNA since a single band has resulted from amplification of the total human genomic DNA by the PCR using primers designed based on each tested GS. Obviously, a desirable primer for human genomic DNA is also a desirable primer for human cDNA and human mRNA.

#### Brief Description of Figures

Fig. 1 shows the preparation of 3' Mbol cDNA library.

Fig. 2 shows the results of tests of primers. A shows the location of primers on the vector; and B shows the electrophoretic patterns of DNA fragments amplified using the primers (A). Primers used are as follows: lane 1, FW (-40)/RV (-14); lane 2, FW (-40)/RV (-36); lane 3, FW (-40)/RV (-71); lane 4: FW (-40)/RV (-29); and lane 5, FW (-47)/RV (-48). Artifacts are indicated by arrows.

Fig. 3 shows the electrophoretic pattern of PCR products using FW(-40) and RV(-14) as primers. The lane at the right end shows the electrophoretic pattern of size markers and the other lanes show the PCR products using FW (-40)/RV (-14) as primers.

Fig. 4 shows the mRNA concentration reflecting the frequency of appearance of each GS in the cDNA library: especially, Figs 4A - 4D; experimental results; Fig. 4E, photographs of colonies; and Fig. 4F,

summary.

Fig. 5 shows the appearance frequencies for various cDNAs in the 3'-directed HepG2 cDNA library.

Fig. 6 shows the genetic mapping of each GS (gs) using PCR.

Fig. 7 shows the genetic mapping of each GS (gs) using PCR.

5 Fig. 8 shows the genetic mapping of each GS (gs) using PCR.

Fig. 9 shows the genetic mapping of each GS (gs) using PCR.

Fig. 10 shows the genetic mapping of each GS (gs) using PCR.

Fig. 11 shows the chromosomal mapping of GS001418 (gs001418) using PCR.

Fig. 12 shows the chromosomal mapping of GS001457 (gs001457) using PCR.

10 Fig. 13 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 14 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 15 summarizes the characteristics of hybrid cells used for Southern hybridization.

Fig. 16 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000152 (clone s14g02) as a probe.

15 Fig. 17 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000041 (clone s650) as a probe.

Fig. 18 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000181 (clone hm01e01) as a probe.

20 Fig. 19 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000055 (clone c13a18) as a probe.

Fig. 20 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000180 (clone s479) as a probe.

Fig. 21 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000094 (clone s173) as a probe.

25 Fig. 22 shows Southern blotting of chromosomal DNA from the hybrid cells using junk (clone hm01g02) as a probe.

Fig. 23 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double cleavage with EcoRI and BamHI.

30 Fig. 24 shows the chromosomal mapping of each GS by Southern-blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 25 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 26 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

35 Preferred embodiments of the invention

In the following section, there will be explained preferred embodiments of the present invention. However, the present invention will not be restricted to these preferred embodiments.

40 [Example 1]

#### Preparation of mRNA

45 Cytoplasmic RNA was extracted from a liver cancer cell line HepG2 (Aden., et al., Nature 282, 615-617, 1979) using standard procedures [Sambrook, J., et al., Molecular Cloning, 2nd ed. (New York: Cold Spring Harbor Laboratory), vol. 1, pp. 7.3-7.36, 1989]. Briefly, HepG2 cells grown in Dulbecco's modified Eagle medium supplemented with 10% FCS were lysed in RNA extraction buffer [0.14 M NaCl, 1.5 mM MgCl<sub>2</sub>, 10 mM Tris-HCl (pH 8.6), 0.5% NP-40, 1 mM DTT, 1000 units/ml RNase inhibitor (Pharmacia)] by using a  
50 Vortex mixer for 30 sec and then left standing on ice for 5 min. Nuclei and other cell debris were precipitated by centrifuging at 12,000 g for 90 sec, and the supernatant was deproteinized with Proteinase K followed by phenol extraction. RNA was precipitated by isopropanol and rinsed with 70% ethanol. Finally, the poly A<sup>+</sup> fraction was collected by oligo dT column fractionation (Aviv., et al., Proc. Natl. Acad. Sci. USA  
55 69, 1408-1412, 1972).



## [Example 2]

## Preparation of vector primer DNA and construction of cDNA libraries

To prepare a vector primer, pUC19 DNA amplified in JM109 cells (Yanisch-Perron, C., et al., *Gene* **33**, 103-119, 1985) was digested with PstI to completion and a poly T-tail was added with terminal transferase (Pharmacia) to a mean length of 26. This process was monitored by the incorporation of <sup>3</sup>H-deoxythymidine triphosphate [Okayama, H., et al., *Methods in Enzymology* (San Diego: Academic Press), vol. **154**, pp. 3-28, 1987]. The product was digested by HincII, and the resulting short fragments were eliminated by chromatography with Sepharose S-300. Then the T-tailed plasmid was purified by an oligo dA column and stored in 50% ethanol at a concentration of 1 µg/µl.

Fig. 1 shows the outline of the construction of the cDNA library. Two micrograms each of the cytoplasmic Poly A<sup>+</sup> RNA and the vector primer DNA were co-precipitated in 70% ethanol containing 0.3 M Na-acetate and the pellet was dissolved in 12 µl of distilled water. For the first strand synthesis, after heat denaturation at 76 °C for 10 min, 4 µl of 5 x reaction buffer [250 mM Tris-HCl (pH 8.3), 375 mM KCl, 15 mM MgCl<sub>2</sub>], 2 µl of 0.1 M DTT and 1 µl of 10 mM each of dATP, dCTP, dGTP and dTTP were added to the sample at 37 °C. The reaction was initiated by the addition of 200 units of reverse transcriptase MMLV-H-RT (BRL), and after incubation at 37 °C for 30 min, stopped by transferring the reaction tube onto ice. For the second strand synthesis, to the aforementioned reaction mixture the following was added: 92 µl of distilled water, 32 µl of 5 x E. coli reaction buffer [100 mM Tris-HCl (pH 7.5), 20 mM MgCl<sub>2</sub>, 50 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 500 mM KCl, 250 µg/ml of BSA, 750 µM βNAD], 3 µl of 10 mM each of dATP, dCTP, dGTP and dTTP, 15 units of E. coli ligase (Pharmacia), 40 units of E. coli polymerase (Pharmacia), and 1.5 units of E. coli RNase H (Pharmacia). The reaction mixture was then incubated at 16 °C for 2 h and heated to 65 °C for 15 min. Then 20 units each of BamHI and MboI were added, and the reaction mixture was incubated at 37 °C for 1 h and heated again at 65 °C for 30 min. Finally, the sample was diluted up to 1 ml with 1 x E. coli reaction buffer, and 100 units of E. coli ligase were added. The resulting mixture was incubated at 16 °C overnight. An aliquot of this mixture was used to transform competent E. coli DH5 cells (Toyobo). Transformants were selected by ampicillin resistance. The product was named "3' MboI cDNA library".

## [Example 3]

## Amplification of cDNA insert by PCR

The plasmid-carrier E. coli colonies were picked into 96-well plates containing 125 µl of LB medium (Davis, R. W., et al., *Advanced Bacterial Genetics*. New York: Cold Spring Harbor Laboratory, 1980) in each well and incubated in a moist chamber at 37 °C for 24 h. A replica culture was made for every plate using a 96-pinned replica device (Sigma) and the master plates were stored at -80 °C for future use. After overnight incubation at 37 °C, 50 µl of the culture from each well of these replicas were transferred to polycarbonate 96-well plates (Techne). Bacteria were collected by centrifugation in an Omnispin H4211 rotor (Sorvall) at 1500 rpm for 5 min, resuspended in 50 µl of water, covered with a layer of mineral oil and lysed at 95 °C for 30 min in a metal bath. Debris were removed by centrifugation at 3600 rpm for 30 min in the same rotor.

Five microliters of the supernatant were added to 20 µl of distilled water and kept at 95 °C for 10 min under a layer of mineral oil. Then the denatured lysate was subjected to PCR by adding 25 µl of 2 x reaction mixture [40 mM Tris-HCl (pH 8.9 at 23 °C), 3 mM MgCl<sub>2</sub>, 50 mM KCl, 200 µg gelatin/ml] containing 5 pmol each of primers, 5 nmol each of dATP, dCTP, dGTP, dTTP and 1.25 units of Taq DNA polymerase (Cetus) at 70 °C. Temperature cycling reactions were carried out immediately after addition of the reaction mixtures using a thermal cycler either for microfuge tubes (PJ1000, Perkin Elmer Cetus) or for a 96-well plate (PHC-3, Techne); 35 repeated cycles of 30 sec at 96 °C, 1 min at 55 °C, and 2 min at 72 °C without a final extension step were performed.

For this method, the correct choice of primers for the PCR reaction is crucial. Therefore, preliminary tests were performed using the following primers with a predicted T<sub>m</sub> of above 60 °C.

The primers tested were a pair of primers, FW(-47) and RV(-48), which are identical to the commercially available 24 mer primers, a second pair of primers, [FW(-40) and RV(-29)], which are a longer version (21 mer) of the well-tested sequencing primers, and the primers RV(-71) and RV(-14), which have a triplet sequence at the 3' terminus identical with that in FW(-40) but is in the opposite orientation (Fig. 2A).

In most of the cases where various combinations of primers were tested, short PCR artifacts appeared, besides the expected major products (Fig. 2B, arrows indicate the PCR artifacts.). These artifacts could be reduced by raising the annealing temperature, lowering the primer concentration or lowering the substrate

concentration but in all cases the yield of the products was not high enough to serve as a template for the sequencing reaction without concentration thereof.

However, since one pair of primers [SW(-40) and RV(-14)] did not yield artifacts (Fig. 3), this pair was selected for further tests, and was found to give reproducible results. Similar results were obtained with randomly selected cDNA clones. Therefore, only this pair of primers SW(-40) and RV(-14) was used as the primers of the present embodiment.

[Example 4]

#### DNA sequencing

The PCR products were drop-dialyzed against TE [10 mM Tris-HCl (pH 8.0), 1 mM EDTA] on millipore filter (VS 0.025  $\mu$ m) for 90 min while stirring. Forty-eight samples are easily applied on a single filter of 150 mm diameter. Without further purification the samples were subjected to the Cycle Sequencing protocol (Applied Biosystems, 1991) using dye labeled primers with minor modifications. For dideoxycytidine sequencing reaction, 2  $\mu$ l of the dialyzed PCR reaction product (about 0.2 pmol of template DNA) were added to 3  $\mu$ l of a reaction mixture containing 0.4 pmol of FAM M13 (-21) Primer (Applied Biosystems) in 160 mM Tris-HCl (pH 8.9), 40 mM  $(\text{NH}_4)_2\text{SO}_4$ , 10 mM  $\text{MgCl}_2$ , 50  $\mu$ M dATP, 12.5  $\mu$ M dCTP, 75  $\mu$ M 7-deaza-dGTP (Boehringer Mannheim Biochemicals), and 50  $\mu$ M dTTP, 25  $\mu$ M dddCTP, 0.8 unit of Taq Polymerase (Perkin Elmer Cetus), and subjected to 15 plus 15 cycles of the reaction (95 °C 30 sec, 60 °C 1 sec, 70 °C 1 min and 95 °C 30 sec, 70 °C 1 min) according to the manufacturer's recommendation in a 96-well plate using a thermal cycler (PHC-3, Techne). The three other sequencing reactions for dideoxyguanosine, dideoxyadenosine, and dideoxythymidine were performed in parallel (with TMRA, JOE, and ROX primers respectively, supplied by Applied Biosystems) in an identical fashion, except that twice the volume of all the ingredients was added to the dideoxyguanosine and dideoxythymidine reactions. Each sample, from a set of four was cooled to 4 °C, pooled, precipitated with ethanol, resuspended in 6  $\mu$ l of a solution of formamide/50 mM EDTA (5/1 by v/v), loaded onto sequencing gel and analyzed by a DNA autosequencer (Model 373A Ver 1.0.1, Applied Biosystems).

[Example 5]

The frequency of appearance of each GS of the cDNA library reflects mRNA population.

To confirm that our 3'-directed regional cDNA library was a non-biased representation of the mRNA population in HepG2 cells, the inserts of four cDNA clones (EF-1 $\alpha$ ,  $\alpha$ -1-antitrypsin, hnRNP core protein A1 and inter- $\alpha$ -trypsin inhibitor) from the clones redundantly obtained by random selection of cDNA were radiolabeled and used as probes in a Northern analysis of poly A<sup>+</sup> mRNA from the HepG2 cells. (The results are shown in Fig. 4A-D, and summarized in Fig. 4F.) The relative band intensity of the four mRNA species demonstrated that their relative ratios were 52, 24, 1 and 1.2, respectively (lane iii in Fig. 4F). Then the same set of probes was used for measuring the number of colonies hybridizing with each probe in the same cDNA library of 8,800 clones (Fig. 4E).

The clonal frequencies were 307, 128, 7 and 9, or in ratio, 44, 17, 1 and 1.3, respectively (lane iv in Fig. 4F). These two estimates agreed, showing that the cDNA library used is a non-biased representation of the mRNA population. The ratio was practically unchanged when different preparations of mRNA from the same cell were tested.

Fig. 4 shows the proportionality of the composition of the 3'-directed cDNA library and of the mRNA. Fig. 4A, 2  $\mu$ g of poly A<sup>+</sup> RNA from HepG2 cells was electrophoresed in lanes 1-4 of a formamide agarose gel containing ethidium bromide (5  $\mu$ g/ml) and then exposed to UV. Lane 5 is the RNA ladder (BRL) used as size markers (kb). In Fig. 4B, the filter was northern blotted using the following <sup>32</sup>P-labeled 3'-specific cDNA probes: Elongation factor-1 $\alpha$  (lane 1),  $\alpha$ -1-antitrypsin (lane 2), hnRNP core protein A1 (lane 3), inter- $\alpha$ -trypsin inhibitor (lane 4). In Fig. 4C, one pmol each of the non-labeled cDNA fragments [EF-1 $\alpha$  (lane 1),  $\alpha$ -1-antitrypsin (lane 2), hnRNP core A1 (lane 3), inter- $\alpha$ -trypsin inhibitor (lane 4), were electrophoresed in a 2% agarose gel, then photographed. Fig. 4D is a Southern analysis of the blotted filter from Fig. 4C, using the same set of radioactive probes. Lane 5 shows the migration pattern of the reference 1 kb ladder (BRL). Hard copies of these screen images were taken at 8 h for b, and 1 h for d. The radioactivity in each band was counted directly in a scinti-scanner ( $\beta$ -603; Betagen) and registered in (i) and (ii) in Fig. 4F. The observed band intensities were corrected based on the band intensities in Fig. 4D (ii in Fig. 4F), and normalized relative to the value of probe 3 (hnRNP core A1, lane iii in Fig. 4F) as 1 (iii in Fig. 4F). These values represent the relative content of each mRNA species in the original mRNA preparation. Fig. 4E

shows the results of colony hybridization of the membranes carrying 8,800 colonies of the 3'-directed cDNA library using the same set of the four radioactive probes. Positive colonies were counted and registered (iv in Fig. 4F), then normalized with the value of HnRNP core protein A1 as 1. The numbers in B, D and E in Fig. 4 represent the probe No. in Fig. 4F. Fig. 4F shows a remarkable agreement between the values of lanes (iii) and (v).

#### [Example 6]

##### Population study of the cDNA library

To analyze further the composition of the cDNA library, 7 and 10 clones were selected from the redundant (group I) and solitary (group II) sequence groups, respectively, and these inserts were used as radiolabeled probes for colony hybridization (Fig. 6). The frequencies of the colonies that hybridized with group I probes were roughly identical to those that were randomly picked and sequenced. These frequencies were about 3.5%-0.1%. Nearly 52% of the cDNA library population consisted of the redundant sequence group containing 173 species. When 8 probes from group II were tested, 18 positive colonies were identified among 26,400 colonies screened, giving an average frequency of 0.007%. Two probes did not hybridize with any of the 26,400 colonies, resulting in the average frequency of <0.004%. Thus, the average frequency of the 10 probes in group II was several orders of magnitude less than the lowest of group I.

The results are summarized in Fig. 5, showing the appearance frequencies of various DNA species in the 3'-directed HepG2 cDNA library. In Fig. 5, seven cDNA probes (a15 through tb042) were selected from the 162 identified genes in the redundant group (group I), and ten (s155 through s632) were randomly chosen from the solitary group (group II). In columns A, B and C, each one of the insert DNAs was radiolabeled and used as a probe for colony hybridization tests of 982 (A), 8,800 (B) or 26,400 colonies (C). NT indicates "not tested". The DDBJ entry names of the 17 clones listed in this table are HUM000A15, HUM000C321, HUM00TB038, HUMHM01B02, HUM0C13A04, HUMHM02D02, HUM00TB042, HUM000S155, HUM000S159, HUM000S639, HUM000S635, HUM000S170, HUM000S154, HUM000S167, HUM000S645, HUM000S647, and HUM000S632.

#### [Example 7]

##### Analyses of sequencing errors

All the sequence data presented in this specification were obtained by repeated cycles of enzymatic amplification of the plasmid inserts, followed by cycle sequencing with Taq polymerase. Sequences of 60 clones that showed data bank matches were examined for discrepancies from the data bank entries. It was found that the accuracy in the region 1-100 bp distant from the cloning site was 98.7%, indicating that the primers or probes designed with the sequence in this region could be obtained practically without any erroneous sequences or even if they contain any errors, they are functionally without problems.

#### [Example 8]

##### Mapping of GS by PCR

##### <cDNA sequence>

cDNA library was constructed from mRNA of DMSO treated HL60 cells. The methods for construction of the 3'-directed cDNA library and for sequence analysis of the library components are the same as described in Examples 1-4.

##### <PCR primer>

Primer design was performed by using the computer software OLIGO 4.0 (National Biosciences) which eliminates possible formation of inter- or intra-molecular secondary structures. In addition to the primer design, transfer of oligonucleotide sequences to the local database and synthesizer were semiautomated using a Macintosh computer linked with a network. DNA oligomers were synthesized on an automated DNA synthesizer (Model 394, Applied Biosystems) on a 40 nmol scale. The synthesized oligomers were used as

PCR primers without further purification.

⟨Preparation of Genomic DNA⟩

The human genomic DNA was extracted from the normal karyotype lymphoblastoid cell line GM0130b. Mouse and Chinese hamster genomic DNAs were purchased from Clontech. Monochromosomal hybrid cells utilized for mapping panel were commonly used ones which have been described previously. Briefly, chromosomes 3, 4, 9, 11, 12, 13, 15, 22 and Y were carried in human-Chinese hamster monochromosomal hybrid cells, and chromosomes 1, 2, 5, 6, 7, 8, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, 21 and X were carried in the human-mouse monochromosomal hybrid cells A9 series. The integrity of the hybrid cells were monitored by *in situ* hybridization.

⟨Amplification by Polymerase Chain Reaction⟩

PCR was performed according to standard protocols (Saiki, R. K., et al., Science 230, 1350-1354, 1985), using 10 pmol of each primer on a whole 20  $\mu$ l scale reaction, with 35 thermal cycles of 30 sec at 94°C, 60 sec at an annealing temperature, and 90 sec at 72°C, using a Perkin-Elmer 9600 thermal cycler. Annealing temperature was determined according to the "optional annealing temperature" estimated by the Program OLIGO.

⟨Analysis of the PCR Products⟩

The PCR products were run on an 8% polyacrylamide non-denatured gel (Acrylamide:Bis-acrylamide = 19:1, 1 mm thick) at 300 V for 1 h, followed by staining in 90 mM Tris-borate, 2 mM EDTA buffer solution containing 0.25  $\mu$ g/ml ethidium bromide for 15 min. The size of the amplification products were determined relative to the 10 bp DNA ladder (BRL). Detection of fluorescence was performed by using a laser fluorescent image analyzer (FM-BIO, Hitachi Software Engineering). The image data were transferred to a computer for analysis.

⟨Results of Analysis of the PCR Products⟩

Among various species of 3'-directed cDNA-GSs obtained from granulocytoid cells, 195 novel GSs which did not match the sequences deposited in Genbank Release 76 were selected and used for designing primers for the PCR. The PCR was performed with these primers using the total human genomic DNA as the template.

Among the 195 primer pairs, 191 (98%) yielded products whose size matched those expected within 5 nt. The results are summarized in Figs. 6 - 10 whose figure legends are as follows: GS, gene signature; CN, clone name; Chromosomal position, chromosome numbers to which GSs were mapped; Sequence of primers, DNA sequences of primers (Sense, sense strand; anti-sense, anti-sense strand); AT, annealing temperature; HO, Observed size of PCR products with total human genomic DNA (nt); HE, Expected size of PCR products with total human genomic DNA (nt); MO, Observed size of PCR products with mouse genomic DNA (nt); CO, Observed size of PCR products with Chinese hamster genomic DNA (nt); G, Number of "hits" of GS in the granulocytoid (DMSO treated HL60) cDNA library after analyzing altogether 1000 clones; T, Total number of "hits" of the GS after analyzing altogether 3000 clones from the three cDNA libraries of HL60 with and without induction by DMSO or TPA. Question marks ("??") indicate that the PCR products did not yield a clear band.

"M" indicates that the PCR products yielded a band which was indistinguishable from the band observed after the reaction using mouse DNA as the template. Similarly, "C" indicates that the PCR products yielded a band which was indistinguishable from the band after the reaction using Chinese hamster DNA as the template.

The overall rate of success of the PCR was 191/195 (98%), although GSs were randomly selected from the cDNA sequences, indicating that the quality of the cDNA library used in this work was reliable, and that the sequence analyses and primer designs were performed appropriately. Thus, the possible chances of failure of the PCR caused by presence of an intron(s) in the relevant cDNA sequences is negligible in working with the GS, as introns virtually do not lie in the poly A proximal 3'-region of vertebrate genes (Wilcox et al., Nucleic Acids Res. 19, 1837-1843, 1991). This is a big advantage compared to the use of partial fragmented cDNA sequences obtained from randomly primed cDNA libraries (Adams et al., Science 252, 1651-1656, 1991) or from 5'-directed cDNA libraries.

# 〈Chromosomal assignments of GS〉

The 191 primer pairs that yielded PCR products from total human DNA were used for chromosomal assignments of the GSs with the monochromosomal hybrid cell panel. At least 119 GSs were assigned to a single chromosome. As an example, GS001418, shown in Fig. 11, was assigned to chromosome number 3. With some clones, extra products were obtained, some of which were assigned to the same chromosome, whereas others to different chromosomes. An example, GS001457, is shown in Fig. 12. Sixty-two (33%) clones yielded the expected PCR products with two or more different chromosomes. Thirty-five cases (18%) yielded PCR products whose size were indistinguishable from background rodent genomic DNA. Among these, 21 GSs produced products indistinguishable from mouse and Chinese hamster DNA. Ten GSs yielded no expected PCR products with the monochromosomal cell panel DNA although the expected PCR products from total human genomic DNA were observed. The 10 cases probably arose from a small deletion in the hybrid cells. Five clones obtained from HepG2 cDNA library have been analyzed also by Southern blot analysis. Four out of the 5 GSs (GS000053, GS000120, GS000271 and GS000279) gave consistent results with those obtained by the PCR. One GS (GS000228), which was uncertainly assigned to chromosome Y because of the weak signal detected by the Southern blot method, was assigned to chromosome 11 by PCR.

## [Example 9]

### Mapping of GS by Southern blot method

#### 〈Cell lines〉

Total human genomic DNA was isolated from the human normal karyotype lymphoblastoid cell line GM0130b. Monochromosomal hybrid cells used as the mapping panel are shown in Fig. 15. Hybrid A9(neo-x)-y cells as described by Koi, et al. (Jpn. J. Cancer Res. 80, 413-418, 1989) were donated by Dr. M. Oshimura, Faculty of Medicine, Tottori University, passaged 3 times and frozen for storage. The loss or rearrangements of chromosomes could have occurred during this period. The GM series was obtained from the Mutant Cell Repository, National Institute of General Medical Science (NIGMS) (Camden, NJ). To confirm that human chromosomes remained intact in the hybrid cells after storage in liquid nitrogen, metaphase spreads of the hybrid cells were monitored by chromosome staining based on *in situ* hybridization using biotinylated total human DNA as the probe (Durnam, D. M., et al., Somatic cell Mol. Geneta. 11, 571-577, 1985). Intact, as well as translocated or fragmented human chromosomes were easily detected by this means. In a hybrid cell mapping panel, chromosomes 11, 12 and 15 were represented by the hybrid cell lines A9(neo-11)-1, A9(neo-12)-4 and A9(neo-15)-2, respectively, and in another panel, they were represented by the hybrid cell lines GM10927A, GM10868 and GM11418, respectively.

#### 〈Isolation of genomic DNA and Southern blotting〉

High molecular weight DNA was extracted from cells using sodium dodecyl sulfate (SDS) and Proteinase K, followed by phenol-chloroform extraction and ethanol precipitation. DNAs were digested overnight with a combination of two restriction enzymes including EcoRI, BamHI and BglII. About 5 µg of each digest was electrophoresed in an 0.8% agarose gel, then transferred to Hybond N<sup>+</sup> membrane (Amersham) with 0.4 N NaOH. The membrane was rinsed in 2 x SSC and stored at 4 °C for subsequent use.

Clones containing a novel sequence and having more than 150 bp were selected as probes. The cDNA inserts of the clones were amplified by the PCR. The PCR products were isolated by electrophoresis through a 2% low-melting temperature agarose gel (Nusieve : SeaPlaque, 3 : 1), followed by excision. The gel was removed by melting at 65 °C and digesting with β-Agarose I (Bio Labs) at 40 °C for 1 h. The probes were labeled with [α-<sup>32</sup>P]dCTP by random priming using a commercial kit (Amersham). Hybridization proceeded at 65 °C in a high salt buffer containing 6xSSC, 1x Denhardt's solution and 0.5% SDS, in the presence of 0.1 mg/ml of sonicated, denatured salmon sperm DNA. The membranes were washed in 2xSSC, 0.1% SDS at 65 °C for 30 min, then twice for 30 min in 0.1xSSC, 0.1% SDS at 65 °C, and analyzed using a Fuji BAS-2000 imaging analyzer.

# <Analyses with Genomic DNA>

Among the HepG2 3'-directed cDNA libraries described in Examples 1 and 2, 160 novel clones were selected and used as probes for Southern blots.

Total human genomic DNA was isolated from a cell line GM0130b that has a normal karyotype, and digested with the restriction enzymes, EcoRI, BamHI and BglII alone or in combination. The GS clones used as probes were the 3'-directed cDNAs. Each of these cDNAs covers a region between the poly(A) site and the nearest MboI site (GATC) (Okubo, K., et al., Nature Genetics 2, 173-179, 1992) and thus do not have restriction sites for BamHI or BglII. In addition, because the average size of GS is 270 bp, the chances of having an EcoRI site in the cDNA moiety were not high. In fact, only 7 clones out of the 160 analyzed had an EcoRI restriction site.

Membranes blotted with digested human genomic DNA were hybridized with radio-labeled GS probes and washed at high stringency. Since the 3'-terminal region of cDNA has, in general, a unique sequence which differs from that of protein encoding regions which tend to have conserved motifs, cross hybridization with unrelated cDNA sequences will not occur under such stringency. Examples of the results of hybridization are shown in Figs. 13 and 14. Clones s503 and s632 (Figs. 13a and 13b; junk) respectively represent unique single band producers. As shown below, 67 clones belonged to this class. The positions of the GS sequence relative to the restriction sites were inferred from the band patterns. Clone s311 (Fig. 13c; GS000092) showed a single band with EcoRI -as well as (EcoRI + BamHI)-digested DNA, but two bands of different sizes in other double digests. The double digestion thus helped resolve multiple GSs. Similar results were obtained with clone c13a08 (Fig. 13d; GS000055), in which there were 2 bands with EcoRI- or (EcoRI + BamHI)-digested DNAs, and 4 when digested with (EcoRI + BglII) or (BamHI + BglII). On the other hand, 4 hybridization bands appeared with clone s479 with EcoRI alone, but the number of bands decreased with (EcoRI + BglII) and (BamHI + BglII) (Fig. 14e; GS000180). These results indicate that genomic DNAs should be digested in various ways to reveal the maximum number of hybridizing fragments. The results of the analysis showed that 41, 10, 7 and 19 clones contained 2, 3, 4 and 5 or more bands, respectively. Clones s14f01 and tw1-46 (Figs. 14f and 14g; GS000407 and junk, respectively) contained at least 10 bands in each lane. Since the EcoRI restriction site is not present in the two GS sequences, the multiplicity of bands is likely to represent the multiple copy number of these genes. Clone kmb07 moved as a smear (Fig. 14h; junk), even after intensive high stringency washes, suggesting that this probe has a repetitious sequence which has not been hitherto identified.

## <Chromosomal assignments>

A set of monochromosomal hybrid cells carrying a single human chromosome in a background of rodent chromosome was collected (Fig. 15). Thirteen cell lines were microcell hybrids established by Koi et al. (Koi, M., et al., Jpn. J. Cancer Res. 80, 413-418, 1989) and the others were obtained from NIGMS. The results of monitoring the human chromosomes in these cell lines by *in situ* hybridization using biotinylated total human DNA are also presented in Fig. 15.

The GSs were assigned to chromosomes using hybrid cell mapping panels. Three types of membranes were prepared, each having DNAs prepared from hybrid cells, and digested with EcoRI, (EcoRI + BamHI), or (BamHI + BglII). Among these three types of membranes, the one which should have yielded the maximum number of bands was used for each GS probe, according to the results of total genomic Southern blots. Examples of hybridization results are shown in Figs. 16 - 22. The numeral on each lane represents the human chromosome numbers which is contained in the hybrid cell, and H stands for the total human chromosomes. Clone s14g02 (GS000152; Fig. 16) that showed a single hybridization band with the total human DNA digested with EcoRI (lane H), showed the corresponding band only with the hybrid cell line containing human chromosome 4. Thus, this GS lies in chromosome 4.

The clone s650 (GS000041; Fig. 17) was assigned to chromosome 12 which showed a characteristic 7.5kb band in the presence of an (EcoRI + BamHI)-digested membrane. However, with an EcoRI digested DNA, the clone could not be assigned, as the human-specific and the cross-reacting rodent DNA fragments overlapped. The single, but shorter fragment band (1.3kb) which appeared in lanes 3, 4, 9, 13 and 22 represents the homologous DNA sequence in Chinese hamster, and the 3.3kb band in other lanes represents the homologous DNA in the mouse.

Clone hm01e01 (GS000181; Fig. 18) exhibited two fragments when hybridized to total human DNA treated with EcoRI alone, and these corresponding bands appeared in lanes 1 and 2. Thus, the two members of this gene family are located on two chromosomes.

Fig. 19 shows that clone c13a08 (GS000055) exhibited 4 bands when hybridized to (BamHI + BglII)- or (EcoRI + BglII)-digested total human DNA, although only 2 bands appeared with EcoRI- or (EcoRI + BamHI)-digested human DNA. Therefore, the (BamHI + BglII)-digested DNA panel was used for this clone. Two bands (12.3kb and 7.5kb) appeared in lane 7, a 5.2kb band in lane 2, and a 3.2kb band in lane 17. Two bands (6.0kb and 3.8kb) that cross-reacted with Chinese hamster DNA appeared in lanes 3, 4, 9, 13 and 22, and a single band (3.5kb) that cross-reacted with mouse DNA appeared in other lanes.

Clone s479 (GS000180; Fig. 20) showed 4 EcoRI fragments with total human DNA. The hybridization to an EcoRI-digested DNA panel yielded in bands of 10.5kb in lanes 7 and 19, 8.5kb in lane 8, 7.8kb in lanes 11 and 12, and 3.5kb in lane 11. Thus, the human specific genes are dispersed among chromosomes 7, 8, 11, 12 and 19, among which the 10.5 and 7.8kb bands in the total DNA both consist of two overlapping fragments. As shown in lane H, the intensity of these overlapping fragments was higher than normal. The 3.5kb band in lane H, as well as in lane 11 was also intense, suggesting that it also represents overlapping fragments.

Clone s173 (GS000094) exhibited 5 bands in EcoRI-cleaved total DNA (Fig. 21). Four corresponding fragments included a 4.5kb fragment in lane 1. Another 4.5kb band was observed in lane 4, indicating that the corresponding band in lane H overlapped. In addition, an intense 3.1kb band was observed in lane 17.

Clone hm01g02 (junk; Fig. 22) exhibited many bands with total DNA, and with those from monochromosomal hybrids. This clone must represent a multiple and closely related family of genes. It also contains a sequence conserved in homologous rodent genes which also give rise to multiple bands. Since most of the human specific and rodent bands overlapped, the chromosomes could not be assigned. Other combinations of restriction enzymes did not resolve the overlap.

The results of the total genomic DNA analyses and the chromosome assignments of 160 GSs are summarized in Figs. 23 - 26. Through total genomic DNA analyses using 4 differently digested human DNAs, 67 clones were categorized into a single band group, 41 in a two band group, 10 in a three band group, 7 in a four band group and 19 in a group that yielded five or more bands. Nine clones did not show any hybridization band under fixed conditions.

Assignment of two band clones showed that the two genes lie in different chromosomes in 15 of them, whereas the gene represented by clone s317 originated from the same chromosome. The three band clones s308 (GS000412) and s401 (GS000224) showed that two of the fragments lie on the same chromosome, and clone hm05g02 (GS000209) and s17a10 (GS000294) showed bands in different chromosomes. Clones displaying four or more bands showed a relatively dispersed distribution among chromosomes. "junk" in Example 9 is the DNA segment cloned by the same method used for GS but is not numbered.

#### [Example 10 Cloning of gene using GS]

[10A. Cloning of a full length cDNA encoding a human ribosomal protein, homologue of yeast S28. Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(1)]

Using a primer ('5'-TGAAATTTATTACTACAGTGTTCACCA-3' (SEQ ID NO:7839)) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00500 and a primer (5'-TAATACGACTCACTATAGGG-3' (SEQ ID NO: 7840)) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, HepG2 cDNA library was amplified by the PCR and a full length cDNA clone encoding a human ribosomal protein, a homologue of yeast ribosomal protein S28 was isolated. (Hori et al., Nucl. Acids Res. 21: 4394, 1993).

[10B. A human ribosomal protein homologous to rat L9 ribosomal protein-Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(2)]

Using a primer 5'-CTTCTTTCTGTAGCCAGGTAAGTCT-3' (SEQ ID NO: 7841) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00418 and a primer (SEQ ID NO: 7840) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, a full length cDNA clone encoding a human ribosomal protein homologous to rat L9 was isolated (Hori et al., Nucl. Acids Res. 21:4395, 1993).

[10C. A human protein homologous to bovine phosphatidylethanolamine-binding protein. Cloning of the full length cDNA by hybridization using a probe comprising a partial sequence of a GS]

By hybridization with the probe,

5'-GATCGTTCTTCATGGGGGTAAGAAAAGCTGGTCTGGAGTTGCTGAATG

TTGCATTAATTGTCCTGTTTGCTGTGTAAGTGAATAAAAATAGAAACCTGAAT

GAAGGAAA-3' (SEQ ID NO:7838),

that comprises a partial sequence of HUMGS00421, a full length cDNA clone encoding a human protein homologous to bovine phosphatidylethanolamine-binding protein was isolated (Hori et al., Gene 140:293, 1994).

[10D. Human mpl-ligand. Cloning of a cDNA coding for the human mpl-ligand using a GS]

This embodiment employs the 5' SLIC (single ligation to single stranded cDNA) method which is an improved version of the 5'RACE (rapid amplification of cDNA ends) method, and is described in Nucleic Acids Res., 19, 5227-5232 (1991).

#### ① Reverse transcription of cDNA and attachment of anchor

The template was prepared using the reagents of the 5'-Amplifinder™ Kit (Toyobo, Inc.) in accordance with the protocol included therewith. Specifically, 2μg of human fetal liver poly A<sup>+</sup>RNA (Clontech Laboratories, Inc.) and 10 pmol of the primer PA-6, a primer corresponding to the 3' end of the gene signature (GS) sequence HUMGS02342 and consisting of the sequence 5'-TTTTCGGCGCTCCCATTTATTCCTT-3' (SEQ ID NO: 7842), were mixed together and then denatured by heating the mixture at 65 °C for 5 min. The cDNA was synthesized by combining the denatured sample with AMW reverse transcriptase, RNase inhibitor, dNTPs, and a reaction buffer, and then heating the resultant mixture at 52 °C for 30 min. EDTA was then added to the mixture to stop the reaction. Thereafter, the RNA was hydrolyzed by adding NaOH to the reaction mixture and heating the resultant mixture at 65 °C for 30 min. The mixture was then neutralized with acetic acid. A suspension of glass beads (GENO-BIND™) and NaI were added to the neutralized solution and the cDNA was adsorbed onto the beads. The cDNA, adsorbed onto the beads, was washed with an aqueous solution of 80% EtOH, and then eluted in 50 μl of distilled water. Glycogen was added to the solution of purified cDNA, and the cDNA was precipitated with EtOH and resuspended in 6 μl of distilled water. The resultant suspension (2.5 μl) was added to a solution containing 4 pmol of AmpliFINDER Anchor (5'-CACGAATTCACCTATCGATTCTGGAACCTTCAGAGG NH<sub>2</sub>-3') (SEQ ID NO: 7843) provided with the Kit, T4 RNA ligase, and a ligation (reaction) buffer. The reaction mixture was incubated at room temperature overnight, and the AmpliFINDER Anchor primer in the reaction mixture was thereby ligated to the 3' end of the cDNA. The ligated product was then used as a template for the subsequent PCR.

#### ② Amplification by PCR

The primary PCR was carried out using the template produced in the procedure described above (①), the Anchor primer, 5'-CTGGTTCGGCCACCTCTGAAGGTTCCAGAATCGATAG-3' (SEQ ID NO: 7846) and the PA-5 primer consisting of the sequence 5'-CTCGCTCGCCATCCTTATACAGGCTCAGTTTTGTCT-3' (SEQ ID NO: 7844). Specifically, 1 μl of the template was mixed with Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-5 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 μl and the PCR was performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.). The reaction mixture was subjected to 40 cycles of the PCR, wherein each cycle consisted of incubating the sample in sequence at 94 °C for 1 min, 63 °C for 1 min, and 72 °C for 3 min and, in the last PCR cycle, at 72 °C for an additional 8 min. The products of the PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of



approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered using a Sephaglas Bandprep Kit™ (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the gel was dissolved in a solution of Nal and the resultant mixture was heated at 60 °C for 10 min. Sephaglas™ BP was added to the gel mixture and the DNA was adsorbed onto the glass beads contained therein. The glass beads, containing the adsorbed DNA, were then washed three times with a Wash Buffer provided with the Kit and eluted in 30 µl of TE buffer (10 mM Tris-HCl pH 8.0, 1mM EDTA).

One µl of the eluted DNA was used as a template in a secondary PCR. In order to enhance the specificity of the secondary PCR, the reaction was performed with PA-4 primer which consisted of the sequence 5'-CTCGCTCGCCCATGTATAGGGACAGCATTCTGAGAG-3' (SEQ ID NO: 7845) and was positioned within the template sequence internal to the PA-5 primer and the Anchor primer. Specifically, 1 µl of the template was mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-4 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 µl preheated at 94 °C for 6 min, and the secondary PCR was then performed under the same conditions described above (①) for the primary PCR. The products of the secondary PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered and purified under the same conditions as described above (①) for the primary PCR.

### ③ Subcloning into plasmid vector

The purified DNA product of the secondary PCR was subcloned into the plasmid vector pUC18 (pharmacia Corp.), using a SureClone™ Ligation Kit (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the purified DNA was added to a solution containing Klenow polymerase, polynucleotide kinase and a reaction buffer, mixed and heated at 37 °C for 30 min in order to create blunt-ended termini and to phosphorylate the 5' terminus of the DNA molecules contained in the reaction mixture. The blunt-ended and phosphorylated DNA was combined with a solution containing 50 ng of a dephosphorylated and Sma I-cleaved pUC18 vector provided with the Ligation Kit, T4 DNA ligase, DTT and a ligation reaction buffer, and the resultant mixture was warmed at 16 °C for 3 hr. One sixth volume of the reaction solution was employed to transform E. coli competent cells using standard methods. Specifically frozen E. coli competent cells (Wako Pure Chemical Industries, Ltd.) were thawed and mixed with the ligated DNA. The resultant mixture was incubated on ice for 20 min, heat-treated at 42 °C for 45 sec, and then incubated on ice for 2 min. A medium [Hi-Competence Broth (Wako Pure Chemical Industries, Ltd.)] was added to the mixture containing the transformed E. coli cells. The mixture was incubated for 37 °C for 1 hr and then spread onto agar plates containing 100 µg/ml Ampicillin, 40 µg/ml X-Gal (6-bromo-4-chloro-3-indolyl-β-D-galactoside), 0.1 mM IPTG (isopropyl-β-D-thiogalactopyranoside) and cultured overnight at 37 °C. White colonies were selected from the colonies which consequently appeared on the agar plates and analyzed by the PCR to determine the presence or absence of the DNA insert. Specifically, a sample of a selected colony was picked with a sterilized toothpick and used to inoculate a 50 µl reaction solution containing 1 unit of Taq DNA polymerase, dNTPs, PCR buffer, 200 µM each of the M13 P4-22 primer consisting of the sequence 5'-CCAGGGTTTCCAGTCACGAC-3' (SEQ ID No: 7847) and M13 P5-22 primer consisting of the sequence 5'-TCACACAGGAAACAGCTATGAC-3' (SEQ ID No: 7848), wherein both primers are comprised of sequences complementary to the pUC18 vector. The resultant mixture was heated at 94 °C for 6 min and then subjected to 30 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence, at 94 °C for 1 min, 55 °C for 1 min, and 72 °C for 2 min. The amplified insert was detected by electrophoresis of the PCR products on an agarose gel and thereby the clone pR02342-2, containing an insert, was selected.

### ④ Sequencing of cDNA

The plasmid DNA was prepared using the QIAprep-Spin Kit (Funakoshi, Ltd.) in accordance with the standard alkali-SDS protocol included therewith. Specifically, E. coli cells transformed with the DNA of clone pR02342-2 were cultured overnight in Luria Broth medium containing 100 µg/ml Ampicillin. The cultured cells were then pelleted by centrifugation and resuspended in P1 solution provided in the Kit. The resultant cell suspension was mixed with the P2 alkali solution of the Kit, incubated at room temperature for 5 min, neutralized with N3 solution of the Kit, incubated on ice for an additional 5 min and then centrifuged. The supernatant obtained from the centrifuged solution was applied to a QIAprep-Spin column. The Spin column

was then washed in sequence with PB and then PE solution of the Kit and the DNA was eluted from the column with TE buffer. Sequencing of the eluted DNA was then carried out using the sequencing kit PRISM™ Terminator Mix (Applied Biosystem Corp). Approximately 1 µg of the purified DNA was mixed with a solution containing 3.3 pmol of either the M13 P4-22 primer or M13 P5-22 primer and 9.5 µl of PRISM™ Terminator Mix. The M13 P4-22 and M13 P5-22 primer were used to sequence both strands of the DNA insert of clone pR02342-2. The resultant mixture was diluted to a final volume of 20 µl with distilled water and subjected to 25 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence at 96 °C for 30 sec, 50 °C for 15 sec, and 60 °C for 4 min. The excess primers and fluorescent dye present in the reaction mixture were removed by gel filtration using a MicroSpin™ S-200 HR column (Pharmacia Corp.) and the DNA products of the sequencing reaction were precipitated with EtOH. The precipitated DNA was resuspended, sequenced using an automated sequencer, "Model 373A" (Applied Biosystem Corp.), and thereafter analyzed to determine the nucleotide sequence.

The analysis of the nucleotide sequence revealed that the insert of clone pR02342-2, including the PA-4 primer, was 608 bp in length. The sequence of this insert was subjected to a search for homologous sequences entered in the Gen Bank data base, and a 100% match was found to a sequence in the cDNA which encodes the human mpl-ligand (Accession No. L 33410, Nature 369, 533-538, 1994). Further comparison of the insert of clone pR02342-2 with the cDNA sequence of the human mpl-ligand revealed that the cloned insert contained 81 bp of the 3' coding region of open reading frame. In addition, the insert of clone pR02342-2 contained an additional sequence extending beyond the 3' end of the human mpl-ligand cDNA sequence registered under Gen Bank Accession No. L 33410. These findings suggest that, using the GS HUMGS02342, the inventors of the present invention succeeded in cloning a cDNA clone pR02342-2, which could possibly have a different and more desirable property for expression than the human mpl-ligand cDNA represented by the sequence registered under Gen Bank Accession No. L 33410.

#### ⑤ Cloning of the full-length cDNA encoding the human mpl-ligand

In order to find an optimal PCR primer, an appropriate computer program is used to search the sequence downstream of the coding region of the human mpl-ligand (clone pR02342-2) and thereby a primer PA-7 is designed and synthesized. A PCR similar to that described above in ② is performed using the template produced by the procedure described above in ①, the Anchor primer, and the PA-7 primer. Specifically, 1 µl of the template is mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-7 primer and Anchor primer. The resultant reaction mixture is diluted with distilled water to a final volume of 50 µl and the PCR is performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.) under conditions similar to that described above in ②. The products of the PCR are then resolved by electrophoresis on a 1% agarose gel and a band greater than 1300 bp in length, representing a product of the PCR, is recovered and cloned into a suitable vector in a manner similar to that described in ③. The cloned DNA is sequenced in a manner similar to that described in ④. The sequence is then compared to that of the human mpl-ligand cDNA registered under Gen Bank Accession No. L 33410 to confirm the presence of the full-length open reading frame.

Alternatively, using the Takara La PCR Kit (Takara Shuzo Inc., Code No. RR011) in accordance with the protocol included therewith, performing the 5'RACE procedure using primers similar to those described above in ②, a cDNA of approximately 2 Kb in length, corresponding to the human mpl-ligand, was isolated.

The tables of appearance frequencies for all GSs related to the present invention are followed by "Sequence Listing" for these GSs, wherein HUMGS numbers after the heading 'clone' represent GS numbers. In the sequence table, N in the base sequence stands for "A or C or G or T or U". However, since nucleic acids in the Sequence Listing are DNAs, "T or U" stands for T in this case.

By the present invention, it has become possible to provide DNA molecules which carry "the information for expression" in various cells and can be used for detecting and diagnosing the cellular abnormalities, recognizing and identifying cells and further efficiently cloning genes which are expressed in a tissue-specific manner, and furthermore cloned DNA molecules which can be used for the production of proteins useful as pharmaceutical products.



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK				
22	00023	00021	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
23	00026	00022	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
24	00028	00023	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
25	00029	00024	5	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
26	00030	00025	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
27	00031	00026	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
28	00033	00027	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
29	00034	00028	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
30	00036	00029	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
31	00037	00030	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
32	00038	00031	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
33	00039	00032	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
34	00040	00033	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
35	00041	00034	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
36	00042	00035	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
37	00043	00036	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
38	00044	00037	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
39	00045	00038	5	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
40	00046	00039	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
41	00047	00040	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
42	00048	00041	10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
43	00049	00042	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
44	00050	00043	16	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
45	00051	00044	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	00053	00045	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
47	00055	00046	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
48	00056	00047	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
49	00057	00048	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
50	00060	00049	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
51	00061	00050	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
52	00062	00051	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
53	00064	00052	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
54	00065	00053	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
55	00066	00054	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
56	00067	00055	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
57	00068	00056	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 2

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
58	00069	00057	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
59	00070	00058	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
60	00071	00059	7	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
61	00072	00060	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
62	00073	00061	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
63	00074	00062	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
64	00075	00063	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
65	00076	00064	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
66	00077	00065	34	1	3	2	5	1	0	0	2	2	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
67	00078	00066	12	1	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
68	00079	00067	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
69	00080	00068	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
70	00081	00069	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
71	00082	00070	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
72	00083	00071	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
73	00084	00072	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
74	00085	00073	26	5	3	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
75	00086	00074	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
76	00087	00075	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
77	00088	00076	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
78	00089	00077	33	1	3	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
79	00090	00078	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
80	00091	00079	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
81	00092	00080	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
82	00093	00081	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
83	00094	00082	9	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
84	00095	00083	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
85	00096	00084	62	6	5	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
86	00097	00085	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
87	00098	00086	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
88	00099	00087	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
89	00100	00088	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90	00101	00089	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
91	00102	00090	44	2	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
92	00103	00091	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
93	00104	00092	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 3

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK		
94	00105	00093	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
95	00106	00094	8	2	1	1	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0								
96	00107	00095	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
97	00108	00096	31	2	3	0	0	1	0	2	0	1	0	3	0	0	0	0	3	6	2	1	1	0	1	2	0	0	3	X63237	94.8 384	1	154	532	
98	00109	00097	5	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
99	00110	00098	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
100	00111	00099	38	7	0	0	1	9	13	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
101	00113	00100	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
102	00114	00101	38	1	1	5	0	1	0	0	3	0	1	3	1	1	0	4	3	1	0	9	0	1	0	0	2	0	X04098	92.2 383	1	1551	1918		
103	00115	00102	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
104	00116	00103	17	2	1	1	1	0	0	0	0	0	0	0	0	0	4	0	0	1	0	0	0	0	0	0	6	1	M14630	95.6 362	1	840	1200		
105	00117	00104	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
106	00118	00105	7	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
107	00119	00106	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
108	00120	00107	5	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
109	00121	00108	4	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
110	00122	00109	4	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0							
111	00123	00110	14	2	0	0	2	0	0	0	0	0	0	0	0	1	1	1	0	1	2	0	2	0	1	0	0	1	0	X55954	98.8 336	1	144	479	
112	00124	00111	6	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
113	00125	00112	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
114	00127	00113	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
115	00128	00114	6	2	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	X54326	98.348	1	4238	4586	
116	00129	00115	11	1	0	0	1	0	0	0	0	1	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	X65923	96.6 348	1	168	518	
117	00130	00116	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
118	00131	00117	6	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
119	00132	00118	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
120	00133	00119	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
121	00134	00120	24	1	0	0	1	0	1	1	1	1	0	1	2	0	4	1	1	0	3	1	1	1	3	0	0	0	0	M16660	99.1 339	1	2205	2543	
122	00135	00121	81	5	4	0	0	14	2	4	2	0	2	0	4	1	1	0	3	5	14	1	12	1	2	4	0	0	0	M10119	99.7 307	1	416	723	
123	00136	00122	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
124	00137	00123	10	2	1	0	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	D00763	98.4 313	1	767	1078
125	00138	00124	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
126	00139	00125	8	1	1	0	1	0	0	0	0	0	0	0	1	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	X03445	93.4 335	1	1698	2029
127	00140	00126	13	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	2	0	0	0	0	0	0						
128	00141	00127	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
129	00142	00128	9	1	0	0	0	0	0	0	0	0	0	0	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0						

Table 4

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK		
130	00143	00129	5	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
131	00144	00130	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
132	00145	00131	2	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
133	00146	00132	8	1	2	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
134	00147	00133	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J05682	98.8	329	1	1245	1618	
135	00148	00134	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
136	00149	00135	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
137	00150	00136	17	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
138	00151	00137	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
139	00152	00138	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
140	00153	00139	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
141	00154	00140	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
142	00155	00141	81	1	0	3	8	0	0	3	0	2	2	3	4	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
143	00156	00142	20	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
144	00157	00143	11	1	0	0	0	8	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
145	00158	00144	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
146	00159	00145	4	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
147	00160	00146	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
148	00161	00147	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
149	00162	00148	47	1	4	3	2	1	0	1	0	1	2	5	2	4	4	2	0	0	2	1	7	1	0	2	1	0	0	0					
150	00163	00149	30	1	0	0	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
151	00164	00150	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
152	00165	00151	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
153	00166	00152	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
154	00167	00153	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
155	00168	00154	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
156	00169	00155	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
157	00170	00156	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
158	00171	00157	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
159	00172	00158	14	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
160	00173	00159	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
161	00174	00160	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
162	00175	00161	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
163	00176	00162	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
164	00177	00163	18	2	2	0	0	1	0	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
165	00178	00164	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 5

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	QA	CA	SA	LA	WA	YA	BA	BC	BE	BF	BGBH	BI	BK	
166	00179	00165	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
167	00180	00166	7	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
168	00181	00167	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
169	00182	00168	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99	97	1	1575	1671
170	00183	00169	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
171	00184	00170	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
172	00185	00171	13	2	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
173	00186	00172	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
174	00187	00173	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
175	00188	00174	11	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
176	00189	00175	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
177	00190	00176	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.9	281	1	1114	1393
178	00191	00177	3	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
179	00192	00178	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
180	00193	00179	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
181	00194	00180	34	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.9	275	1	1265	1538
182	00195	00181	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
183	00196	00182	67	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
184	00197	00183	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.9	274	4	193	462
185	00198	00184	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.8	273	1	687	2036
186	00199	00185	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
187	00200	00186	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
188	00201	00187	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96	253	1	4989	5243
189	00202	00188	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
190	00203	00189	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
191	00204	00190	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
192	00205	00191	5	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
193	00206	00192	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
194	00207	00193	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
195	00209	00194	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
196	00210	00195	14	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	384	1	1135	1529
197	00211	00196	128	8	24	2	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
198	00212	00197	16	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.8	272	1	275	557
199	00213	00198	8	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
200	00215	00199	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
201	00216	00200	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

Table 6



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
202	00217	00201	5	1	0	0	0	0	0	1	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
203	00218	00202	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
204	00219	00203	13	2	1	0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0	1	0	1	0	2	2013388	99.5	220	1	1216	1435		
205	00220	00204	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
206	00221	00205	4	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0							
207	00222	00206	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
208	00223	00207	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
209	00224	00208	8	1	1	0	0	0	0	1	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0						
210	00225	00209	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
211	00226	00210	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
212	00227	00211	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
213	00228	00212	9	2	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	2	0	0	0	1	0	0	X17206	98.5	202	31	733	934
214	00230	00213	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
215	00231	00214	6	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	1	0	0							
216	00232	00215	3	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
217	00233	00216	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
218	00234	00217	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
219	00235	00218	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
220	00236	00219	11	1	1	0	0	0	1	1	1	1	1	0	1	0	0	0	0	2	0	0	0	0	0	0	0	1						
221	00237	00220	11	2	0	0	0	0	1	0	0	1	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
222	00238	00221	2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	976	
223	00239	00222	7	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	3	0	0	0	0	0			
224	00240	00223	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
225	00241	00224	12	1	0	0	2	0	0	0	0	1	0	1	0	0	0	0	0	1	1	0	0	0	1	1	3	0	0	0	0	0	258	602
226	00242	00225	5	2	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
227	00243	00226	7	1	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1179	1412
228	00244	00227	65	2	0	14	1	0	0	0	0	0	1	2	3	0	1	3	7	2	4	11	3	0	1	1	4	1	0	0	0	0	1109	1761
229	00245	00228	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0			
230	00246	00229	26	3	5	0	1	0	1	1	0	3	1	0	1	0	1	0	2	2	1	1	0	0	1	0	0	0	0	0	0	0		
231	00247	00230	2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
232	00248	00231	7	1	0	0	0	1	1	1	1	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		
233	00249	00232	9	1	0	5	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2607	2828
234	00250	00233	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0			
235	00251	00234	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
236	00252	00235	5	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		
237	00253	00236	16	2	1	2	0	0	0	1	0	0	0	0	2	0	0	0	2	1	0	1	0	0	0	0	1	0	0	0	0	0		

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
238	00254	00237	38	1	0	0	2	0	0	1	2	1	0	1	0	2	0	1	3	0	0	0	0	0	1	3	20	0	0	M24096	98.1	214	1	1152	1365
239	00255	00238	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
240	00256	00239	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
241	00257	00240	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
242	00258	00241	6	1	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	0	X04588	95.4	217	3	1857	2077
243	00259	00242	2	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
244	00260	00243	4	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0						
245	00261	00244	17	2	1	0	1	0	1	0	0	0	0	1	0	1	1	1	0	0	0	0	3	0	2	0	2	0	0	X65460	99	204	1	1607	1809
246	00262	00245	50	2	7	2	0	1	1	2	0	3	6	0	1	3	0	0	3	0	1	2	0	0	4	0	6	0	2	M17885	98.6	211	1	888	1097
247	00263	00246	2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
248	00264	00247	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
249	00265	00248	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
250	00266	00249	3	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
251	00267	00250	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	X55330	99.1	107	83	1	2150
252	00268	00251	5	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
253	00269	00252	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X63679	98.3	116	1	1152	1267
254	00270	00253	9	1	0	0	0	0	0	0	0	0	1	0	1	0	3	0	1	0	0	0	1	0	0	0	0	0	0	X04526	95.2	209	1	2887	3088
255	00271	00254	24	2	0	1	2	0	1	0	0	2	0	0	0	5	0	1	2	0	1	1	0	0	2	0	4	0	0	X75683	99	210	1	92	301
256	00272	00255	9	1	0	0	0	0	0	1	2	0	0	0	1	0	0	0	1	0	1	0	0	0	1	0	1	0	0	X05262	100	197	1	931	1148
257	00273	00256	119	9	6	4	13	2	11	2	1	12	14	0	6	0	6	0	3	1	3	0	0	2	3	15	0	0	0	X64899	94.8	192	1	626	819
258	00274	00257	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
259	00275	00258	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
260	00276	00259	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0	0							
261	00277	00260	36	3	0	0	0	8	14	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M29882	100	191	1	234	424
262	00278	00261	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
263	00279	00262	10	2	0	1	1	0	0	0	0	0	0	2	3	0	0	0	0	1	0	0	0	0	0	0	0	0							
264	00280	00263	3	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
265	00281	00264	8	3	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	1	0	0	X64228	99.5	196	1	6389	6597
266	00282	00265	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2036	2226	
267	00283	00266	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
268	00284	00267	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0							
269	00285	00268	89	6	14	1	8	0	3	4	1	4	3	5	3	5	0	2	5	1	1	4	1	3	2	0	8	1							
270	00286	00269	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
271	00287	00270	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
272	00288	00271	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
273	00289	00272	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK			
274	00290	00273	85	5	9	3	8	4	2	1	1	1	1	7	4	1	4	5	0	2	6	5	3	6	1	0	2	0	5	0	X66699	99.5	184	1	163	349
275	00291	00274	8	1	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	1	0	1	0	0	0	1	1	0							
276	00292	00275	49	4	12	1	0	2	1	1	4	6	4	0	0	2	0	0	0	5	4	0	1	0	1	0	1	0	0	0	M60854	100	181	1	358	538
277	00293	00276	74	6	13	1	6	2	4	3	3	2	5	0	1	0	4	0	0	2	2	0	0	0	1	5	0	11	3							
278	00294	00277	5	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0							
279	00295	00278	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0							
280	00296	00279	8	1	4	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	M86737	100	183	1	264	2839
281	00297	00280	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
282	00298	00281	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
283	00299	00282	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
284	00300	00283	24	2	1	0	2	0	1	0	0	1	1	2	0	3	1	4	2	0	1	1	0	0	1	1	0	0	0	0	M37104	98.3	179	1	294	471
285	00301	00284	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
286	00302	00285	4	1	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
287	00303	00286	17	2	2	0	0	0	0	0	1	0	0	2	0	0	0	0	0	1	2	0	0	0	0	0	0	2	2	2	L09260	96	176	1	1141	1322
288	00304	00287	48	2	1	2	2	1	0	1	1	3	2	2	3	1	0	4	2	6	0	3	0	1	4	3	3	1	0	M26880	99.4	175	1	2088	2309	
289	00305	00288	46	1	6	0	2	2	3	1	2	1	4	4	2	2	0	3	0	1	4	1	0	2	2	1	2	0	0							
290	00306	00289	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0							
291	00307	00290	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
292	00308	00291	10	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	3	1	0	2	0	0	0	0	0	Y00052	96.7	183	1	542	723
293	00309	00292	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
294	00310	00293	6	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
295	00311	00294	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	M72709	98.8	85	1	1634	1717	
296	00312	00295	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
297	00313	00296	17	1	0	1	0	1	0	1	0	0	1	0	0	0	1	0	2	1	0	3	2	0	0	0	2	0	0	Y00472	96.8	63	1	767	829	
298	00314	00297	45	1	3	1	3	1	0	1	5	1	1	3	2	0	7	2	0	3	2	0	3	0	4	3	2	0	2	X06617	96.4	168	1	378	543	
299	00315	00298	21	3	4	1	0	0	0	1	0	1	0	3	0	0	0	1	0	0	3	0	0	0	0	0	0	2	0	L06498	99.4	161	1	345	505	
300	00316	00299	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	S63912	96.8	63	1	1126	3043	
301	00317	00300	10	1	0	0	0	0	3	0	2	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0							
302	00320	00301	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
303	00322	00302	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
304	00323	00303	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
305	00325	00304	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
306	00327	00305	20	1	3	1	0	0	0	1	2	0	0	0	0	2	1	0	0	0	0	2	3	0	0	3	0	0	1	0	X03342	96.4	169	1	328	505
307	00328	00306	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
308	00329	00307	5	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	1	0							
309	00330	00308	8	1	0	2	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						

Table 9

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK			
310	00331	00309	6	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
311	00332	00310	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
312	00333	00311	16	1	0	0	3	0	0	0	0	1	4	0	0	0	0	0	2	2	0	1	0	0	0	0	0	0	0	0	0	0			
313	00334	00312	3	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
314	00335	00313	86	1	16	4	3	1	1	0	3	7	3	1	6	6	1	3	2	1	1	1	4	2	5	0	10	3	M36072	100	165	1	727	891	
315	00336	00314	47	1	2	2	2	0	1	0	0	5	6	0	1	2	0	3	4	3	1	1	0	1	8	0	3	0	Z12962	96	3	162	1	308	478
316	00337	00315	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	1	0	0	0	0	0	0	0	0	0		
317	00338	00316	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
318	00339	00317	13	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	6	0	0	0	0	0	0	0	0		
319	00340	00318	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
320	00341	00319	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
321	00342	00320	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
322	00343	00321	12	2	0	0	1	0	0	0	2	1	0	0	0	3	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	
323	00344	00322	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
324	00346	00323	9	1	0	0	0	0	0	0	1	1	0	0	1	0	0	1	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	
325	00347	00324	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
326	00348	00325	10	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
327	00349	00326	29	2	2	0	0	1	0	0	2	1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
328	00350	00327	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
329	00351	00328	7	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
330	00352	00329	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
331	00353	00330	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
332	00354	00331	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
333	00355	00332	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
334	00356	00333	43	1	17	0	2	2	1	3	0	0	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
335	00357	00334	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
336	00358	00335	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
337	00359	00336	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
338	00360	00337	19	2	2	1	0	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
339	00361	00338	11	1	0	1	0	0	0	0	0	2	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
340	00362	00339	19	1	0	0	0	0	0	0	0	2	0	12	2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
341	00363	00340	29	1	0	0	0	0	1	0	1	1	0	5	0	2	0	1	1	3	2	2	1	3	1	1	1	0	0	0	0	0	0	0	
342	00364	00341	632	17	0	0	0	0	227	109	#	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
343	00365	00342	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
344	00366	00343	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
345	00367	00344	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK			
346	00368	00345	11	1	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	3	0	0	1	0	0	0	1	M31627	98.6	141	1	1657	1818		
347	00369	00346	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L10379	98.6	142	1	1581	1725		
348	00370	00347	7	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	3	0	0								
349	00372	00348	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
350	00373	00349	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
351	00374	00350	10	1	1	0	0	1	2	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
352	00375	00351	36	2	3	0	3	1	2	0	0	3	5	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0							
353	00376	00352	21	2	0	0	0	1	0	0	0	1	1	1	0	0	0	0	1	4	1	3	1	0	2	1	0	1	6						
354	00377	00353	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
355	00378	00354	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
356	00379	00355	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
357	00380	00356	47	1	12	0	1	0	1	3	0	2	5	2	0	1	3	1	1	1	1	1	1	1	2	0	3	1							
358	00381	00357	22	1	0	2	6	0	0	0	0	0	0	0	6	0	1	0	0	0	0	0	0	0	0	0	0	0							
359	00382	00358	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
360	00383	00359	28	3	1	3	0	1	0	0	2	0	0	1	3	0	0	0	1	3	2	1	0	0	0	0	0	0	0						
361	00384	00360	10	1	0	0	0	0	0	0	2	0	1	0	1	0	0	0	2	0	0	0	0	0	0	0	0	3	J04031	97.8	136	1	2977	3112	
362	00385	00361	4	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
363	00386	00362	6	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
364	00387	00363	5	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L11932	100	126	1	1667	1792	
365	00388	00364	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
366	00389	00365	4	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
367	00390	00366	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
368	00391	00367	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
369	00392	00368	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
370	00393	00369	2	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
371	00394	00370	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
372	00395	00371	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
373	00396	00372	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
374	00397	00373	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
375	00398	00374	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
376	00399	00375	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
377	00400	00376	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
378	00401	00377	16	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.9	118	1	1622	1751	
379	00402	00378	39	1	0	0	2	2	0	0	0	1	0	0	2	0	0	0	0	2	1	1	0	1	0	3	0	L24521	94.5	220	1	1024	1240		
380	00403	00379	21	7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	22	0	0	0	97.6	125	1	917	1060	
381	00404	00380	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	TA	GA	IA	KA	MA	QA	CA	SA	LA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK	
418	00442	00417	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
419	00443	00418	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
420	00444	00419	71	6	10	1	4	2	4	1	1	0	3	1	0	5	0	0	1	4	8	5	5	0	3	5	0	2	0	0	0	0	0	0	0	
421	00445	00420	3	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
422	00446	00421	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
423	00447	00422	38	2	6	1	1	0	3	2	0	2	6	2	0	1	0	0	3	1	1	1	0	1	1	1	0	3	0	0	0	0	0	0	0	
424	00448	00423	17	1	0	1	1	0	0	0	0	1	2	0	1	0	1	0	1	0	2	0	1	2	0	1	0	1	0	0	0	0	0	0	0	
425	00450	00424	30	3	2	2	2	0	0	0	0	0	0	0	0	2	1	0	2	0	3	1	10	0	2	0	0	0	0	0	0	0	0	0	0	
426	00451	00425	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
427	00453	00426	4	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
428	00454	00427	7	1	0	0	1	0	0	0	0	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
429	00455	00428	10	2	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	0	2	0	0	0	0	0	0		
430	00456	00429	18	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	1	0	1	0	1	0	8	0	0	0	0	0	0		
431	00457	00430	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
432	00458	00431	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
433	00459	00432	8	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
434	00460	00433	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
435	00461	00434	3	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
436	00462	00435	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
437	00463	00436	26	2	2	0	1	1	0	0	0	0	0	0	1	0	0	2	0	2	2	3	1	1	2	4	0	0	0	0	0	0	0	0	0	
438	00464	00437	18	1	1	2	0	0	1	0	0	0	1	3	0	1	0	0	0	2	2	2	1	1	1	0	0	0	0	0	0	0	0	0	0	
439	00465	00438	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
440	00466	00439	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
441	00467	00440	4	1	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
442	00468	00441	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
443	00469	00442	6	1	1	1	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
444	00470	00443	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
445	00471	00444	8	1	0	1	0	0	0	1	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
446	00473	00445	10	1	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	1	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
447	00474	00446	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
448	00475	00447	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
449	00477	00448	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
450	00478	00449	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
451	00479	00450	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
452	00480	00451	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
453	00481	00452	24	1	1	0	0	0	1	0	3	0	0	2	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 13

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
490	00545	00489	36			3	0	2	0	0	1	2	3	0	1	3	1	0	2	1	1	0	1	3	0	7	1M94314	93.4	439	1	75	556
491	00546	00490	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
492	00547	00491	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
493	00548	00492	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0M64716	94.4	478	2	24	497	
494	00549	00493	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
495	00551	00494	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
496	00552	00495	4	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
497	00553	00496	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
498	00554	00497	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
499	00555	00498	4	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0D14662	97.5	481	1	395	1653	
500	00556	00499	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
501	00557	00500	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
502	00558	00501	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
503	00560	00502	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
504	00561	00503	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
505	00562	00504	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
506	00564	00505	2	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
507	00565	00506	70	4	2	5	0	1	1	1	1	1	1	4	5	1	1	0	4	6	2	1	1	2	0	2M30684	96.4	415	1	519	929	
508	00567	00507	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0L06432	95.9	98	162	332	549	
509	00568	00508	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
510	00569	00509	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
511	00571	00510	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
512	00572	00511	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
513	00573	00512	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
514	00574	00513	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
515	00575	00514	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0J04564	93.5	370	4	736	1099	
516	00576	00515	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
517	00577	00516	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
518	00578	00517	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
519	00579	00518	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X52317	96.5	342	1	40	869	
520	00580	00519	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
521	00581	00520	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
522	00582	00521	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
523	00583	00522	34	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
524	00584	00523	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X73460	95.8	378	1	900	1272	
525	00585	00524	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 15

Table 16

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
526	00586	00525	6		1	0	0	1	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
527	00589	00526	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
528	00590	00527	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
529	00591	00528	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
530	00592	00529	15		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
531	00593	00530	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
532	00594	00531	17		3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
533	00595	00532	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
534	00596	00533	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
535	00597	00534	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
536	00598	00535	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
537	00599	00536	4		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
538	00600	00537	12		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
539	00601	00538	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
540	00602	00539	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
541	00603	00540	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
542	00604	00541	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
543	00606	00542	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
544	00607	00543	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
545	00608	00544	22		5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
546	00609	00545	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
547	00610	00546	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
548	00611	00547	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
549	00612	00548	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
550	00614	00549	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
551	00615	00550	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
552	00616	00551	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
553	00617	00552	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
554	00618	00553	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
555	00619	00554	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
556	00620	00555	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
557	00621	00556	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
558	00622	00557	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
559	00623	00558	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
560	00624	00559	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
561	00625	00560	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
562	00626	00561	4		2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
563	00627	00562	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
564	00628	00563	4		1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
565	00629	00564	3		1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0							
566	00630	00565	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
567	00631	00566	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
568	00632	00567	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
569	00633	00568	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
570	00634	00569	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
571	00635	00570	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
572	00636	00571	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
573	00637	00572	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
574	00638	00573	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
575	00639	00574	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
576	00640	00575	10		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
577	00641	00576	8		2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
578	00642	00577	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
579	00643	00578	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
580	00644	00579	24		5	0	2	0	1	1	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0							
581	00645	00580	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
582	00646	00581	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
583	00647	00582	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
584	00648	00583	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
585	00649	00584	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
586	00650	00585	52		14	2	6	0	2	0	1	1	2	1	6	3	2	0	0	0	0	0	0	0	0	0	0							
587	00651	00586	9		4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
588	00652	00587	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
589	00653	00588	13		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
590	00654	00589	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
591	00655	00590	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
592	00656	00591	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
593	00657	00592	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
594	00658	00593	6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
595	00659	00594	9		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
596	00660	00595	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
597	00661	00596	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 17

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
598	00664	00597	3		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
599	00665	00598	2		1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
600	00666	00599	5		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	98.4	248	1	1335	1692
601	00667	00600	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
602	00668	00601	8		2	0	1	0	0	0	1	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
603	00669	00602	2		1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
604	00670	00603	12		1	0	0	0	0	2	0	0	2	1	0	0	0	0	0	1	1	0	0	0	0	0	1	0	98.4	249	1	600	851
605	00671	00604	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
606	00672	00605	7		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.9	241	1	2915	3319
607	00673	00606	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.2	240	1	2728	2969
608	00674	00607	5		1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
609	00675	00608	31		4	1	0	0	1	0	2	1	1	0	0	0	2	5	0	0	1	0	2	0	0	0	6	0	100	237	1	291	530
610	00676	00609	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
611	00677	00610	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
612	00678	00611	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
613	00679	00612	15		1	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
614	00680	00613	1		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
615	00681	00614	7		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
616	00682	00615	3		1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	238	1	2484	2739
617	00683	00616	20		1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.2	254	1	1304	3043
618	00684	00617	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	96.1	230	1	194	422
619	00685	00618	18		2	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.8	237	1	1728	3755
620	00686	00619	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
621	00687	00620	16		1	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
622	00689	00621	40		1	1	2	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	246	1	1494	1741
623	00690	00622	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
624	00691	00623	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
625	00692	00624	6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
626	00693	00625	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
627	00694	00626	3		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
628	00695	00627	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
629	00696	00628	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
630	00697	00629	7		2	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.9	226	1	1640	1880
631	00698	00630	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
632	00699	00631	1		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
633	00700	00632	1		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 18

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
634	00701	00633	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
635	00702	00634	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
636	00703	00635	17	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	172	1	466	635	
637	00704	00636	45	4	1	0	0	0	1	0	1	1	6	1	2	3	2	0	0	0	0	0	0	0	0	0	0	100	217	1	506	722	
638	00705	00637	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
639	00706	00638	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
640	00707	00639	10	1	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	92.3	209	1	887	1093	
641	00708	00640	32	1	0	2	0	0	1	0	3	3	3	2	0	1	0	0	0	0	0	0	0	0	0	0	0						
642	00710	00641	2	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	98.4	127	84	3	135	
643	00711	00642	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
644	00712	00643	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
645	00713	00644	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
646	00714	00645	13	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99	202	1	531	732	
647	00715	00646	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
648	00716	00647	48	5	3	3	0	0	0	0	2	1	3	0	1	3	1	0	0	0	0	0	0	0	0	0	0	94	200	1	291	495	
649	00717	00648	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.5	198	1	2231	2444	
650	00718	00649	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
651	00719	00650	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
652	00720	00651	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
653	00721	00652	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
654	00722	00653	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
655	00723	00654	11	1	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	L10376	97	202	1	509	753
656	00725	00655	10	1	0	0	0	0	0	1	0	1	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0					
657	00726	00656	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
658	00727	00657	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
659	00728	00658	5	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
660	00729	00659	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.5	133	1	932	1064	
661	00730	00660	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
662	00731	00661	2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
663	00732	00662	47	6	3	4	0	0	1	5	1	1	1	0	1	6	2	0	2	7	0	4	3	0	0	0	0	0					
664	00733	00663	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
665	00734	00664	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
666	00735	00665	11	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
667	00736	00666	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
668	00737	00667	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
669	00738	00668	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 19

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	DE	BF	BG	BH	BI	BK
670	00739	00669	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
671	00740	00670	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
672	00741	00671	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
673	00742	00672	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
674	00743	00673	54	7	1	7	2	6	1	0	1	0	8	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
675	00745	00674	4	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
676	00746	00675	13	1	2	1	0	0	0	0	0	0	0	0	0	1	0	2	0	1	0	1	1	2	0	0	0	0	0	0	0	0	0
677	00747	00676	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
678	00748	00677	5	1	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
679	00749	00678	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
680	00750	00679	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
681	00751	00680	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
682	00752	00681	4	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
683	00753	00682	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
684	00754	00683	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
685	00755	00684	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
686	00757	00685	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
687	00758	00686	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
688	00759	00687	25	4	1	1	0	0	1	0	0	0	2	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
689	00760	00688	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
690	00761	00689	10	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
691	00762	00690	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
692	00763	00691	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
693	00764	00692	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
694	00765	00693	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
695	00766	00694	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
696	00768	00695	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
697	00769	00696	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
698	00770	00697	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
699	00771	00698	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
700	00772	00699	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
701	00773	00700	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
702	00774	00701	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
703	00775	00702	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
704	00777	00703	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
705	00778	00704	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 20

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
706	00779	00705	3	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
707	00780	00706	3	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
708	00781	00707	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
709	00782	00708	8	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
710	00783	00709	5	1	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
711	00784	00710	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
712	00785	00711	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
713	00786	00712	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
714	00787	00713	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
715	00788	00714	4	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
716	00789	00715	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
717	00790	00716	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
718	00791	00717	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
719	00792	00718	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
720	00793	00719	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
721	00794	00720	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
722	00795	00721	42	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
723	00796	00722	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
724	00797	00723	36	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
725	00798	00724	4	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
726	00799	00725	13	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
727	00800	00726	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
728	00801	00727	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
729	00802	00728	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
730	00803	00729	7	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
731	00804	00730	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
732	00805	00731	6	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
733	00806	00732	7	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
734	00807	00733	23	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
735	00808	00734	8	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
736	00809	00735	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
737	00810	00736	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
738	00811	00737	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
739	00813	00738	7	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
740	00814	00739	8	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
741	00815	00740	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 21

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
742	00816	00741	14	1	5	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
743	00817	00742	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
744	00818	00743	20	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
745	00819	00744	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
746	00820	00745	18	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
747	00821	00746	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
748	00822	00747	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
749	00823	00748	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
750	00824	00749	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
751	00825	00750	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
752	00826	00751	6	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
753	00827	00752	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
754	00828	00753	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
755	00829	00754	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
756	00830	00755	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
757	00831	00756	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
758	00832	00757	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
759	00833	00758	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
760	00834	00759	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
761	00835	00760	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
762	00836	00761	8	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
763	00837	00762	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
764	00839	00763	7	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
765	00840	00764	8	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
766	00841	00765	10	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
767	00842	00766	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
768	00843	00767	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
769	00844	00768	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
770	00845	00769	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
771	00846	00770	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
772	00847	00771	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
773	00848	00772	12	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
774	00849	00773	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
775	00850	00774	12	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
776	00851	00775	14	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
777	00852	00776	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 22



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
778	00853	00777	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
779	00854	00778	8		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
780	00855	00779	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
781	00856	00780	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
782	00857	00781	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
783	00858	00782	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
784	00859	00783	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
785	00860	00784	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
786	00861	00785	34		6	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
787	00862	00786	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
788	00863	00787	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
789	00864	00788	5		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
790	00865	00789	56		9	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
791	00866	00790	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
792	00867	00791	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
793	00868	00792	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
794	00869	00793	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
795	00870	00794	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
796	00871	00795	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
797	00872	00796	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
798	00873	00797	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
799	00874	00798	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
800	00875	00799	21		2	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
801	00876	00800	9		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
802	00877	00801	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
803	00878	00802	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
804	00879	00803	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
805	00880	00804	5		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
806	00882	00805	20		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
807	00883	00806	5		1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
808	00884	00807	3		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
809	00885	00808	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
810	00886	00809	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
811	00887	00810	14		2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
812	00889	00811	17		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
813	00890	00812	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 23

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AB	AC	AD	AE	AF	AG	AH	AI	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AW	AX	AY	BA	BB	BC	BE	BF	BG	BH	BI	BK				
814	00891	00813	5		1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
815	00892	00814	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
816	00894	00815	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
817	00895	00816	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
818	00896	00817	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
819	00897	00818	10		2	1	0	0	0	2	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
820	00898	00819	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
821	00900	00820	27		1	0	2	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
822	00903	00821	3		1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
823	00904	00822	8		1	0	0	0	0	1	0	1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
824	00905	00823	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
825	00906	00824	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
826	00908	00825	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
827	00910	00826	2		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
828	00911	00827	9		1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
829	00912	00828	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
830	00913	00829	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
831	00914	00830	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
832	00915	00831	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
833	00917	00832	43		3	1	3	0	0	3	3	2	1	1	5	6	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
834	00918	00833	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
835	00919	00834	7		1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
836	00920	00835	4		1	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0</											

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
850	00955	00849	6		3	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
851	00972	00850	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
852	00973	00851	2	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
853	00974	00852	59	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
854	00976	00853	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
855	00977	00854	5	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
856	00978	00855	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
857	00979	00856	3	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
858	00980	00857	12	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
859	00981	00858	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
860	00982	00859	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
861	00983	00860	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
862	00984	00861	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
863	00985	00862	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
864	00986	00863	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
865	00987	00864	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
866	00988	00865	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
867	00989	00866	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
868	00990	00867	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
869	00991	00868	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
870	00992	00869	3	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
871	00993	00870	2	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
872	00994	00871	19	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
873	00995	00872	23	23	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
874	00996	00873	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
875	00997	00874	2	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
876	00998	00875	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
877	00999	00876	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
878	01000	00877	3	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
879	01001	00878	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
880	01002	00879	2	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
881	01003	00880	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
882	01004	00881	4	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
883	01005	00882	2	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
884	01006	00883	3	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
885	01007	00884	33	33	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 25

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
886	01009	00885	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
887	01010	00886	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
888	01011	00887	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
889	01012	00888	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
890	01013	00889	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
891	01015	00890	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
892	01016	00891	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
893	01017	00892	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
894	01018	00893	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
895	01019	00894	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
896	01020	00895	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
897	01021	00896	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
898	01023	00897	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
899	01024	00898	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
900	01025	00899	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
901	01026	00900	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
902	01027	00901	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
903	01028	00902	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
904	01029	00903	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
905	01030	00904	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
906	01032	00905	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
907	01033	00906	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
908	01034	00907	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
909	01035	00908	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
910	01036	00909	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
911	01037	00910	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
912	01038	00911	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
913	01039	00912	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
914	01040	00913	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
915	01041	00914	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
916	01042	00915	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
917	01043	00916	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
918	01044	00917	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
919	01045	00918	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
920	01046	00919	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
921	01047	00920	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 26

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK
922	01048	00921	5		0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	96.9	382	1	708	1089
923	01049	00922	2		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
924	01051	00923	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
925	01052	00924	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
926	01053	00925	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.3	380	24	3711	4221	
927	01054	00926	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
928	01055	00927	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
929	01057	00928	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
930	01061	00929	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	347	1	1115	1460	
931	01062	00930	8		0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	1	0	0	0	97.2	394	1	1011	1441	
932	01063	00931	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
933	01064	00932	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
934	01065	00933	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
935	01066	00934	2		0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
936	01067	00935	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
937	01068	00936	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
938	01069	00937	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
939	01070	00938	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
940	01071	00939	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
941	01072	00940	8		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
942	01073	00941	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
943	01074	00942	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
944	01075	00943	10		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
945	01076	00944	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
946	01077	00945	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
947	01078	00946	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
948	01079	00947	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
949	01080	00948	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
950	01081	00949	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
951	01082	00950	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
952	01083	00951	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
953	01084	00952	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
954	01085	00953	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
955	01086	00954	8		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
956	01087	00955	18		0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
957	01088	00956	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 27

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
958	01089	00957	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0M16592	91.8	367	1	1410	1926	
959	01090	00958	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
960	01091	00959	5		0	3	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
961	01092	00960	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0D12902	93	343	16	1	1391	
962	01093	00961	2		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
963	01094	00962	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
964	01095	00963	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
965	01096	00964	9		0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
966	01097	00965	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
967	01098	00966	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
968	01099	00967	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
969	01100	00968	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
970	01101	00969	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
971	01102	00970	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
972	01103	00971	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
973	01104	00972	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
974	01105	00973	8		0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
975	01106	00974	16		0	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
976	01107	00975	11		0	2	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
977	01108	00976	5		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
978	01109	00977	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
979	01110	00978	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
980	01111	00979	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
981	01112	00980	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
982	01115	00981	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
983	01116	00982	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
984	01117	00983	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
985	01118	00984	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
986	01119	00985	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
987	01120	00986	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
988	01122	00987	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
989	01123	00988	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
990	01126	00989	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
991	01127	00990	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
992	01128	00991	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
993	01129	00992	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 28

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1030	01168	01029	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
1031	01169	01030	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
1032	01170	01031	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1033	01171	01032	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1034	01172	01033	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1035	01173	01034	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1036	01174	01035	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1037	01175	01036	14		0	1	2	1	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1038	01176	01037	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1039	01177	01038	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1040	01178	01039	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1041	01179	01040	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1042	01180	01041	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1043	01181	01042	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1044	01182	01043	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1045	01183	01044	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1046	01184	01045	7		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1047	01186	01046	1		0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1048	01187	01047	8		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1049	01188	01048	5		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1050	01189	01049	13		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1051	01191	01050	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1052	01192	01051	8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1053	01193	01052	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1054	01194	01053	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1055	01195	01054	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1056	01196	01055	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1057	01197	01056	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1058	01198	01057	10		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1059	01199	01058	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1060	01200	01059	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1061	01201	01060	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1062	01202	01061	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1063	01203	01062	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1064	01204	01063	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1065	01205	01064	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 30



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1066	01207	01065	5		0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0						
1067	01208	01066	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1068	01209	01067	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1069	01210	01068	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1070	01211	01069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1071	01212	01070	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1072	01213	01071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1073	01214	01072	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1074	01215	01073	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1075	01216	01074	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1076	01217	01075	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1077	01218	01076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1078	01219	01077	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1079	01220	01078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1080	01221	01079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1081	01222	01080	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1082	01223	01081	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1083	01224	01082	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1084	01225	01083	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1085	01226	01084	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1086	01227	01085	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1087	01228	01086	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1088	01229	01087	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1089	01230	01088	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1090	01231	01089	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1091	01232	01090	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1092	01233	01091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1093	01235	01092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1094	01236	01093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1095	01237	01094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1096	01238	01095	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1097	01239	01096	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1098	01240	01097	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1099	01241	01098	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1100	01242	01099	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1101	01243	01100	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 31

[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1174	01319	01173	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1175	01320	01174	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1176	01321	01175	19		0	3	2	1	2	0	1	1	0	0	1	0	2	0	0	0	0	0	0	2	1	0							
1177	01322	01176	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1178	01323	01177	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1179	01324	01178	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1180	01325	01179	17		0	1	0	0	0	0	0	0	0	2	0	1	0	1	0	2	1	0	2	3	1	0	L26247	98.5	203	1	455	660	
1181	01326	01180	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1182	01327	01181	4		0	2	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	M74524	100	199	1	1543	1743		
1183	01328	01182	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	D16217	93.2	251	1	2131	2493		
1184	01329	01183	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1185	01330	01184	4		0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	M13450	99.3	146	1	820	1069		
1186	01331	01185	3		0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
1187	01332	01186	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1188	01333	01187	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L16862	99.5	196	1	1867	2848		
1189	01334	01188	7		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1190	01335	01189	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M33195	98.9	186	1	400	591		
1191	01336	01190	4		0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1192	01337	01191	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1193	01338	01192	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1194	01339	01193	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1195	01340	01194	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X69838	98.9	188	1	3190	3391		
1196	01341	01195	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1197	01342	01196	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1198	01343	01197	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1199	01344	01198	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1200	01345	01199	4		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1201	01346	01200	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J04739	98.3	180	1	1634	1813	
1202	01347	01201	5		0	2	0	0	0	0	0	1	0	0	1	2	4	0	0	0	0	0	0	0	0	0	0						
1203	01348	01202	13		0	2	0	0	0	0	0	1	0	0	1	2	4	0	0	0	0	0	0	0	0	0	0						
1204	01349	01203	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1205	01350	01204	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1206	01351	01205	7		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1207	01352	01206	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1208	01353	01207	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1209	01354	01208	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 34

Table 35

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK		
1210	01355	01209	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1211	01356	01210	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1212	01357	01211	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1213	01358	01212	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1214	01359	01213	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L22473	95.3	127	1	453	579	
1215	01360	01214	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1216	01361	01215	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1217	01362	01216	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1218	01363	01217	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1219	01364	01218	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1220	01365	01219	4		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1221	01366	01220	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1222	01367	01221	21		0	3	1	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	729505	97.2	216	1	1324	1558
1223	01368	01222	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1224	01369	01223	5		0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1225	01370	01224	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1226	01371	01225	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1227	01372	01226	7		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X06233	91.4	58	1	405	462	
1228	01373	01227	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1229	01374	01228	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1230	01375	01229	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1231	01377	01230	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1232	01378	01231	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1233	01379	01232	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1234	01380	01233	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1235	01381	01234	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1236	01382	01235	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1237	01383	01236	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1238	01384	01237	16		0	1	1	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1239	01385	01238	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1240	01386	01239	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M86667	100	124	41	1287	1580	
1241	01387	01240	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1242	01388	01241	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L10342	99.4	163	1	2	2225	
1243	01389	01242	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1244	01390	01243	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1245	01391	01244	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 36

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1246	01392	01245	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1247	01393	01246	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1248	01394	01247	12		0	4	0	0	0	0	0	0	0	1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1249	01395	01248	7		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1250	01396	01249	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1251	01397	01250	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1252	01398	01251	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1253	01400	01252	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1254	01401	01253	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1255	01402	01254	7		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1256	01403	01255	6		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1257	01404	01256	16		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1258	01405	01257	4		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1259	01406	01258	7		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1260	01407	01259	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1261	01408	01260	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1262	01409	01261	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1263	01410	01262	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1264	01411	01263	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1265	01412	01264	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1266	01413	01265	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1267	01414	01266	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1268	01415	01267	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1269	01416	01268	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1270	01417	01269	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1271	01418	01270	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1272	01419	01271	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1273	01420	01272	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1274	01421	01273	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1275	01422	01274	3		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1276	01423	01275	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1277	01424	01276	12		0	2	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1278	01426	01277	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1279	01427	01278	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1280	01428	01279	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1281	01429	01280	4		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1282	01430	01281	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1283	01431	01282	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1284	01432	01283	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1285	01433	01284	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1286	01434	01285	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1287	01435	01286	7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1288	01436	01287	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1289	01437	01288	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1290	01438	01289	3		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1291	01439	01290	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1292	01440	01291	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1293	01441	01292	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1294	01442	01293	4		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1295	01443	01294	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1296	01444	01295	3		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1297	01445	01296	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1298	01446	01297	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1299	01447	01298	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1300	01448	01299	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1301	01449	01300	10		0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1302	01450	01301	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1303	01451	01302	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1304	01452	01303	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1305	01453	01304	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1306	01454	01305	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1307	01455	01306	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1308	01456	01307	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1309	01457	01308	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1310	01458	01309	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1311	01459	01310	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1312	01460	01311	2		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1313	01461	01312	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1314	01462	01313	6		0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1315	01463	01314	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1316	01464	01315	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1317	01466	01316	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 37

Table 38

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
1318	01467	01317	4		0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1319	01468	01318	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1320	01469	01319	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1321	01470	01320	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1322	01471	01321	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1323	01472	01322	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1324	01473	01323	9		0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1325	01474	01324	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1326	01475	01325	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1327	01476	01326	19		0	4	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1328	01477	01327	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1329	01478	01328	5		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1330	01479	01329	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1331	01481	01330	3		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1332	01482	01331	2		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1333	01483	01332	9		0	2	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1334	01484	01333	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1335	01485	01334	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1336	01486	01335	3		0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1337	01487	01336	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1338	01488	01337	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1339	01489	01338	5		0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1340	01490	01339	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1341	01491	01340	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1342	01492	01341	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1343	01493	01342	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1344	01494	01343	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1345	01495	01344	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1346	01496	01345	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1347	01497	01346	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1348	01498	01347	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1349	01499	01348	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1350	01500	01349	3		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1351	01501	01350	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1352	01502	01351	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1353	01503	01352	9		0	1	2	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0					



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK
1354	01505	01353	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1355	01506	01354	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	406			2327	
1356	01507	01355	5	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.1	112	1	1923	1760	
1357	01508	01356	13	13	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1358	01509	01357	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1359	01510	01358	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1360	01511	01359	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1361	01512	01360	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1362	01513	01361	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1363	01514	01362	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1364	01515	01363	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1365	01516	01364	7	7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.6	110	1	3448	4221	
1366	01517	01365	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1367	01518	01366	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1368	01519	01367	3	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1369	01520	01368	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1370	01521	01369	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1371	01522	01370	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1372	01523	01371	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1373	01524	01372	7	7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.5	231	62	1	229	
1374	01525	01373	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1375	01526	01374	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1376	01527	01375	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1377	01528	01376	16	16	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1378	01529	01377	7	7	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1379	01530	01378	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1380	01531	01379	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1381	01532	01380	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1382	01533	01381	19	19	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.1	105	1	2333	2455	
1383	01534	01382	8	8	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1384	01535	01383	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1385	01536	01384	2	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1386	01537	01385	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1387	01538	01386	12	12	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1388	01539	01387	1	1	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1389	01540	01388	6	6	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1390	01541	01389	6	6	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 39

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1390	01542	01389	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1391	01543	01390	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1392	01544	01391	4	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1393	01545	01392	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1394	01546	01393	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1395	01547	01394	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1396	01548	01395	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1397	01549	01396	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1398	01550	01397	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1399	01551	01398	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1400	01552	01399	10	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1401	01553	01400	5	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1402	01554	01401	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1403	01555	01402	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1404	01556	01403	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1405	01557	01404	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1406	01558	01405	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1407	01560	01406	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1408	01561	01407	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1409	01562	01408	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1410	01563	01409	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1411	01564	01410	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1412	01565	01411	6	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1413	01566	01412	9	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1414	01567	01413	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1415	01568	01414	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1416	01569	01415	6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1417	01570	01416	7	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1418	01571	01417	10	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1419	01572	01418	4	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1420	01573	01419	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1421	01574	01420	11	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1422	01575	01421	6	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1423	01576	01422	6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1424	01577	01423	5	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1425	01578	01424	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 40

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	CA	AS	JA	WA	YB	AB	BC	BE	BF	BG	BH	BI	BK
1426	01579	01425	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1427	01580	01426	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1428	01581	01427	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1429	01582	01428	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1430	01583	01429	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1431	01584	01430	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1432	01585	01431	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1433	01586	01432	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1434	01587	01433	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1435	01588	01434	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1436	01589	01435	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1437	01590	01436	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1438	01591	01437	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1439	01592	01438	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1440	01593	01439	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1441	01594	01440	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1442	01595	01441	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1443	01596	01442	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1444	01597	01443	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1445	01598	01444	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1446	01599	01445	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1447	01600	01446	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1448	01601	01447	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1449	01602	01448	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1450	01603	01449	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1451	01604	01450	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1452	01605	01451	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1453	01606	01452	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1454	01607	01453	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1455	01608	01454	23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1456	01609	01455	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1457	01610	01456	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1458	01611	01457	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1459	01612	01458	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1460	01614	01459	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1461	01615	01460	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 41

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
1462	01616	01461	32		0	1	3	1	0	0	0	0	0	0	3	0	0	1	0	5	11	0	0	2	1	0	0	3	03558	98.2	55	1	588	642
1463	01617	01462	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1464	01618	01463	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1465	01619	01464	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1466	01620	01465	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1467	01621	01466	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1468	01622	01467	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1469	01623	01468	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1470	01624	01469	8		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1471	01625	01470	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1472	01626	01471	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1473	01627	01472	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1474	01628	01473	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1475	01629	01474	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1476	01630	01475	9		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1477	01632	01476	11		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1478	01633	01477	7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1479	01642	01478	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1480	01671	01479	35		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1481	01673	01480	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1482	01686	01481	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1483	01687	01482	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1484	01688	01483	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1485	01689	01484	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1486	01691	01485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1487	01692	01486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1488	01693	01487	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1489	01694	01488	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1490	01695	01489	11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1491	01696	01490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1492	01697	01491	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1493	01698	01492	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1494	01699	01493	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1495	01700	01494	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1496	01701	01495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1497	01702	01496	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 42

Table 43

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
1498	01703	01497	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1499	01704	01498	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1500	01705	01499	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1501	01706	01500	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1502	01707	01501	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1503	01708	01502	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1504	01709	01503	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1505	01710	01504	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1506	01711	01505	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1507	01713	01506	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1508	01714	01507	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1509	01715	01508	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1510	01718	01509	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1511	01719	01510	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1512	01720	01511	43		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1513	01721	01512	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1514	01722	01513	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1515	01724	01514	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1516	01726	01515	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1517	01727	01516	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1518	01728	01517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1519	01729	01518	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1520	01730	01519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1521	01731	01520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1522	01732	01521	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1523	01733	01522	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1524	01734	01523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1525	01735	01524	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1526	01736	01525	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1527	01737	01526	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1528	01738	01527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1529	01739	01528	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1530	01740	01529	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1531	01741	01530	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1532	01742	01531	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1533	01745	01532	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	KA	MA	QA	SA	TA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
1534	01746	01533	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1535	01747	01534	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1536	01748	01535	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1537	01749	01536	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1538	01750	01537	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1539	01751	01538	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1540	01752	01539	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1541	01753	01540	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1542	01754	01541	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1543	01755	01542	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1544	01756	01543	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1545	01758	01544	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1546	01759	01545	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1547	01760	01546	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1548	01761	01547	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1549	01763	01548	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1550	01764	01549	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1551	01765	01550	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1552	01766	01551	63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1553	01767	01552	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1554	01768	01553	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1555	01769	01554	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1556	01770	01555	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1557	01771	01556	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1558	01772	01557	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1559	01773	01558	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1560	01774	01559	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1561	01775	01560	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1562	01776	01561	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1563	01777	01562	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1564	01778	01563	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1565	01779	01564	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1566	01780	01565	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1567	01781	01566	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1568	01782	01567	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1569	01783	01568	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 44

Table 45

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
1570	01784	01569	2		0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
1571	01785	01570	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99	301	1	1101	1401	
1572	01786	01571	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1573	01787	01572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1574	01788	01573	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1575	01789	01574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1576	01790	01575	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1577	01791	01576	34		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95	9	295	1	1011	1301
1578	01792	01577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1579	01793	01578	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1580	01794	01579	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1581	01795	01580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1582	01796	01581	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1583	01797	01582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1584	01798	01583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1585	01799	01584	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1586	01800	01585	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1587	01801	01586	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1588	01802	01587	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1589	01803	01588	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1590	01804	01589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1591	01805	01590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1592	01806	01591	26		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1593	01807	01592	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1594	01808	01593	47		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1595	01809	01594	19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1596	01810	01595	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1597	01811	01596	39		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1598	01812	01597	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1599	01813	01598	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1600	01814	01599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1601	01815	01600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1602	01816	01601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1603	01817	01602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1604	01818	01603	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1605	01819	01604	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BH	BI	BK	
1606	01820	01605	9		0	0	1	0	0	0	0	0	1	0	0	1	0	3	0	0	0	0	0	0	0	0	0						
1607	01821	01606	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1608	01822	01607	7		0	0	2	0	0	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
1609	01823	01608	24		0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
1610	01824	01609	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1611	01825	01610	3		0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
1612	01826	01611	6		0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
1613	01827	01612	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1614	01828	01613	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1615	01829	01614	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1616	01830	01615	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1617	01831	01616	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1618	01832	01617	8		0	0	1	0	0	0	2	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0						
1619	01833	01618	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1620	01834	01619	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1621	01835	01620	5		0	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
1622	01836	01621	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1623	01837	01622	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1624	01838	01623	2		0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
1625	01839	01624	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1626	01840	01625	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1627	01841	01626	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1628	01842	01627	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1629	01843	01628	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1630	01844	01629	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1631	01845	01630	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1632	01846	01631	2		0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1633	01847	01632	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1634	01848	01633	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1635	01849	01634	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1636	01850	01635	4		0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
1637	01851	01636	1		0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
1638	01852	01637	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1639	01853	01638	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1640	01854	01639	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1641	01855	01640	7		0	0	1	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 46



[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK			
1678	01893	01677	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1679	01895	01678	7		0	0	1	0	0	0	0	1	0	0	0	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0				
1680	01896	01679	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1681	01897	01680	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1682	01898	01681	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1683	01899	01682	14		0	0	2	0	0	0	0	2	0	0	0	3	1	0	0	1	1	3	0	0	0	0	0	0	0	0	0	1104			
1684	01900	01683	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1685	01901	01684	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1686	01902	01685	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1687	01903	01686	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2804			
1688	01904	01687	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1689	01905	01688	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1690	01906	01689	3		0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1691	01907	01690	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1692	01908	01691	21		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1693	01909	01692	4		0	0	1	0	0	0	2	0	0	0	0	0	0	0	3	9	0	1	0	0	0	0	0	0	0	0	0	1871			
1694	01910	01693	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	699			
1695	01911	01694	10		0	0	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	852		
1696	01912	01695	5		0	0	1	0	0	2	0	0	0	0	0	0	0	0	2	1	0	2	0	0	0	0	0	0	0	0	0	0			
1697	01913	01696	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2593			
1698	01914	01697	3		0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1699	01915	01698	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1700	01916	01699	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1701	01917	01700	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1702	01918	01701	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1703	01919	01702	111		0	0	5	0	1	0	3	5	6	12	3	2	0	0	7	23	5	2	3	6	22	3	0	0	0	0	0	0	0		
1704	01920	01703	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1705	01921	01704	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1706	01922	01705	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1707	01923	01706	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1708	01924	01707	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1709	01925	01708	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1710	01926	01709	24		0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1711	01927	01710	3		0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1712	01928	01711	10		0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1713	01929	01712	19		0	0	1	0	0	1	0	4	0	0	0	0	0	2	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	
1714	01930	01713	19		0	0	1	0	0	1	0	4	0	0	0	0	0	2	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 48

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	OK			
1714	01930	01713	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1715	01931	01714	4	0	0	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1716	01932	01715	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1717	01933	01716	10	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	4	1	0	0	0	0	2	0	0	0	0	0	0	0	0		
1718	01934	01717	5	0	0	1	1	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1719	01935	01718	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1720	01936	01719	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1721	01937	01720	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1722	01938	01721	3	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1723	01939	01722	3	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1724	01940	01723	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1725	01941	01724	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1726	01943	01725	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1727	01944	01726	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1728	01945	01727	7	0	0	0	1	1	0	0	0	1	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1729	01946	01728	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1730	01947	01729	6	0	0	0	1	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1731	01948	01730	4	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1732	01949	01731	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1733	01950	01732	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1734	01951	01733	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1735	01952	01734	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1736	01953	01735	17	0	0	0	2	2	0	0	0	1	0	1	0	3	0	2	0	1	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0
1737	01954	01736	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1738	01955	01737	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1739	01956	01738	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1740	01957	01739	4	0	0	0	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1741	01958	01740	6	0	0	0	1	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1742	01959	01741	5	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1743	01960	01742	6	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1744	01961	01743	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1745	01962	01744	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1746	01963	01745	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1747	01964	01746	6	0	0	0	2	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1748	01965	01747	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1749	01966	01748	8	0	0	0	0	2	0	0	0	0	0	0	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1750	01967	01749	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1751	01968	01750	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1752	01969	01751	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1753	01970	01752	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1754	01971	01753	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1755	01972	01754	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1756	01973	01755	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1757	01974	01756	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1758	01975	01757	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1759	01976	01758	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1760	01977	01759	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1761	01978	01760	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1762	01979	01761	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0</								

Table 49

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BI	BK		
1786	02007	01785	15		0	0	1	0	0	0	0	1	0	2	0	0	0	2	0	1	4	0	0	1	0	0	1	2	0	0	100	56	1	1064	1119
1787	02010	01786	7		0	0	1	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0						
1788	02011	01787	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0						
1789	02012	01788	16		0	0	2	0	0	0	2	2	0	1	0	1	0	0	0	1	0	1	1	1	3	0	0	1	0	0					
1790	02013	01789	12		0	0	2	0	0	0	0	0	2	0	0	0	0	0	0	1	2	0	0	1	1	1	0	0	0						
1791	02025	01790	8		0	0	1	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0						
1792	02039	01791	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1793	02040	01792	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1794	02041	01793	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1795	02042	01794	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1796	02043	01795	8		0	0	0	7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
1797	02044	01796	5		0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1798	02045	01797	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1799	02046	01798	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1800	02047	01799	13		0	0	0	2	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1801	02048	01800	5		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1802	02049	01801	20		0	0	0	1	0	0	1	0	0	10	0	0	0	0	0	3	0	0	4	0	0	1	0	0	0						
1803	02050	01802	5		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1804	02051	01803	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1805	02052	01804	2		0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
1806	02053	01805	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1807	02054	01806	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1808	02055	01807	2		0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1809	02056	01808	2		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1810	02057	01809	5		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1811	02058	01810	5		0	0	0	1	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1812	02059	01811	6		0	0	0	1	0	0	0	1	0	1	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0						
1813	02060	01812	8		0	0	0	1	1	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1814	02062	01813	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1815	02063	01814	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1816	02064	01815	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1817	02065	01816	2		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1818	02066	01817	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1819	02067	01818	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1820	02068	01819	3		0	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1821	02069	01820	7		0	0	0	0	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 51

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Table 53

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1858	02107	01857	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X65551	98.2 218	100 208	1 1262	1 8718	11435
1859	02108	01858	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X16609	98.2 219	98.6 70	1 1884	1 5919	7252
1860	02110	01859	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1861	02111	01860	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1862	02112	01861	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1863	02113	01862	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1864	02115	01863	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1865	02116	01864	12		0	0	0	3	2	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M12272	100 208	96.8 188	11 5234		
1866	02117	01865	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M14057	98.6 70	99.5 197	1 8075	18878	1486
1867	02118	01866	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M14982	96.8 188	95.3 191	1 1773	1963	2171
1868	02119	01867	8		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1869	02120	01868	19		0	0	0	3	12	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1870	02121	01869	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1871	02122	01870	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1872	02123	01871	28		0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1873	02124	01872	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1874	02126	01873	7		0	0	0	0	6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1875	02127	01874	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1876	02128	01875	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1877	02129	01876	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1878	02130	01877	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1879	02131	01878	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1880	02132	01879	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1881	02133	01880	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1882	02134	01881	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1883	02135	01882	6		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1884	02136	01883	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1885	02137	01884	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1886	02138	01885	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1887	02139	01886	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1888	02140	01887	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1889	02141	01888	8		0	0	0	5	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1890	02142	01889	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1891	02143	01890	3		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1892	02144	01891	8		0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1893	02145	01892	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1894	02146	01893	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1895	02147	01894	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1896	02148	01895	21		0	0	0	3	6	6	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1897	02149	01896	4		0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1898	02150	01897	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1899	02151	01898	14		0	0	0	9	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1900	02152	01899	7		0	0	0	1	0	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1901	02153	01900	6		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1902	02154	01901	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1903	02155	01902	28		0	0	0	7	3	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1904	02156	01903	8		0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1905	02157	01904	35		0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1906	02158	01905	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1907	02159	01906	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1908	02160	01907	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1909	02161	01908	9		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1910	02162	01909	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1911	02163	01910	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1912	02164	01911	5		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1913	02165	01912	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1914	02166	01913	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1915	02167	01914	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1916	02168	01915	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1917	02169	01916	9		0	0	0	2	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1918	02170	01917	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1919	02171	01918	6		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1920	02172	01919	4		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1921	02173	01920	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1922	02174	01921	25		0	0	0	4	1	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1923	02175	01922	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1924	02176	01923	13		0	0	0	3	1	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1925	02177	01924	7		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1926	02178	01925	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1927	02179	01926	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1928	02180	01927	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1929	02181	01928	14		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 54



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
1930	02182	01929	3		0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1931	02183	01930	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1932	02184	01931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1933	02185	01932	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1934	02186	01933	68		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96	99	1	1551
1935	02187	01934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1676
1936	02188	01935	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1937	02189	01936	11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1938	02191	01937	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8	83	1	842	
1939	02192	01938	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	923
1940	02193	01939	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1941	02194	01940			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1942	02195	01941	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1943	02196	01942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1944	02197	01943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1945	02198	01944	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1946	02199	01945	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1947	02200	01946	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1948	02202	01947	32		0	0	0	0	15	12	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1949	02203	01948	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1950	02204	01949	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1951	02205	01950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1952	02206	01951	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1953	02207	01952	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1954	02208	01953	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1955	02209	01954	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1956	02210	01955	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1957	02211	01956	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1958	02212	01957	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1959	02213	01958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1960	02214	01959	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1961	02215	01960	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1962	02216	01961	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1963	02237	01962	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1964	02238	01963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1965	02239	01964	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 55

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	DE	BF	BG	BH	BI	BK
1966	02240	01965	5		0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0						
1967	02241	01966	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.1	416	1	1523	1941
1968	02242	01967	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1969	02243	01968	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1970	02244	01969	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.5	399	1	610	1162
1971	02245	01970	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1972	02246	01971	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1973	02247	01972	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.7	380	1	1496	1872
1974	02248	01973	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1975	02249	01974	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.8	374	1	2279	2807
1976	02250	01975	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1977	02252	01976	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1978	02254	01977	3		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1979	02255	01978	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1980	02256	01979	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1981	02257	01980	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.1	339	1	930	1268
1982	02258	01981	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6	210	1	306	1239
1983	02259	01982	10		0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1984	02260	01983	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1985	02261	01984	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1986	02262	01985	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1987	02263	01986	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1988	02264	01987	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1989	02266	01988	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1990	02268	01989	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1991	02269	01990	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1992	02270	01991	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1993	02271	01992	12		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1994	02272	01993	9		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1995	02274	01994	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1996	02275	01995	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1997	02276	01996	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1998	02277	01997	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1999	02278	01998	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2000	02279	01999	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2001	02280	02000	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 56

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
2002	02281	02001	1																													
2003	02282	02002	1																													
2004	02283	02003	1																													
2005	02285	02004	10																													
2006	02287	02005	1																													
2007	02288	02006	1																													
2008	02289	02007	1																													
2009	02290	02008	16																													
2010	02291	02009	1																													
2011	02292	02010	1																													
2012	02293	02011	1																													
2013	02294	02012	1																													
2014	02295	02013	1																													
2015	02296	02014	2																													
2016	02297	02015	2																													
2017	02298	02016	1																													
2018	02299	02017	4																													
2019	02300	02018	3																													
2020	02301	02019	1																													
2021	02302	02020	5																													
2022	02303	02021	1																													
2023	02304	02022	1																													
2024	02305	02023	2																													
2025	02306	02024	1																													
2026	02307	02025	1																													
2027	02308	02026	3																													
2028	02309	02027	18																													
2029	02310	02028	3																													
2030	02311	02029	6																													
2031	02312	02030	5																													
2032	02313	02031	6																													
2033	02314	02032	2																													
2034	02315	02033	1																													
2035	02316	02034	12																													
2036	02317	02035	5																													
2037	02318	02036	2																													

Table 57

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BGRH	BI	BK
2038	02319	02037	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2	132	1	657	793
2039	02321	02038	7		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3	137	1	1095	1231
2040	02322	02039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.1	129	10	1673	1801
2041	02323	02040	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2042	02324	02041	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2043	02325	02042	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2044	02326	02043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2045	02327	02044	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2046	02328	02045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2047	02329	02046	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2048	02330	02047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2049	02331	02048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2050	02332	02049	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2051	02333	02050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2052	02334	02051	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2053	02336	02052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2054	02337	02053	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2055	02338	02054	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2056	02339	02055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2057	02340	02056	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2058	02341	02057	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2059	02342	02058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2060	02343	02059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2061	02345	02060	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2062	02346	02061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2063	02347	02062	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2064	02348	02063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2065	02349	02064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2066	02350	02065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2067	02351	02066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2068	02352	02067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2069	02353	02068	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2070	02354	02069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2071	02355	02070	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2072	02356	02071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2073	02357	02072	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 58

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AK	AM	AO	CA	CS	AL	AW	AY	BA	BC	BE	BF	BG	BI	BK		
2074	02358	02073	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X69078	97.9	95	1	3127	3228	
2075	02359	02074	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2076	02360	02075	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2077	02361	02076	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2078	02362	02077	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2079	02363	02078	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2080	02364	02079	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2081	02365	02080	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2082	02366	02081	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2083	02367	02082	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2084	02368	02083	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2085	02369	02084	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Y00317	98.5	67	1	2027	2093
2086	02370	02085	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2087	02371	02086	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2088	02372	02087	6		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2089	02373	02088	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2090	02374	02089	38		0	0	0	0	1	1	1	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2091	02375	02090	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2092	02376	02091	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2093	02377	02092	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X64594	100	56	1	1839	1927
2094	02378	02093	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2095	02379	02094	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2096	02380	02095	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2097	02382	02096	13		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2098	02399	02097	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2099	02400	02098	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2100	02401	02099	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2101	02402	02100	6		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2102	02403	02101	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X03557	100	273	1	1370	1642
2103	02404	02102	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2104	02406	02103	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2105	02408	02104	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2106	02409	02105	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J05037	94.8	305	1	1093	1393
2107	02411	02106	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M62401	97.4	378	1	1500	1880
2108	02412	02107	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2109	02413	02108	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 59



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
2146	02452	02145	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
2147	02453	02146	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2148	02454	02147	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2149	02455	02148	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2150	02456	02149	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2151	02457	02150	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2152	02458	02151	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2153	02459	02152	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2154	02461	02153	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2155	02462	02154	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2156	02463	02155	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2157	02464	02156	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2158	02465	02157	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2159	02466	02158	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2160	02467	02159	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2161	02468	02160	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2162	02469	02161	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2163	02471	02162	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2164	02472	02163	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2165	02473	02164	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2166	02474	02165	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2167	02475	02166	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2168	02476	02167	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2169	02477	02168	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2170	02478	02169	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2171	02479	02170	6		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2172	02480	02171	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2173	02481	02172	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2174	02482	02173	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2175	02483	02174	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2176	02484	02175	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2177	02486	02176	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2178	02487	02177	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2179	02488	02178	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2180	02489	02179	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2181	02490	02180	16		0	0	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 61





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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2218	02528	02217	2										1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2219	02529	02218	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2220	02531	02219	3										0	0	1	0	0	0	0	0	0	0	0	0	0	1	0						
2221	02532	02220	3										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2222	02534	02221	5										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2223	02535	02222	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2224	02537	02223	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2225	02538	02224	2										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2226	02540	02225	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2227	02542	02226	33										0	0	12	1	0	0	0	0	0	0	0	0	0	0	0						
2228	02543	02227	2										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2229	02544	02228	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2230	02545	02229	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2231	02546	02230	19										0	0	18	0	0	0	0	0	0	0	0	0	0	0	0						
2232	02547	02231	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2233	02548	02232	8										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2234	02549	02233	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2235	02551	02234	2										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2236	02552	02235	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2237	02553	02236	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2238	02554	02237	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2239	02555	02238	8										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2240	02556	02239	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2241	02557	02240	5										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2242	02559	02241	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2243	02560	02242	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2244	02562	02243	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2245	02563	02244	5										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2246	02564	02245	5										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2247	02565	02246	4										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2248	02567	02247	2										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2249	02568	02248	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2250	02569	02249	3										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2251	02570	02250	2										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2252	02571	02251	9										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2253	02572	02252	1										0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 63

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2254	02573	02253	1		0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2255	02574	02254	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2256	02575	02255	3		0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2257	02576	02256	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2258	02577	02257	3		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2259	02578	02258	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2260	02580	02259	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2261	02581	02260	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2262	02582	02261	5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2263	02583	02262	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2264	02585	02263	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2265	02586	02264	5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2266	02588	02265	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2267	02589	02266	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2268	02590	02267	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2269	02591	02268	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2270	02592	02269	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2271	02593	02270	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2272	02612	02271	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2273	02627	02272	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2274	02628	02273	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2275	02629	02274	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2276	02630	02275	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2277	02631	02276	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2278	02632	02277	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2279	02633	02278	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2280	02634	02279	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2281	02635	02280	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2282	02637	02281	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2283	02638	02282	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2284	02639	02283	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2285	02640	02284	9		0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2286	02641	02285	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2287	02642	02286	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2288	02643	02287	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2289	02644	02288	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2290	02645	02289	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2291	02646	02290	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2292	02648	02291	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2293	02650	02292	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2294	02651	02293	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2295	02652	02294	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2296	02653	02295	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2297	02654	02296	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2298	02656	02297	20		0	0	0	0	0	0	3	3	0	0	1	2	0	2	3	2	0	0	0	0	0	0	0						
2299	02657	02298	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2300	02658	02299	6		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2301	02659	02300	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2302	02660	02301	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2303	02661	02302	3		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2304	02662	02303	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2305	02663	02304	4		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2306	02664	02305	5		0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2307	02665	02306	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2308	02666	02307	2		0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2309	02667	02308	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2310	02668	02309	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2311	02669	02310	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2312	02670	02311	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2313	02672	02312	5		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2314	02673	02313	5		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2315	02675	02314	2		0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2316	02676	02315	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2317	02677	02316	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2318	02678	02317	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2319	02679	02318	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2320	02680	02319	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2321	02681	02320	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2322	02682	02321	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2323	02684	02322	13		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2324	02685	02323	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2325	02686	02324	1		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2326	02687	02325	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2327	02688	02326	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2328	02689	02327	4		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2329	02690	02328	4		0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2330	02691	02329	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2331	02692	02330	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2332	02693	02331	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2333	02694	02332	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2334	02695	02333	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2335	02696	02334	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2336	02697	02335	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2337	02698	02336	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2338	02699	02337	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2339	02700	02338	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2340	02701	02339	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2341	02702	02340	5		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2342	02703	02341	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2343	02704	02342	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2344	02705	02343	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2345	02706	02344	13		0	0	0	0	0	0	2	0	0	0	0	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2346	02707	02345	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2347	02708	02346	8		0	0	0	0	0	0	2	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2348	02709	02347	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2349	02710	02348	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2350	02711	02349	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2351	02712	02350	8		0	0	0	0	0	0	1	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2352	02713	02351	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2353	02714	02352	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2354	02715	02353	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2355	02716	02354	18		0	0	0	0	0	0	2	8	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2356	02717	02355	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2357	02718	02356	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2358	02719	02357	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2359	02721	02358	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2360	02722	02359	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2361	02723	02360	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 66



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2398	02765	02397	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2399	02767	02398	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2400	02768	02399	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2401	02769	02400	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2402	02770	02401	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2403	02771	02402	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2404	02772	02403	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2405	02773	02404	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2406	02774	02405	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2407	02775	02406	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2408	02776	02407	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2409	02777	02408	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2410	02778	02409	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2411	02779	02410	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2412	02780	02411	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2413	02781	02412	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2414	02782	02413	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2415	02783	02414	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2416	02785	02415	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2417	02786	02416	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2418	02787	02417	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2419	02788	02418	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2420	02789	02419	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2421	02790	02420	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2422	02791	02421	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2423	02792	02422	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2424	02793	02423	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2425	02794	02424	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2426	02795	02425	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2427	02796	02426	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2428	02797	02427	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2429	02798	02428	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2430	02799	02429	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2431	02800	02430	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2432	02801	02431	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2433	02802	02432	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 68

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK		
2434	02803	02433	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
2435	02804	02434	5		0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	2	0								
2436	02805	02435	4		0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0							
2437	02806	02436	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2438	02807	02437	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2439	02808	02438	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2440	02809	02439	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2441	02810	02440	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X70991	95.4	174	1	2015	2192	
2442	02811	02441	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2443	02812	02442	12		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	165	1	3377	3541	
2444	02813	02443	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2445	02814	02444	15		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2446	02815	02445	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2447	02816	02446	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2448	02817	02447	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2449	02818	02448	5		0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2450	02819	02449	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2451	02820	02450	29		0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X02490	91.9	135	14	435	568	
2452	02821	02451	22		0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	X68277	93.4	409	1	1601	2000
2453	02822	02452	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2454	02823	02453	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2455	02824	02454	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2456	02825	02455	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2457	02826	02456	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2458	02827	02457	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2459	02828	02458	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.7	158	1	4303	4460
2460	02829	02459	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
2461	02830	02460	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2462	02831	02461	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2463	02832	02462	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2464	02833	02463	7		0	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	90.4	407	1	4603	5122
2465	02834	02464	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2466	02835	02465	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2467	02836	02466	3		0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.7	150	1	1084	1233
2468	02837	02467	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2469	02838	02468	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 69

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2470	02839	02469	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2471	02840	02470	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2472	02843	02471	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2473	02844	02472	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2474	02845	02473	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2475	02846	02474	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2476	02847	02475	11		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2477	02848	02476	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2478	02849	02477	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2479	02850	02478	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2480	02851	02479	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2481	02852	02480	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2482	02853	02481	8		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2483	02854	02482	4		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2484	02855	02483	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2485	02856	02484	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2486	02857	02485	3		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2487	02858	02486	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2488	02859	02487	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2489	02860	02488	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2490	02861	02489	10		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2491	02862	02490	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2492	02863	02491	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2493	02864	02492	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2494	02865	02493	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2495	02866	02494	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2496	02867	02495	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2497	02868	02496	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2498	02869	02497	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2499	02870	02498	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2500	02872	02499	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2501	02873	02500	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2502	02874	02501	6		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2503	02875	02502	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2504	02876	02503	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2505	02877	02504	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 70



Table 71

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AO	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2506	02878	02505	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2507	02879	02506	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2508	02880	02507	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2509	02881	02508	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2510	02882	02509	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2511	02883	02510	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2512	02884	02511	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2513	02885	02512	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2514	02886	02513	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2515	02887	02514	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2516	02888	02515	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2517	02889	02516	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2518	02890	02517	6		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2519	02891	02518	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2520	02893	02519	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2521	02894	02520	89		0	0	0	0	0	0	87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2522	02895	02521	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2523	02896	02522	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2524	02897	02523	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2525	02898	02524	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2526	02899	02525	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2527	02900	02526	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2528	02901	02527	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2529	02902	02528	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2530	02903	02529	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2531	02904	02530	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2532	02905	02531	8		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2533	02906	02532	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2534	02907	02533	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2535	02908	02534	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2536	02909	02535	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2537	02910	02536	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2538	02911	02537	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2539	02912	02538	3		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2540	02913	02539	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2541	02914	02540	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2542	02915	02541	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0						
2543	02916	02542	8		0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	2	3	0	0	0	0	0	0						
2544	02917	02543	3		0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0						
2545	02919	02544	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2546	02920	02545	3		0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0						
2547	02921	02546	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2548	02922	02547	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
2549	02923	02548	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2550	02924	02549	3		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
2551	02925	02550	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2552	02926	02551	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2553	02927	02552	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2554	02928	02553	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
2555	02929	02554	4		0	0	0	0	0	0	1	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0						
2556	02930	02555	2		0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0						
2557	02931	02556	15		0	0	0	0	0	0	1	1	0	0	1	0	0	0	6	0	1	0	2	0	0	0	1						
2558	02932	02557	4		0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
2559	02933	02558	2		0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
2560	02934	02559	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2561	02935	02560	4																														

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK
2614	02999	02613	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2615	03002	02614	3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2616	03005	02615	3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2617	03028	02616	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2618	03030	02617	3	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2619	03031	02618	3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2620	03053	02619	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2621	03055	02620	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2622	03056	02621	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2623	03058	02622	3	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2624	03059	02623	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2625	03060	02624	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2626	03061	02625	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2627	03062	02626	6	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2628	03063	02627	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2629	03064	02628	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2630	03065	02629	4	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2631	03066	02630	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2632	03067	02631	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2633	03068	02632	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2634	03069	02633	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2635	03070	02634	3	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2636	03071	02635	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2637	03072	02636	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2638	03073	02637	5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2639	03074	02638	44	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2640	03075	02639	5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2641	03077	02640	5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2642	03078	02641	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2643	03079	02642	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2644	03080	02643	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2645	03081	02644	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2646	03082	02645	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2647	03083	02646	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2648	03084	02647	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2649	03085	02648	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 74

Table 75

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AI	AK	AM	AN	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
2650	03086	02649	5		0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3	298	1	394	691
2651	03087	02650	8		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	545630				
2652	03088	02651	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2653	03089	02652	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2654	03090	02653	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2655	03091	02654	1		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
2656	03092	02655	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2657	03094	02656	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2658	03095	02657	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2659	03096	02658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2660	03097	02659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2661	03098	02660	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2662	03099	02661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2663	03100	02662	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2664	03101	02663	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2665	03102	02664	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2666	03103	02665	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2667	03104	02666	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2668	03105	02667	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2669	03106	02668	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2670	03108	02669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2671	03109	02670	13		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2672	03110	02671	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2673	03111	02672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2674	03112	02673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2675	03115	02674	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2676	03116	02675	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2677	03117	02676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2678	03118	02677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2679	03119	02678	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2680	03120	02679	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2681	03121	02680	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2682	03122	02681	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2683	03123	02682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2684	03124	02683	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2685	03125	02684	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AO	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
2686	03126	02685	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
2687	03127	02686	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2688	03128	02687	19		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96	224	1	500	725	
2689	03129	02688	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2690	03131	02689	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2691	03132	02690	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2692	03133	02691	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2693	03134	02692	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2694	03135	02693	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2695	03136	02694	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2696	03138	02695	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98	5	205	1	507	719
2697	03139	02696	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2698	03140	02697	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2699	03141	02698	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2700	03142	02699	9		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2701	03145	02700	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99	5	210	1	1121	1330
2702	03146	02701	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2703	03147	02702	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2704	03148	02703	12		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2705	03149	02704	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2706	03150	02705	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2707	03151	02706	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2708	03152	02707	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2709	03153	02708	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2710	03154	02709	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2711	03155	02710	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2712	03156	02711	15		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2713	03157	02712	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2714	03159	02713	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2715	03160	02714	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2716	03162	02715	4		0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2717	03163	02716	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2718	03164	02717	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2719	03166	02718	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2720	03167	02719	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2721	03168	02720	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 76

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2722	03169	02721	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2723	03170	02722	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2724	03171	02723	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2725	03172	02724	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2726	03173	02725	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2727	03175	02726	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2728	03176	02727	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2729	03177	02728	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2730	03178	02729	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2731	03179	02730	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2732	03180	02731	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2733	03181	02732	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2734	03182	02733	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2735	03183	02734	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2736	03185	02735	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2737	03186	02736	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2738	03187	02737	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2739	03188	02738	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2740	03189	02739	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2741	03190	02740	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2742	03192	02741	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2743	03193	02742	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2744	03194	02743	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2745	03195	02744	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2746	03196	02745	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2747	03197	02746	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2748	03198	02747	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2749	03200	02748	52		0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2750	03201	02749	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2751	03202	02750	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2752	03204	02751	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2753	03205	02752	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2754	03206	02753	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2755	03207	02754	9		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2756	03208	02755	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2757	03212	02756	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 77

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBI	BI	BK
2758	03213	02757	3		0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0					
2759	03214	02758	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2760	03215	02759	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2761	03216	02760	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.3	406	1	3055	3634
2762	03217	02761	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2763	03218	02762	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2764	03219	02763	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2765	03220	02764	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2766	03221	02765	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2767	03222	02766	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2768	03223	02767	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2769	03224	02768	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2770	03225	02769	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2771	03227	02770	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2772	03229	02771	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2773	03230	02772	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2774	03231	02773	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2775	03233	02774	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2776	03234	02775	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2777	03235	02776	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2778	03236	02777	2		0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2779	03237	02778	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2780	03239	02779	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2781	03240	02780	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2782	03241	02781	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2783	03242	02782	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2784	03243	02783	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2785	03244	02784	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2786	03245	02785	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2787	03247	02786	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2788	03248	02787	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2789	03249	02788	6		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2790	03251	02789	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2791	03252	02790	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2792	03253	02791	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2793	03255	02792	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 78





	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AK	AM	AQ	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK
2830	03326	02829	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2831	03331	02830	24	0	0	0	0	0	0	0	0	1	10	1	0	0	0	0	0	0	0	0	0	0	0	0					
2832	03332	02831	6	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
2833	03356	02832	2	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
2834	03374	02833	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
2835	03375	02834	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2836	03376	02835	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2837	03377	02836	4	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
2838	03378	02837	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2839	03379	02838	3	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
2840	03380	02839	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2841	03381	02840	3	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2842	03382	02841	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2843	03383	02842	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2844	03384	02843	3	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2845	03385	02844	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2846	03386	02845	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2847	03387	02846	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2848	03388	02847	3	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2849	03389	02848	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2850																															

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	IA	AK	MA	QA	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2866	03406	02865	2										2	0	0	0	0	0	0	0	0	0	0	0	0	0						
2867	03407	02866	1										1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2868	03408	02867	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2869	03409	02868	2										2	0	0	0	0	0	0	0	0	0	0	0	0	0						
2870	03410	02869	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2871	03411	02870	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2872	03412	02871	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2873	03413	02872	3										2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2	323	1	7170	7496
2874	03414	02873	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2875	03415	02874	2										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2876	03416	02875	4										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2877	03417	02876	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2878	03418	02877	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2879	03419	02878	7										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2880	03420	02879	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2881	03421	02880	4										2	1	0	0	0	0	0	0	0	0	0	0	0	0						
2882	03422	02881	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2883	03423	02882	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2884	03424	02883	4										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2885	03426	02884	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2886	03427	02885	2										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2887	03428	02886	3										2	0	0	0	0	0	0	0	0	0	0	0	0	0						
2888	03429	02887	4										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2889	03430	02888	4										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2890	03431	02889	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2891	03432	02890	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2892	03433	02891	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2893	03434	02892	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2894	03435	02893	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2895	03436	02894	3										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2896	03437	02895	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2897	03438	02896	1										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2898	03439	02897	6										0	2	0	0	0	0	0	0	0	0	0	0	0	0						
2899	03440	02898	2										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2900	03441	02899	4										0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2901	03442	02900	2										2	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 81

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AI	AK	AM	AO	AS	AW	AY	B	BC	DE	BF	BG	BH	BI	BK
2938	03480	02937	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2939	03481	02938	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2940	03482	02939	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2941	03483	02940	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2942	03484	02941	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2943	03485	02942	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2944	03486	02943	7		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2945	03487	02944	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2946	03488	02945	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2947	03489	02946	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2948	03490	02947	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2949	03491	02948	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2950	03492	02949	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2951	03493	02950	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2952	03494	02951	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2953	03495	02952	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2954	03496	02953	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2955	03497	02954	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2956	03498	02955	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2957	03499	02956	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2958	03500	02957	4		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0							
2959	03501	02958	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2960	03502	02959	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2961	03503	02960	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2962	03504	02961	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2963	03505	02962	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2964	03506	02963	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2965	03507	02964	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2966	03508	02965	3		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0							
2967	03509	02966	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2968	03510	02967	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2969	03511	02968	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2970	03512	02969	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2971	03513	02970	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2972	03514	02971	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
2973	03515	02972	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							

Table 83

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AL	AK	AN	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BI	BK
2974	03516	02973	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2975	03517	02974	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2976	03518	02975	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2977	03519	02976	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2978	03520	02977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2979	03521	02978	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2980	03522	02979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2981	03523	02980	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2982	03524	02981	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2983	03525	02982	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2984	03526	02983	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2985	03527	02984	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2986	03528	02985	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2987	03529	02986	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2988	03530	02987	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2989	03531	02988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2990	03532	02989	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2991	03533	02990	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2992	03534	02991	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2993	03535	02992	9		0																												

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
3010	03552	03009	4	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0					
3011	03553	03010	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3012	03554	03011	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3013	03555	03012	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3014	03556	03013	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3015	03557	03014	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3016	03558	03015	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3017	03559	03016	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3018	03560	03017	4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3019	03561	03018	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3020	03562	03019	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3021	03563	03020	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3022	03564	03021	11	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3023	03565	03022	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3024	03566	03023	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3025	03567	03024	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3026	03568	03025	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3027	03569	03026	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3028	03570	03027	4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3029	03571	03028	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3030	03572	03029	3	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3031	03573	03030	9	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3032	03574	03031	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3033	03575	03032	17	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3034	03576	03033	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3035	03577	03034	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3036	03578	03035	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3037	03579	03036	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3038	03580	03037	3	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3039	03581	03038	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3040	03582	03039	6	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3041	03583	03040	4	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3042	03584	03041	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3043	03585	03042	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3044	03586	03043	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3045	03587	03044	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 85

[illegible]





	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3118	03603	03117	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3119	03604	03118	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3120	03605	03119	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3121	03606	03120	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3122	03608	03121	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3123	03609	03122	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3124	03600	03123	4	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3125	03691	03124	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3126	03693	03125	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3127	03694	03126	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3128	03695	03127	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3129	03696	03128	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3130	03697	03129	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3131	03698	03130	13	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3132	03699	03131	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3133	03701	03132	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3134	03702	03133	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3135	03703	03134	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3136	03704	03135	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
3154	03723	03153	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3155	03724	03154	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3156	03725	03155	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3157	03726	03156	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3158	03727	03157	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3159	03728	03158	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3160	03729	03159	3		0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3161	03730	03160	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3162	03731	03161	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3163	03732	03162	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3164	03733	03163	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3165	03734	03164	7		0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3166	03736	03165	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3167	03737	03166	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3168	03738	03167	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3169	03739	03168	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3170	03740	03169	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3171	03741	03170	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3172	03742	03171	3		0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3173	03743	03172	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3174	03744	03173	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3175	03745	03174	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3176	03746	03175	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3177	03747	03176	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3178	03748	03177	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3179	03749	03178	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3180	03750	03179	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3181	03751	03180	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3182	03752	03181	8		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3183	03753	03182	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3184	03754	03183	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3185	03755	03184	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3186	03756	03185	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3187	03757	03186	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3188	03758	03187	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3189	03759	03188	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 89

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3190	03760	03189	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3191	03761	03190	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3192	03762	03191	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3193	03763	03192	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3194	03764	03193	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3195	03765	03194	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3196	03766	03195	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3197	03767	03196	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3198	03768	03197	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3199	03769	03198	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3200	03770	03199	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3201	03771	03200	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3202	03772	03201	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3203	03773	03202	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3204	03774	03203	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3205	03775	03204	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3206	03776	03205	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3207	03777	03206	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3208	03778	03207	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3209	03779	03208	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3210	03780	03209	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3211	03781	03210	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3212	03782	03211	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3213	03783	03212	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3214	03784	03213	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3215	03785	03214	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3216	03786	03215	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3217	03787	03216	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3218	03788	03217	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3219	03789	03218	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3220	03790	03219	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3221	03791	03220	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3222	03792	03221	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3223	03793	03222	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3224	03794	03223	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3225	03795	03224	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 90

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AK	AM	AN	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
3226	03796	03225	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3227	03797	03226	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3228	03798	03227	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3229	03799	03228	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3230	03800	03229	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3231	03801	03230	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3232	03802	03231	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3233	03803	03232	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3234	03804	03233	7		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3235	03805	03234	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3236	03806	03235	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3237	03807	03236	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3238	03808	03237	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3239	03809	03238	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3240	03810	03239	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3241	03811	03240	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3242	03812	03241	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3243	03813	03242	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3244	03814	03243	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3245	03815	03244	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3246	03816	03245	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3247	03817	03246	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3248	03818	03247	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3249	03819	03248	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3250	03820	03249	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3251	03821	03250	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3252	03822	03251	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3253	03823	03252	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3254	03824	03253	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3255	03825	03254	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3256	03826	03255	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3257	03827	03256	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3258	03828	03257	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3259	03829	03258	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3260	03830	03259	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3261	03831	03260	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					

Table 91

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK
3262	03832	03261	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3263	03833	03262	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3264	03835	03263	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3265	03836	03264	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3266	03837	03265	13	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	7	1	0	0	0	0	0	0	0	0	0	0	0	0
3267	03838	03266	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3268	03839	03267	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3269	03840	03268	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3270	03841	03269	3	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3271	03842	03270	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3272	03843	03271	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3273	03844	03272	50	0	0	0	0	0	0	0	0	0	0	25	0	0	0	0	8	3	0	9	0	5	0	0	0	0	0	0	0	0
3274	03845	03273	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3275	03846	03274	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3276	03847	03275	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3277	03848	03276	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
3278	03849	03277	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
3279	03850	03278	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3280	03851	03279																														

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3298	03870	03297	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3299	03871	03298	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0						
3300	03872	03299	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3301	03873	03300	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3302	03874	03301	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3303	03875	03302	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3304	03876	03303	5		0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	1	0	0						
3305	03877	03304	2		0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0						
3306	03878	03305	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3307	03879	03306	7		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0						
3308	03880	03307	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3309	03881	03308	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3310	03882	03309	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3311	03883	03310	1		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3312	03884	03311	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3313	03885	03312	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3314	03886	03313	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3315	03887	03314	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3316	03888	03315	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3317	03889	03316	4		0</																												

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3370	03942	03369	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3371	03943	03370	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3372	03944	03371	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3373	03945	03372	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3374	03946	03373	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3375	03947	03374	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3376	03948	03375	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3377	03949	03376	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3378	03951	03377	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3379	03952	03378	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3380	03954	03379	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3381	03955	03380	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3382	03956	03381	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3383	03958	03382	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3384	03959	03383	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3385	03960	03384	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3386	03961	03385	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3387	03962	03386	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3388	03963	03387	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3389	03964	03388	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3390	03965	03389	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3391	03966	03390	15		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3392	03967	03391	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3393	03968	03392	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3394	03969	03393	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3395	03971	03394	8		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3396	03972	03395	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3397	03973	03396	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3398	03974	03397	5		0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3399	03975	03398	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3400	03976	03399	5		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3401	03977	03400	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3402	03978	03401	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3403	03979	03402	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3404	03980	03403	8		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3405	03981	03404	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

Table 95

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3406	03982	03405	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3407	03984	03406	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3408	03985	03407	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3409	03986	03408	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3410	03987	03409	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3411	03988	03410	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3412	03989	03411	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3413	03993	03412	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3414	04020	03413	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3415	04021	03414	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3416	04022	03415	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3417	04023	03416	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3418	04024	03417	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3419	04025	03418	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3420	04026	03419	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3421	04028	03420	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3422	04029	03421	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3423	04030	03422	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3424	04031	03423	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3425	04032	03424	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3426	04033	03425	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3427	04034	03426	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3428	04035	03427	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3429	04036	03428	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3430	04037	03429	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3431	04039	03430	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3432	04040	03431	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3433	04041	03432	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3434	04042	03433	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3435	04044	03434	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3436	04045	03435	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3437	04046	03436	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3438	04047	03437	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3439	04048	03438	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3440	04049	03439	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3441	04050	03440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 96

Table 97

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3442	04051	03441	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0						
3443	04052	03442	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3444	04053	03443	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3445	04054	03444	9		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3446	04055	03445	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3447	04056	03446	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3448	04057	03447	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3449	04058	03448	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3450	04059	03449	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3451	04060	03450	4		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3452	04061	03451	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3453	04062	03452	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3454	04063	03453	4		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3455	04064	03454	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3456	04065	03455	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3457	04066	03456	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3458	04067	03457	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3459	04068	03458	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3460	04069	03459	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3461	04070	03460	3		0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0						
3462	04071	03461	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3463	04072	03462	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3464	04073	03463	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3465	04074	03464	5		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3466	04075	03465	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3467	04076	03466	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3468	04077	03467	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3469	04078	03468	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3470	04079	03469	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3471	04080	03470	10		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3472	04081	03471	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3473	04082	03472	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3474	04083	03473	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3475	04084	03474	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3476	04086	03475	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3477	04087	03476	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3478	04088	03477	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3479	04089	03478	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3480	04090	03479	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3481	04091	03480	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3482	04092	03481	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3483	04093	03482	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3484	04094	03483	13		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3485	04095	03484	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3486	04096	03485	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3487	04097	03486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3488	04098	03487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3489	04099	03488	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3490	04100	03489	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3491	04101	03490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3492	04102	03491	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3493	04103	03492	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3494	04104	03493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3495	04105	03494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3496	04106	03495	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3497	04107	03496	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3498	04108	03497	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3499	04109	03498	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3500	04110	03499	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3501	04111	03500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3502	04112	03501	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3503	04113	03502	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3504	04114	03503	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3505	04115	03504	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3506	04116	03505	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3507	04117	03506	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3508	04118	03507	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3509	04119	03508	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3510	04120	03509	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3511	04121	03510	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3512	04122	03511	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3513	04123	03512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
3514	04125	03513	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3515	04126	03514	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3516	04127	03515	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3517	04128	03516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3518	04129	03517	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3519	04130	03518	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3520	04131	03519	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3521	04132	03520	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3522	04133	03521	7		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3523	04134	03522	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3524	04135	03523	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3525	04136	03524	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3526	04137	03525	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3527	04139	03526	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3528	04140	03527	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3529	04141	03528	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3530	04142	03529	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3531	04143	03530	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3532	04144	03531	11		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3533	04145	03532	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3534	04146	03533	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3535	04147	03534	6		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3536	04148	03535	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3537	04149	03536	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3538	04150	03537	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3539	04151	03538	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3540	04152	03539	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3541	04153	03540	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3542	04154	03541	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3543	04155	03542	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3544	04156	03543	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3545	04157	03544	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3546	04158	03545	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3547	04159	03546	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3548	04160	03547	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3549	04161	03548	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3550	04162	03549	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3551	04163	03550	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3552	04164	03551	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3553	04165	03552	6		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3554	04166	03553	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	03592	96.1	127	1	990	1116
3555	04167	03554	5		0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	056738	96.2	132	1	533	1452
3556	04169	03555	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3557	04170	03556	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3558	04171	03557	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3559	04172	03558	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3560	04173	03559	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3561	04174	03560	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3562	04175	03561	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3563	04176	03562	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3564	04177	03563	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3565	04179	03564	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3566	04180	03565	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3567	04181	03566	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3568	04182	03567	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3569	04183	03568	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3570	04184	03569	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3571	04186	03570	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3572	04187	03571	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3573	04188	03572	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3574	04189	03573	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3575	04190	03574	10		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3576	04191	03575	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3577	04192	03576	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3578	04193	03577	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3579	04194	03578	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3580	04195	03579	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3581	04196	03580	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3582	04197	03581	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3583	04198	03582	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3584	04199	03583	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3585	04200	03584	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
3586	04201	03585	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0					
3587	04202	03586	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3588	04203	03587	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3589	04204	03588	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3590	04205	03589	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3591	04206	03590	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3592	04207	03591	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3593	04210	03592	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3594	04211	03593	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3595	04213	03594	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3596	04214	03595	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3597	04215	03596	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3598	04216	03597	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3599	04218	03598	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3600	04219	03599	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3601	04220	03600	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3602	04247	03601	3		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
3603	04248	03602	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3604	04249	03603	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3605	04250	03604	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3606	04252	03605	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3607	04253	03606	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3608	04256	03607	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3609	04257	03608	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3610	04258	03609	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3611	04259	03610	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3612	04261	03611	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3613	04264	03612	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3614	04265	03613	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3615	04266	03614	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
3616	04267	03615	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
3617	04268	03616	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3618	04269	03617	3		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
3619	04270	03618	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3620	04271	03619	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
3621	04272	03620	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					

Table 101

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AL	AM	AN	AO	AS	AW	AY	BAB	BE	BF	BG	BH	BI	BK
3622	04273	03621	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3623	04274	03622	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3624	04275	03623	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0						
3625	04276	03624	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3626	04278	03625	4		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0						
3627	04279	03626	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3628	04280	03627	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3629	04281	03628	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3630	04282	03629	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3631	04284	03630	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3632	04285	03631	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3633	04286	03632	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3634	04287	03633	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0						
3635	04288	03634	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0						
3636	04289	03635	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0						
3637	04290	03636	8		0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0						
3638	04291	03637	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3639	04292	03638	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3640	04293	03639	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3641	04294	03640	6		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0							



[illegible]

Table 104

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
3730	04388	03729	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3731	04389	03730	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3732	04390	03731	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3733	04391	03732	3		0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0					
3734	04392	03733	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3735	04393	03734	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3736	04394	03735	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3737	04395	03736	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3738	04396	03737	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3739	04397	03738	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3740	04398	03739	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3741	04399	03740	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3742	04400	03741	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3743	04401	03742	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3744	04402	03743	7		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3745	04403	03744	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3746	04404	03745	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3747	04405	03746	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3748	04406	03747	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3749	04407	03748	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3750	04408	03749	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3751	04409	03750	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3752	04410	03751	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3753	04411	03752	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3754	04412	03753	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3755	04414	03754	5		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3756	04415	03755	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3757	04416	03756	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3758	04417	03757	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3759	04418	03758	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3760	04419	03759	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3761	04420	03760	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3762	04421	03761	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3763	04422	03762	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3764	04423	03763	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3765	04424	03764	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					

Table 105

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
3766	04425	03765	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3767	04426	03766	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3768	04427	03767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3769	04428	03768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3770	04429	03769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3771	04430	03770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3772	04431	03771	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3773	04432	03772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3774	04433	03773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3775	04434	03774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3776	04435	03775	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3777	04436	03776	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3778	04437	03777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3779	04439	03778	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3780	04440	03779	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3781	04441	03780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3782	04442	03781	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3783	04443	03782	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3784	04445	03783	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3785	04446	03784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3786	04447	03785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3787	04448	03786	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3788	04449	03787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3789	04450	03788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3790	04452	03789	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3791	04453	03790	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3792	04454	03791	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3793	04455	03792	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3794	04456	03793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3795	04457	03794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3796	04460	03795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3797	04462	03796	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3798	04463	03797	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3799	04464	03798	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3800	04465	03799	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3801	04466	03800	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 106



A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
3838	04511	03837	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3839	04512	03838	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3840	04513	03839	2	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3841	04514	03840	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0					
3842	04515	03841	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3843	04516	03842	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3844	04517	03843	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3845	04518	03844	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0					
3846	04519	03845	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3847	04520	03846	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3848	04521	03847	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3849	04522	03848	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3850	04523	03849	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3851	04525	03850	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3852	04527	03851	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3853	04528	03852	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3854	04529	03853	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3855	04530	03854	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3856	04531	03855	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3857	04532	03856	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0					
3858	04533	03857	4	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0</										

Table 109

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3874	04597	03873	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3875	04598	03874	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3876	04599	03875	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3877	04600	03876	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3878	04601	03877	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3879	04602	03878	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3880	04603	03879	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3881	04604	03880	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3882	04605	03881	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3883	04606	03882	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3884	04607	03883	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3885	04608	03884	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3886	04609	03885	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3887	04610	03886	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3888	04611	03887	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3889	04612	03888	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3890	04613	03889	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3891	04614	03890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3892	04615	03891	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3893	04616	03892	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3894	04617	03893	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3895	04618	03894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3896	04619	03895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3897	04620	03896	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3898	04621	03897	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3899	04623	03898	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3900	04624	03899	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3901	04625	03900	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3902	04626	03901	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3903	04627	03902	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3904	04628	03903	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3905	04629	03904	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3906	04630	03905	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3907	04631	03906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3908	04632	03907	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3909	04633	03908	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AI	AK	AM	AO	AS	AL	AW	AY	BABC	BE	BF	BG	BH	BI	BK
3910	04634	03909	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3911	04635	03910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
3912	04636	03911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3913	04637	03912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3914	04638	03913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3915	04639	03914	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3916	04640	03915	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3917	04641	03916	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3918	04642	03917	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3919	04643	03918	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3920	04644	03919	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3921	04645	03920	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3922	04646	03921	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3923	04647	03922	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3924	04648	03923	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3925	04649	03924	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3926	04650	03925	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3927	04651	03926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3928	04652	03927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3929	04653	03928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3930	04654	03929	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3931	04655	03930	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3932	04656	03931	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3933	04657	03932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3934	04658	03933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3935	04659	03934	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3936	04660	03935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3937	04661	03936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3938	04662	03937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3939	04663	03938	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3940	04664	03939	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3941	04665	03940	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3942	04666	03941	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3943	04667	03942	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3944	04668	03943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3945	04669	03944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 110



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
3946	04670	03945	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3947	04671	03946	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3948	04672	03947	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3949	04673	03948	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3950	04674	03949	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3951	04675	03950	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3952	04676	03951	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0					
3953	04677	03952	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3954	04678	03953	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3955	04679	03954	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3956	04680	03955	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3957	04681	03956	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3958	04682	03957	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3959	04683	03958	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3960	04684	03959	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3961	04685	03960	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3962	04686	03961	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3963	04687	03962	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3964	04688	03963	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3965	04689	03964	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3966	04690	03965	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3967	04691	03966	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3968	04692	03967	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3969	04693	03968	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3970	04694	03969	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3971	04695	03970	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3972	04696	03971	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3973	04697	03972	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3974	04698	03973	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3975	04699	03974	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3976	04700	03975	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3977	04701	03976	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3978	04702	03977	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3979	04703	03978	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3980	04704	03979	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3981	04705	03980	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					

Table 111

Table 112

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BI	BK
3982	04706	03981	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3983	04707	03982	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3984	04708	03983	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3985	04709	03984	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3986	04710	03985	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3987	04711	03986	7		0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3988	04712	03987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3989	04713	03988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3990	04714	03989	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3991	04715	03990	5		0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0
3992	04716	03991	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3993	04717	03992	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3994	04718	03993	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3995	04719	03994	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3996	04720	03995	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3997	04721	03996	4		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3998	04722	03997	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3999	04723	03998	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4000	04724	03999	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4001	04725	04000	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4002	04728	04001	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4003	04729	04002	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4004	04730	04003	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4005	04732	04004	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4006	04733	04005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4007	04734	04006	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4008	04735	04007	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4009	04736	04008	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4010	04737	04009	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4011	04738	04010	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4012	04739	04011	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4013	04740	04012	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4014	04741	04013	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4015	04742	04014	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4016	04743	04015	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4017	04744	04016	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4018	04745	04017	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4019	04746	04018	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4020	04747	04019	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4021	04748	04020	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4022	04750	04021	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4023	04751	04022	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4024	04752	04023	3		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4025	04753	04024	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4026	04754	04025	8		0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0	0						
4027	04755	04026	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4028	04756	04027	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4029	04757	04028	5		0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0						
4030	04758	04029	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4031	04759	04030	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4032	04760	04031	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4033	04761	04032	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4034	04762	04033	6		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4035	04763	04034	4		0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0						
4036	04764	04035	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4037	04765	04036	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4038	04766	04037	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4039	04767	04038	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4040	04768	04039	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4041	04769	04040	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4042	04770	04041	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4043	04771	04042	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4044	04772	04043	4		0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0						
4045	04773	04044	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4046	04774	04045	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4047	04775	04046	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4048	04776	04047	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4049	04777	04048	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4050	04778	04049	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4051	04779	04050	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4052	04780	04051	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4053	04781	04052	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						

Table 113

Table 114

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	ACA	AF	AG	AI	AK	AMA	ACA	AS	AL	AW	AY	BA	BC	BE	BF	BG	BI	DK
4090	04819	04089	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4091	04820	04090	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4092	04821	04091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4093	04822	04092	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4094	04823	04093	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4095	04824	04094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4096	04826	04095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4097	04827	04096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4098	04828	04097	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4099	04829	04098	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4100	04830	04099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4101	04831	04100	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4102	04832	04101	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4103	04833	04102	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4104	04834	04103	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4105	04835	04104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4106	04836	04105	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4107	04837	04106	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4108	04838	04107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4109	04839	04108	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4110	04840	04109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4111	04841	04110	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4112	04842	04111	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4113	04843	04112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4114	04844	04113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4115	04845	04114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4116	04846	04115	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4117	04847	04116	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4118	04848	04117	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4119	04850	04118	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4120	04851	04119	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4121	04852	04120	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4122	04853	04121	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4123	04854	04122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4124	04855	04123	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4125	04856	04124	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 115

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
4126	04859	04125	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4127	04860	04126	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4128	04861	04127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4129	04862	04128	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4130	04863	04129	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4131	04864	04130	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4132	04865	04131	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4133	04866	04132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4134	04867	04133	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4135	04868	04134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4136	04869	04135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4137	04870	04136	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4138	04872	04137	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4139	04873	04138	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4140	04874	04139	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4141	04875	04140	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4142	04877	04141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4143	04878	04142	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4144	04879	04143	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4145	04881	04144	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4146	04882	04145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4147	04883	04146	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4148	04884	04147	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4149	04885	04148	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4150	04886	04149	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4151	04887	04150	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4152	04888	04151	25		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4153	04889	04152	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4154	04890	04153	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4155	04891	04154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4156	04892	04155	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4157	04893	04156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4158	04894	04157	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4159	04895	04158	14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4160	04897	04159	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4161	04898	04160	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 116

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
4162	04900	04161	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4163	04902	04162	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4164	04903	04163	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4165	04904	04164	5	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	1	0	0	0	0	0					
4166	04905	04165	5	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	0	0	0	0	0	0	0					
4167	04907	04166	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
4168	04908	04167	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4169	04909	04168	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4170	04910	04169	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4171	04912	04170	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4172	04913	04171	4	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0					
4173	04914	04172	6	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0					
4174	04915	04173	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
4175	04916	04174	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4176	04917	04175	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0					
4177	04918	04176	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4178	04919	04177	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4179	04920	04178	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4180	04921	04179	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4181	04922	04180	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4182	04923	04181	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4183	04924	04182	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4184	04925	04183	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4185	04926	04184	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4186	04927	04185	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4187	04928	04186	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0					
4188	04929	04187	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4189	04930	04188	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4190	04940	04189	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4191	04945	04190	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
4192	04947	04191	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4193	04948	04192	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0					
4194	04950	04193	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4195	04965	04194	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4196	04985	04195	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0					
4197	04986	04196	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					

Table 117

Table 118

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4198	04987	04197	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
4199	04988	04198	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
4200	04989	04199	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4201	04990	04200	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4202	04991	04201	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4203	04992	04202	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4204	04993	04203	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4205	04994	04204	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4206	04997	04205	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4207	04998	04206	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4208	04999	04207	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4209	05001	04208	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4210	05002	04209	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4211	05003	04210	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4212	05004	04211	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4213	05005	04212	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4214	05006	04213	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4215	05007	04214	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4216	05008	04215	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4217	05009	04216	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4218	05010	04217	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4219	05011	04218	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4220	05013	04219	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4221	05014	04220	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4222	05016	04221	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4223	05018	04222	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4224	05019	04223	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4225	05021	04224	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4226	05023	04225	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4227	05024	04226	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4228	05025	04227	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4229	05026	04228	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4230	05027	04229	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4231	05028	04230	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4232	05029	04231	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0</											



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK
4234	05031	04233	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4235	05033	04234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4236	05034	04235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4237	05035	04236	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4238	05037	04237	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4239	05039	04238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4240	05040	04239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4241	05041	04240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4242	05042	04241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4243	05043	04242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4244	05044	04243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4245	05045	04244	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4246	05046	04245	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4247	05047	04246	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4248	05051	04247	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4249	05052	04248	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4250	05053	04249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4251	05054	04250	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4252	05055	04251	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4253	05056	04252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4254	05058	04253	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4255	05059	04254	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4256	05060	04255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4257	05061	04256	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4258	05062	04257	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4259	05063	04258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4260	05064	04259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4261	05065	04260	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4262	05066	04261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4263	05068	04262	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4264	05069	04263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4265	05070	04264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4266	05071	04265	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4267	05073	04266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4268	05074	04267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4269	05075	04268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 119

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AV	AW	BA	BC	BE	BF	BG	BH	BI	BK
4270	05076	04269	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4271	05077	04270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4272	05079	04271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4273	05080	04272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4274	05081	04273	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4275	05082	04274	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	
4276	05083	04275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	
4277	05085	04276	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	
4278	05086	04277	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4279	05087	04278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4280	05088	04279	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4281	05089	04280	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4282	05090	04281	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4283	05092	04282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4284	05094	04283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4285	05095	04284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4286	05096	04285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4287	05099	04286	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4288	05100	04287	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4289	05102	04288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4290	05103	04289	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	
4291	05104	04290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4292	05105	04291	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4293	05106	04292	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4294	05107	04293	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4295	05108	04294	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	
4296	05109	04295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4297	05110	04296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4298	05111	04297	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	3	0	0	0	0	0	0	0	0	0	0	0	
4299	05112	04298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4300	05113	04299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4301	05114	04300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4302	05115	04301	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	
4303	05116	04302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4304	05117	04303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
4305	05118	04304	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	

Table 120

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4306	05119	04305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4307	05120	04306	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4308	05121	04307	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4309	05122	04308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4310	05123	04309	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4311	05124	04310	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4312	05127	04311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4313	05128	04312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4314	05129	04313	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4315	05130	04314	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4316	05132	04315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4317	05133	04316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4318	05134	04317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4319	05135	04318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4320	05136	04319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4321	05137	04320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4322	05138	04321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4323	05139	04322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4324	05140	04323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4325	05141	04324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4326	05142	04325	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4327	05143	04326	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4328	05144	04327	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4329	05145	04328	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4330	05147	04329	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4331	05148	04330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4332	05149	04331	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4333	05150	04332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4334	05151	04333	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4335	05152	04334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4336	05153	04335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4337	05155	04336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4338	05157	04337	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4339	05158	04338	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4340	05159	04339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4341	05160	04340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 121

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AI	AK	AM	AA	CA	AS	AL	AW	AY	B	C	DE	BF	BG	BH	BI	BK
4342	05161	04341	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4343	05162	04342	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4344	05163	04343	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4345	05164	04344	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4346	05165	04345	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4347	05166	04346	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4348	05168	04347	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4349	05169	04348	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4350	05170	04349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4351	05172	04350	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4352	05173	04351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4353	05174	04352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4354	05176	04353	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4355	05177	04354	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4356	05178	04355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4357	05180	04356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4358	05181	04357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4359	05182	04358	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4360	05183	04359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4361	05184	04360	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4362	05185	04361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4363	05186	04362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4364	05187	04363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4365	05188	04364	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4366	05190	04365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4367	05191	04366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4368	05192	04367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4369	05194	04368	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4370	05195	04369	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4371	05196	04370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4372	05197	04371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4373	05198	04372	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4374	05199	04373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4375	05200	04374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4376	05201	04375	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
4377	05203	04376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								

Table 122

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4378	05204	04377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4379	05205	04378	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4380	05206	04379	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4381	05207	04380	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4382	05208	04381	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4383	05209	04382	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4384	05210	04383	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4385	05211	04384	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4386	05212	04385	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4387	05213	04386	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4388	05214	04387	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4389	05215	04388	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4390	05216	04389	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4391	05217	04390	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4392	05218	04391	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4393	05219	04392	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4394	05220	04393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4395	05221	04394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4396	05223	04395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4397	05224	04396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4398	05227	04397	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4399	05228	04398	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4400	05229	04399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4401	05230	04400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4402	05231	04401	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4403	05232	04402	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4404	05233	04403	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4405	05234	04404	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4406	05235	04405	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4407	05236	04406	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4408	05237	04407	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4409	05238	04408	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4410	05239	04409	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4411	05240	04410	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4412	05241	04411	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4413	05242	04412	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 123

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
4414	05243	04413	1																												
4415	05244	04414	4																												
4416	05245	04415	1																												
4417	05246	04416	1																												
4418	05247	04417	1																												
4419	05248	04418	2																												
4420	05249	04419	1																												
4421	05251	04420	2																												
4422	05252	04421	1																												
4423	05253	04422	1																												
4424	05254	04423	1																												
4425	05255	04424	1																												
4426	05259	04425	1																												
4427	05260	04426	2																												
4428	05262	04427	1																												
4429	05263	04428	2																												
4430	05264	04429	2																												
4431	05266	04430	1																												
4432	05267	04431	2																												
4433	05269	04432	1																												
4434	05270	04433	1																												
4435	05271	04434	2																												
4436	05272	04435	1																												
4437	05273	04436	3																												
4438	05274	04437	1																												
4439	05275	04438	1																												
4440	05276	04439	1																												

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BI	BK	
4450	05287	04449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4451	05288	04450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4452	05289	04451	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	003643	99.2	118	1	1263	1380
4453	05290	04452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0053799	100	290	1	792	1081
4454	05291	04453	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4455	05292	04454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4456	05293	04455	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0						
4457	05294	04456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4458	05295	04457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4459	05296	04458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4460	05297	04459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4461	05298	04460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	022969	98.5	130	1	3405	3786
4462	05300	04461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4463	05301	04462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4464	05302	04463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4465	05303	04464	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4466	05304	04465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4467	05305	04466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4468	05306	04467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4469	05307	04468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	X68148	98.354				3031
4470	05308	04469	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	Y00971	96.9	64	1	2392	2457
4471	05309	04470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4472	05310	04471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4473	05311	04472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4474	05312	04473	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4475	05313	04474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4476	05314	04475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4477	05315	04476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4478	05316	04477	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4479	05318	04478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4480	05319	04479	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4481	05320	04480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4482	05321	04481	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4483	05322	04482	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4484	05323	04483	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4485	05325	04484	5		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
4486	05326	04485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4487	05327	04486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4488	05328	04487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4489	05329	04488	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4490	05331	04489	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4491	05332	04490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4492	05333	04491	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4493	05334	04492	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4494	05335	04493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4495	05336	04494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4496	05337	04495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4497	05339	04496	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4498	05340	04497	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4499	05341	04498	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4500	05342	04499	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
4501	05343	04500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4502	05344	04501	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4503	05345	04502	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4504	05346	04503	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4505	05347	04504	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4506	05349	04505	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4507	05350	04506	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4508	05351	04507	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4509	05352	04508	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4510	05353	04509	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4511	05354	04510	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
4512	05355	04511	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4513	05356	04512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4514	05357	04513	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4515	05359	04514	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4516	05360	04515	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4517	05361	04516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4518	05362	04517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4519	05363	04518	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4520	05364	04519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4521	05365	04520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					

Table 126



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4522	05366	04521	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	100	79			
4523	05367	04522	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	4363	4446	
4524	05368	04523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4525	05370	04524	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4526	05371	04525	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4527	05372	04526	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4528	05373	04527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4529	05374	04528	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4530	05375	04529	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4531	05376	04530	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4532	05377	04531	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4533	05378	04532	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4534	05379	04533	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4535	05381	04534	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4536	05382	04535	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4537	05383	04536	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4538	05384	04537	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4539	05387	04538	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0				
4540	05388	04539	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0				
4541	05389	04540	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0				
4542	05390	04541	32		0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0				
4543	05391	04542	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0				
4544	05392	04543	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0				
4545	05393	04544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4546	05394	04545	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4547	05395	04546	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4548	05396	04547	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0				
4549	05398	04548	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4550	05399	04549	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4551	05400	04550	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4552	05401	04551	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4553	05402	04552	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4554	05404	04553	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4555	05406	04554	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4556	05407	04555	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
4557	05408	04556	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				

Table 127

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4558	05409	04557	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4559	05410	04558	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4560	05411	04559	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	0	0						
4561	05412	04560	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	2	0	0	0	0	0						
4562	05413	04561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4563	05414	04562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4564	05415	04563	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4565	05416	04564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4566	05417	04565	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0						
4567	05418	04566	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4568	05419	04567	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4569	05420	04568	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0						
4570	05421	04569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4571	05422	04570	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4572	05423	04571	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4573	05424	04572	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4574	05425	04573	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4575	05427	04574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4576	05428	04575	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4577	05429	04576	1		0																												

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AI	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4594	05446	04593	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4595	05447	04594	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4596	05448	04595	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4597	05451	04596	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4598	05452	04597	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4599	05453	04598	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4600	05454	04599	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4601	05455	04600	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4602	05456	04601	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4603	05458	04602	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4604	05459	04603	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4605	05460	04604	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4606	05461	04605	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4607	05462	04606	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4608	05464	04607	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4609	05465	04608	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4610	05466	04609	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4611	05467	04610	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4612	05468	04611	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4613	05469	04612	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4614	05470	04613	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4615	05471	04614	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4616	05472	04615	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4617	05474	04616	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4618	05475	04617	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4619	05476	04618	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4620	05477	04619	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4621	05478	04620	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4622	05479	04621	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4623	05480	04622	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4624	05481	04623	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4625	05482	04624	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4626	05483	04625	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4627	05484	04626	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4628	05485	04627	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4629	05486	04628	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 129

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK
4666	05532	04665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4667	05533	04666	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4668	05534	04667	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4669	05535	04668	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4670	05536	04669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4671	05538	04670	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4672	05539	04671	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4673	05540	04672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4674	05541	04673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4675	05544	04674	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4676	05545	04675	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4677	05547	04676	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4678	05548	04677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4679	05551	04678	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4680	05552	04679	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4681	05553	04680	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4682	05555	04681	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4683	05556	04682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4684	05558	04683	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4685	05559	04684	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4686	05560	04685	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4687	05561	04686	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4688	05562	04687	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4689	05563	04688	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4690	05564	04689	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4691	05565	04690	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4692	05566	04691	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4693	05567	04692	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4694	05568	04693	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4695	05570	04694	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4696	05571	04695	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4697	05572	04696	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4698	05573	04697	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4699	05574	04698	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4700	05575	04699	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4701	05576	04700	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 131

[illegible]

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AI	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4738	05623	04737	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4739	05624	04738	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4740	05625	04739	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4741	05627	04740	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4742	05628	04741	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4743	05629	04742	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4744	05630	04743	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4745	05631	04744	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4746	05632	04745	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4747	05634	04746	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4748	05635	04747	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4749	05636	04748	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4750	05637	04749	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4751	05639	04750	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4752	05640	04751	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4753	05642	04752	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4754	05643	04753	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4755	05644	04754	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4756	05645	04755	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4757	05646	04756	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4758	05647	04757	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4759	05648	04758	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4760	05649	04759	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4761	05650	04760	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4762	05651	04761	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4763	05652	04762	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4764	05653	04763	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4765	05654	04764	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4766	05655	04765	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4767	05656	04766	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4768	05657	04767	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4769	05658	04768	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4770	05659	04769	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4771	05660	04770	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4772	05661	04771	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4773	05662	04772	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 133

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
4774	05665	04773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4775	05667	04774	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4776	05668	04775	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4777	05669	04776	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4778	05671	04777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4779	05673	04778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4780	05674	04779	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4781	05676	04780	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4782	05679	04781	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4783	05680	04782	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4784	05681	04783	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4785	05682	04784	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4786	05683	04785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4787	05684	04786	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4788	05685	04787	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4789	05686	04788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4790	05687	04789	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4791	05688	04790	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4792	05689	04791	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4793	05690	04792	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4794	05692	04793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4795	05693	04794	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4796	05694	04795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4797	05695	04796	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4798	05696	04797	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4799	05697	04798	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4800	05701	04799	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4801	05704	04800	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4802	05707	04801	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4803	05708	04802	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4804	05709	04803	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4805	05710	04804	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4806	05711	04805	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4807	05714	04806	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4808	05715	04807	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4809	05716	04808	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 134



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AN	AW	AY	B	BC	BE	BF	BG	BI	BK
4810	05718	04809	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4811	05719	04810	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4812	05720	04811	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4813	05721	04812	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4814	05722	04813	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4815	05723	04814	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4816	05724	04815	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4817	05725	04816	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4818	05726	04817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4819	05727	04818	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4820	05729	04819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4821	05730	04820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4822	05731	04821	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4823	05732	04822	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4824	05733	04823	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4825	05734	04824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4826	05735	04825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4827	05736	04826	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4828	05738	04827	17		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4829	05741	04828	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4830	05742	04829	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4831	05743	04830	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4832	05747	04831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4833	05748	04832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4834	05749	04833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4835	05751	04834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4836	05752	04835	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4837	05754	04836	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4838	05755	04837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4839	05756	04838	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4840	05757	04839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4841	05758	04840	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4842	05759	04841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4843	05763	04842	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4844	05765	04843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4845	05767	04844	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 135

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK			
4846	05768	04845	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	X02571	97.3	73	130	1430	1512		
4847	05769	04846	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4848	05770	04847	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4849	05772	04848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4850	05773	04849	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4851	05774	04850	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4852	05775	04851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	3150	4186			
4853	05776	04852	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4854	05777	04853	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0								
4855	05778	04854	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4856	05779	04855	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4857	05780	04856	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3	0	0	0	0	X00269	90.5	359	1	1268	1617		
4858	05781	04857	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4859	05782	04858	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4860	05783	04859	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	1	0	0	0	0	0	0	0	0	0	1
4861	05784	04860	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4862	05785	04861	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4863	05787	04862	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4864	05789	04863	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4865	05790	04864	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4866	05792	04865	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4867	05793	04866	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4868	05794	04867	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4869	05795	04868	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0								
4870	05796	04869	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4871	05797	04870	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4872	05798	04871	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	1	5181	5784			
4873	05799	04872	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0								
4874	05801	04873	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	84	1	1936	2027		
4875	05804	04874	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4876	05807	04875	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4877	05808	04876	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1	2	0	0	0	0	0	0	0	0	0	0
4878	05810	04877	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4879	05813	04878	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
4880	05814	04879	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0								
4881	05815	04880	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	IA	KA	MA	QA	CA	SA	IA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
4882	05816	04881	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4883	05817	04882	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4884	05818	04883	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4885	05819	04884	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4886	05820	04885	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4887	05821	04886	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4888	05823	04887	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4889	05824	04888	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4890	05825	04889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4891	05826	04890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4892	05827	04891	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4893	05829	04892	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4894	05830	04893	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4895	05831	04894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4896	05832	04895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4897	05833	04896	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4898	05834	04897	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4899	05835	04898	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4900	05836	04899	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4901	05837	04900	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4902	05838	04901	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4903	05839	04902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4904	05840	04903	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4905	05841	04904	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4906	05842	04905	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4907	05843	04906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4908	05844	04907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4909	05845	04908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4910	05846	04909	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4911	05847	04910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4912	05848	04911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4913	05849	04912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4914	05850	04913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4915	05851	04914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4916	05852	04915	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4917	05854	04916	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 137

BNSDOCID: <EP\_0679716A1 | >

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4954	05899	04953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4955	05900	04954	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4956	05902	04955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4957	05903	04956	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4958	05907	04957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4959	05908	04958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4960	05912	04959	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4961	05913	04960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4962	05914	04961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4963	05916	04962	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4964	05917	04963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4965	05918	04964	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4966	05919	04965	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4967	05920	04966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4968	05921	04967	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4969	05923	04968	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4970	05925	04969	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4971	05926	04970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4972	05927	04971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4973	05928	04972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4974	05932	04973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4975	05933	04974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4976	05934	04975	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4977	05937	04976	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4978	05938	04977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4979	05939	04978	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4980	05940	04979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4981	05941	04980	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4982	05942	04981	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4983	05943	04982	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4984	05946	04983	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0						
4985	05947	04984	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4986	05948	04985	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4987	05949	04986	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4988	05951	04987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4989	05952	04988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						

Table 139

Table 140

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	CI	AK	AM	CA	CA	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4990	05953	04989	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4991	05954	04990	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4992	05955	04991	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4993	05956	04992	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4994	05957	04993	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4995	05959	04994	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4996	05960	04995	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4997	05961	04996	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4998	05962	04997	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4999	05963	04998	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5000	05964	04999	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5001	05966	05000	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5002	05967	05001	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5003	05968	05002	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5004	05969	05003	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5005	05970	05004	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5006	05974	05005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5007	05975	05006	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5008	05976	05007	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5009	05978	05008	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5010	05980	05009	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5011	05981	05010	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5012	05982	05011	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5013	05983	05012	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5014	05984	05013	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5015	05987	05014	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5016	05988	05015	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5017	05989	05016	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5018	05991	05017	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5019	05992	05018	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5020	05993	05019	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5021	05994	05020	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5022	05996	05021	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5023	05997	05022	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5024	05998	05023	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5025	05999	05024	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 141

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
5026	06000	05025	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5027	06001	05026	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5028	06004	05027	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5029	06005	05028	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5030	06008	05029	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5031	06010	05030	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5032	06011	05031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5033	06013	05032	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5034	06014	05033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5035	06015	05034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5036	06016	05035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5037	06017	05036	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5038	06018	05037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5039	06020	05038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5040	06021	05039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5041	06022	05040	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5042	06023	05041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5043	06024	05042	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5044	06025	05043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5045	06026	05044	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5046	06027	05045	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5047	06028	05046	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5048	06030	05047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5049	06031	05048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5050	06032	05049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5051	06034	05050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5052	06035	05051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5053	06036	05052	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5054	06038	05053	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5055	06039	05054	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5056	06040	05055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5057	06041	05056	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5058	06042	05057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5059	06043	05058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5060	06044	05059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5061	06045	05060	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					

	A	B	C	E	G	I	K	M	Q	S	U	W	Y	AA	AC	AF	AG	AK	AM	AO	AS	AW	BAB	BE	BF	BG	BH	BI	BK
5062	06046	05061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5063	06047	05062	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5064	06048	05063	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5065	06049	05064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5066	06050	05065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5067	06051	05066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5068	06052	05067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5069	06053	05068	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0						
5070	06054	05069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5071	06055	05070	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5072	06056	05071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5073	06057	05072	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5074	06059	05073	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5075	06060	05074	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5076	06061	05075	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5077	06062	05076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5078	06064	05077	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5079	06065	05078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5080	06066	05079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5081	06067	05080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5082	06068	05081	3		0	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0						
5083	06069	05082	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						



Table 143

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5098	06086	05097	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5099	06087	05098	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5100	06089	05099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5101	06090	05100	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5102	06091	05101	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5103	06092	05102	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5104	06093	05103	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5105	06094	05104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5106	06095	05105	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5107	06097	05106	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5108	06098	05107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5109	06100	05108	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5110	06101	05109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5111	06102	05110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5112	06103	05111	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5113	06104	05112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5114	06105	05113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5115	06107	05114	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5116	06108	05115	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5117	06109	05116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5118	06110	05117	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5119	06111	05118	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5120	06112	05119	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5121	06113	05120	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5122	06114	05121	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5123	06115	05122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5124	06116	05123	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5125	06117	05124	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5126	06118	05125	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5127	06119	05126	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5128	06122	05127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5129	06123	05128	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5130	06125	05129	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5131	06126	05130	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5132	06127	05131	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5133	06128	05132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

[illegible]

Table 145

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AT	AW	AY	BABC	BE	BF	BGBH	BI	BK
5170	06173	05169	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5171	06174	05170	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5172	06175	05171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5173	06176	05172	3		0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0					
5174	06177	05173	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5175	06179	05174	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5176	06180	05175	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5177	06181	05176	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
5178	06182	05177	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5179	06183	05178	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5180	06184	05179	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5181	06185	05180	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5182	06186	05181	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5183	06187	05182	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5184	06188	05183	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5185	06189	05184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5186	06190	05185	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5187	06191	05186	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5188	06192	05187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5189	06195	05188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5190	06196	05189	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5191	06197	05190	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
5192	06198	05191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5193	06199	05192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5194	06200	05193	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5195	06201	05194	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5196	06202	05195	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5197	06203	05196	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5198	06204	05197	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5199	06205	05198	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5200	06206	05199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5201	06207	05200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5202	06208	05201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5203	06209	05202	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
5204	06210	05203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5205	06211	05204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					

Table 146

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5206	06213	05205	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5207	06215	05206	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5208	06216	05207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5209	06217	05208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5210	06218	05209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5211	06219	05210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5212	06220	05211	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5213	06221	05212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5214	06222	05213	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5215	06224	05214	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5216	06225	05215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5217	06226	05216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5218	06227	05217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5219	06228	05218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5220	06229	05219	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5221	06230	05220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5222	06232	05221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5223	06233	05222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5224	06234	05223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5225	06235	05224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5226	06236	05225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5227	06237	05226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5228	06238	05227	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5229	06240	05228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5230	06241	05229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5231	06243	05230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5232	06244	05231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5233	06246	05232	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5234	06247	05233	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5235	06248	05234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5236	06249	05235	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5237	06250	05236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5238	06251	05237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5239	06253	05238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5240	06254	05239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5241	06255	05240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						

Table 147

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AL	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	DE	BF	BG	BH	BI	BK
5242	06256	05241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5243	06257	05242	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5244	06258	05243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5245	06259	05244	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5246	06260	05245	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	XS2056	98.5	68	1	1297	1364
5247	06261	05246	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5248	06262	05247	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5249	06264	05248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5250	06267	05249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5251	06268	05250	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5252	06269	05251	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5253	06270	05252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5254	06271	05253	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5255	06272	05254	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5256	06273	05255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0M80359	93.9	181	1	2062	2914
5257	06274	05256	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5258	06275	05257	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0M90104	94.2	173	1	1700	1879
5259	06277	05258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5260	06278	05259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5261	06279	05260	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5262	06280	05261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5263	06281	05262	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5264	06282	05263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0M64784	95.6	338	1	638	1138
5265	06283	05264	11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5266	06284	05265	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	9XS2426	100	102	1	1574	1677
5267	06286	05266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5268	06288	05267	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5269	06289	05268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5270	06290	05269	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5271	06291	05270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5272	06292	05271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5273	06293	05272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5274	06294	05273	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5275	06295	05274	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5276	06296	05275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5277	06297	05276	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0M86400	92.4	197	1	1196	2834

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
5314	06338	05313	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5315	06339	05314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5316	06341	05315	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5317	06343	05316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5318	06344	05317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5319	06345	05318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5320	06346	05319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5321	06347	05320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5322	06348	05321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5323	06350	05322	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5324	06351	05323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5325	06353	05324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5326	06354	05325	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5327	06355	05326	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5328	06356	05327	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5329	06357	05328	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5330	06358	05329	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5331	06359	05330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5332	06360	05331	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5333	06361	05332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5334	06362	05333	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5335	06363	05334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5336	06364	05335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5337	06365	05336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5338	06366	05337	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		X02994	96.8 217	1	1282	1498
5339	06367	05338	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5340	06369	05339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5341	06370	05340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5342	06371	05341	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5343	06372	05342	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5344	06373	05343	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5345	06374	05344	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5346	06376	05345	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5347	06377	05346	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5348	06378	05347	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5349	06379	05348	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		X03751	99.1 323	1	660	1103

Table 149

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
5350	06380	05349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5351	06381	05350	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5352	06382	05351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5353	06383	05352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5354	06384	05353	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5355	06385	05354	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5356	06386	05355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5357	06387	05356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5358	06388	05357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5359	06389	05358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5360	06390	05359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5361	06392	05360	26		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5362	06393	05361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5363	06394	05362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5364	06395	05363	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5365	06396	05364	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5366	06397	05365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5367	06398	05366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5368	06399	05367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5369	06400	05368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5370	06401	05369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5371	06402	05370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5372	06403	05371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5373	06404	05372	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5374	06405	05373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5375	06407	05374	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5376	06408	05375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5377	06409	05376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5378	06410	05377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5379	06411	05378	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5380	06412	05379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5381	06413	05380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5382	06414	05381	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5383	06415	05382	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5384	06416	05383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5385	06417	05384	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 150



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5386	06418	05385	1																														
5387	06419	05386	2																														
5388	06420	05387	1																														
5389	06421	05388	2																														
5390	06422	05389	1																														
5391	06423	05390	1																														
5392	06424	05391	2																														
5393	06425	05392	1																														
5394	06426	05393	1																														
5395	06427	05394	1																														
5396	06428	05395	1																														
5397	06429	05396	1																														
5398	06430	05397	1																														
5399	06431	05398	1																														
5400	06432	05399	1																														
5401	06433	05400	1																														
5402	06434	05401	4																														
5403	06435	05402	2																														
5404	06436	05403	1																														
5405	06437	05404	1																														
5406	06438	05405	1																														
5407	06439	05406	3																														
5408	06440	05407	1																														
5409	06441	05408	1																														
5410	06442	05409	2																														
5411	06443	05410	2																														
5412	06444	05411	1																														
5413	06445	05412	1																														
5414	06446	05413	1																														
5415	06447	05414	3																														
5416	06448	05415	3																														
5417	06449	05416	4																														
5418	06450	05417	1																														
5419	06451	05418	1																														
5420	06452	05419	1																														
5421	06453	05420	1																														

Table 151

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5422	06454	05421	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0L10910	95.1	205	1	2334	2595	
5423	06455	05422	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5424	06456	05423	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5425	06457	05424	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5426	06458	05425	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5427	06459	05426	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5428	06460	05427	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0M59465	100	183	1	4244	4426	
5429	06461	05428	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5430	06462	05429	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5431	06463	05430	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5432	06464	05431	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5433	06465	05432	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5434	06466	05433	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5435	06468	05434	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5436	06469	05435	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5437	06470	05436	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5438	06471	05437	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5439	06472	05438	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5440	06473	05439	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0X63657	9					

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
5458	06493	05157	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5459	06496	05458	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5460	06498	05459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5461	06499	05460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5462	06500	05461	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2187
5463	06501	05462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5464	06502	05463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5465	06503	05464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5466	06504	05465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5467	06505	05466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5468	06506	05467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5469	06507	05468	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5470	06508	05469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5471	06509	05470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5472	06510	05471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5473	06511	05472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5474	06512	05473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5475	06513	05474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5476	06514	05475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5477	06515	05476	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5478	06516	05477	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5479	06517	05478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5480	06518	05479	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5481	06519	05480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5482	06520	05481	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5483	06521	05482	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5484	06522	05483	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5485	06523	05484	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5486	06524	05485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5487	06525	05486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5488	06526	05487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5489	06527	05488	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5490	06528	05489	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5491	06529	05490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5492	06530	05491	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5493	06531	05492	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 153

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
5494	06532	05493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5495	06533	05494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5496	06536	05495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5497	06537	05496	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5498	06538	05497	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5499	06539	05498	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5500	06540	05499	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5501	06541	05500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5502	06542	05501	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5503	06544	05502	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5504	06545	05503	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5505	06546	05504	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5506	06547	05505	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5507	06548	05506	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5508	06549	05507	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5509	06550	05508	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5510	06551	05509	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5511	06552	05510	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5512	06553	05511	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5513	06555	05512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5514	06556	05513	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5515	06557	05514	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5516	06558	05515	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5517	06559	05516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5518	06560	05517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5519	06561	05518	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5520	06563	05519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5521	06564	05520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5522	06565	05521	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5523	06566	05522	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5524	06567	05523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5525	06569	05524	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5526	06571	05525	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5527	06572	05526	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5528	06573	05527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5529	06574	05528	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 154

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AI	AK	AM	AO	AS	AL	AW	AY	BA	BC	BE	BF	BG	BI	BK
5530	06576	05529	1																													
5531	06577	05530	1																													
5532	06578	05531	1																													
5533	06579	05532	2																													
5534	06580	05533	1																													
5535	06581	05534	1																													
5536	06582	05535	2																													
5537	06583	05536	3																													
5538	06584	05537	1																													
5539	06585	05538	1																													
5540	06586	05539	1																													
5541	06587	05540	1																													
5542	06588	05541	1																													
5543	06590	05542	3																													
5544	06592	05543	2																													
5545	06593	05544	1																													
5546	06594	05545	1																													
5547	06595	05546	1																													
5548	06596	05547	2																													
5549	06597	05548	1																													
5550	06599	05549	1																													
5551	06600	05550	1																													
5552	06601	05551	1																													
5553	06602	05552	1																													
5554	06603	05553	1																													
5555	06604	05554	2																													
5556	06605	05555	1																													
5557	06606	05556	2																													
5558	06607	05557	2																													
5559	06608	05558	1																													
5560	06609	05559	1																													
5561	06610	05560	2																													
5562	06611	05561	1																													
5563	06612	05562	1																													
5564	06613	05563	2																													
5565	06614	05564	1																													

Table 155

[illegible]

Table 157

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AJ	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
5638	06698	05637	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5639	06699	05638	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5640	06700	05639	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5641	06701	05640	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5642	06702	05641	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5643	06703	05642	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5644	06704	05643	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5645	06705	05644	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5646	06706	05645	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5647	06707	05646	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5648	06709	05647	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5649	06710	05648	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5650	06711	05649	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5651	06712	05650	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5652	06713	05651	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5653	06714	05652	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5654	06715	05653	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5655	06716	05654	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5656	06717	05655	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5657	06718	05656	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
5658	06719	05657	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5659	06720	05658	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5660	06721	05659	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5661	06724	05660	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5662	06725	05661	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5663	06726	05662	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
5664	06727	05663	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5665	06728	05664	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5666	06730	05665	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5667	06731	05666	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5668	06732	05667	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5669	06733	05668	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5670	06734	05669	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5671	06735	05670	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5672	06736	05671	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5673	06737	05672	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					

Table 158



[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AI	AK	AM	AN	AO	CA	CS	AS	AW	BA	BC	BE	BF	BG	BI	BK
5710	06778	05709	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5711	06780	05710	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5712	06781	05711	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5713	06783	05712	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5714	06784	05713	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5715	06785	05714	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5716	06786	05715	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	005633	100 214	1 2887	3117	
5717	06787	05716	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5718	06788	05717	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5719	06789	05718	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5720	06790	05719	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5721	06791	05720	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5722	06792	05721	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5723	06794	05722	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0D21163	98 3 363	1 2923	3784	
5724	06795	05723	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5725	06796	05724	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5726	06797	05725	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5727	06798	05726	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5728	06800	05727	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5729	06801	05728	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5730	06802	05729	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5731	06803	05730	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5732	06804	05731	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5733	06805	05732	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5734	06806	05733	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5735	06807	05734	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5736	06808	05735	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5737	06809	05736	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5738	06810	05737	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5739	06811	05738	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5740	06812	05739	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5741	06813	05740	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	007956	98 4 127	1 2780	2955	
5742	06815	05741	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5743	06816	05742	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	006985	93 3 195	1 1175	1550	
5744	06817	05743	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5745	06818	05744	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 160

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AJ	AK	AM	AN	AO	AP	AQ	AR	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5746	06819	05745	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5747	06820	05746	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5748	06821	05747	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5749	06823	05748	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5750	06824	05749	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5751	06825	05750	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5752	06826	05751	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5753	06827	05752	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5754	06828	05753	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5755	06829	05754	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5756	06830	05755	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5757	06831	05756	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5758	06832	05757	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5759	06833	05758	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5760	06834	05759	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5761	06835	05760	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5762	06836	05761	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5763	06837	05762	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5764	06838	05763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5765	06839	05764	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5766	06840	05765	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5767	06841	05766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5768	06842	05767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5769	06843	05768	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5770	06844	05769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5771	06845	05770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5772	06846	05771	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5773	06848	05772	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5774	06850	05773	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5775	06851	05774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5776	06852	05775	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5777	06854	05776	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5778	06855	05777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5779	06856	05778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5780	06857	05779	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5781	06858	05780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 161

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5818	06904	05817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5819	06906	05818	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5820	06909	05819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5821	06910	05820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5822	06911	05821	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5823	06912	05822	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5824	06913	05823	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5825	06915	05824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5826	06916	05825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5827	06917	05826	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5828	06919	05827	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5829	06920	05828	27		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5830	06922	05829	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5831	06923	05830	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5832	06927	05831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5833	06928	05832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5834	06929	05833	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5835	06930	05834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5836	06931	05835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5837	06932	05836	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5838	06933	05837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5839	06934	05838	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5840	06935	05839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5841	06936	05840	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5842	06937	05841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5843	06938	05842	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5844	06939	05843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5845	06941	05844	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5846	06942	05845	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5847	06943	05846	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5848	06945	05847	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5849	06946	05848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5850	06947	05849	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5851	06948	05850	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5852	06949	05851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5853	06951	05852	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 163

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5854	06952	05853	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5855	06953	05854	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5856	06954	05855	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5857	06955	05856	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5858	06956	05857	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5859	06957	05858	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5860	06959	05859	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5861	06960	05860	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5862	06961	05861	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5863	06963	05862	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5864	06964	05863	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5865	06965	05864	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5866	06966	05865	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5867	06967	05866	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5868	06969	05867	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5869	06971	05868	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5870	06972	05869	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5871	06973	05870	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5872	06975	05871	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5873	06977	05872	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5874	06978	05873	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5875	06979	05874	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5876	06981	05875	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5877	06982	05876	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5878	06983	05877	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5879	06984	05878	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5880	06985	05879	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5881	06986	05880	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5882	06987	05881	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5883	06988	05882	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5884	06989	05883	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5885	06990	05884	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5886	06991	05885	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5887	06992	05886	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5888	06993	05887	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5889	06994	05888	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 164

[illegible]

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Table 166



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
5962	07079	05961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5963	07080	05962	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5964	07081	05963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5965	07082	05964	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5966	07083	05965	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5967	07084	05966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5968	07085	05967	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5969	07086	05968	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5970	07087	05969	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5971	07088	05970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5972	07089	05971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5973	07091	05972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5974	07093	05973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5975	07094	05974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5976	07095	05975	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5977	07096	05976	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5978	07097	05977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5979	07098	05978	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5980	07099	05979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5981	07100	05980	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5982	07101	05981	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5983	07102	05982	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5984	07103	05983	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5985	07104	05984	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5986	07105	05985	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5987	07106	05986	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5988	07108	05987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5989	07110	05988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5990	07111	05989	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5991	07112	05990	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5992	07113	05991	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5993	07114	05992	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5994	07115	05993	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5995	07116	05994	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5996	07117	05995	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5997	07118	05996	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 167

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5998	07119	05997	1																													
5999	07120	05998	1																													
6000	07121	05999	1																													
6001	07122	06000	1																													
6002	07123	06001	1																													
6003	07124	06002	1																													
6004	07125	06003	1																													
6005	07126	06004	1																													
6006	07127	06005	1																													
6007	07128	06006	1																													
6008	07129	06007	1																													
6009	07130	06008	1																													
6010	07131	06009	1																													
6011	07132	06010	1																													
6012	07133	06011	1																													
6013	07134	06012	1																													
6014	07135	06013	2																													
6015	07136	06014	2																													
6016	07137	06015	1																													
6017	07138	06016	1																													
6018	07139	06017	2																													
6019	07140	06018	3																													
6020	07141	06019	1																													
6021	07142	06020	1																													
6022	07143	06021	1																													
6023	07144	06022	2																													
6024	07145	06023	1																													
6025	07146	06024	1																													
6026	07147	06025	1																													
6027	07150	06026	1																													
6028	07151	06027	1																													
6029	07152	06028	1																													
6030	07153	06029	1																													
6031	07154	06030	1																													
6032	07156	06031	1																													
6033	07157	06032	1																													

Table 168

Table 169

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6034	07158	06033	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6035	07160	06034	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6036	07161	06035	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6037	07162	06036	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6038	07163	06037	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6039	07164	06038	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6040	07165	06039	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6041	07166	06040	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6042	07167	06041	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6043	07169	06042	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6044	07170	06043	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6045	07171	06044	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6046	07173	06045	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6047	07174	06046	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6048	07175	06047	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6049	07178	06048	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6050	07179	06049	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6051	07180	06050	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6052	07181	06051	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6053	07182	06052	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6054	07183	06053	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6055	07185	06054	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6056	07186	06055	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6057	07187	06056	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6058	07188	06057	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6059	07192	06058	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6060	07193	06059	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6061	07194	06060	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6062	07195	06061	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6063	07196	06062	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6064	07199	06063	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6065	07200	06064	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6066	07201	06065	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6067	07202	06066	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6068	07204	06067	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6069	07206	06068	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6106	07259	06105	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6107	07261	06106	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6108	07263	06107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6109	07264	06108	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6110	07265	06109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6111	07266	06110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6112	07267	06111	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6113	07268	06112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6114	07269	06113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6115	07270	06114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6116	07272	06115	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6117	07274	06116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6118	07275	06117	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6119	07276	06118	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6120	07277	06119	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6121	07278	06120	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6122	07279	06121	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6123	07280	06122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6124	07281	06123	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6125	07282	06124	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6126	07283	06125	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6127	07284	06126	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6128	07285	06127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6129	07286	06128	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6130	07287	06129	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6131	07288	06130	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6132	07289	06131	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6133	07290	06132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6134	07291	06133	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6135	07292	06134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6136	07293	06135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6137	07294	06136	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6138	07295	06137	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6139	07296	06138	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6140	07297	06139	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6141	07298	06140	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 171

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6142	07299	06141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6143	07300	06142	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6144	07301	06143	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6145	07302	06144	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6146	07303	06145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6147	07304	06146	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6148	07305	06147	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6149	07306	06148	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6150	07307	06149	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6151	07308	06150	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6152	07309	06151	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6153	07311	06152	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6154	07312	06153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6155	07313	06154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6156	07315	06155	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6157	07316	06156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6158	07317	06157	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6159	07318	06158	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6160	07319	06159	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6161	07320	06160	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6162	07321	06161	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6163	07322	06162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6164	07323	06163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6165	07324	06164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6166	07325	06165	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6167	07326	06166	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6168	07327	06167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6169	07328	06168	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6170	07329	06169	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6171	07330	06170	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6172	07331	06171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6173	07332	06172	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6174	07333	06173	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6175	07334	06174	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6176	07335	06175	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6177	07336	06176	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 172



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6214	07374	06213	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6215	07375	06214	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6216	07376	06215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6217	07377	06216	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0							
6218	07378	06217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6219	07379	06218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6220	07380	06219	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6221	07381	06220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6222	07382	06221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6223	07383	06222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6224	07384	06223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6225	07385	06224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6226	07386	06225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6227	07387	06226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		M77016	94	234	1	1369	2665
6228	07388	06227	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6229	07389	06228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6230	07390	06229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6231	07391	06230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6232	07392	06231	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6233	07393	06232	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6234	07394	06233	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6235	07395	06234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		J03068	92.9	141	1	2175	3317
6236	07396	06235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6237	07397	06236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6238	07398	06237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6239	07399	06238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6240	07400	06239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6241	07401	06240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6242	07402	06241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6243	07403	06242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6244	07404	06243	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6245	07405	06244	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6246	07406	06245	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6247	07407	06246	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6248	07408	06247	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6249	07409	06248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							



[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6286	07447	06285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6287	07448	06286	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6288	07449	06287	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6289	07450	06288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6290	07451	06289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6291	07452	06290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6292	07453	06291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6293	07454	06292	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6294	07455	06293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6295	07456	06294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6296	07457	06295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6297	07458	06296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6298	07459	06297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6299	07460	06298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6300	07461	06299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6301	07462	06300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6302	07463	06301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6303	07464	06302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6304	07465	06303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6305	07466	06304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6306	07467	06305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6307	07468	06306	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6308	07469	06307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6309	07470	06308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6310	07471	06309	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6311	07472	06310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6312	07473	06311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6313	07474	06312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6314	07475	06313	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6315	07476	06314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6316	07477	06315	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6317	07478	06316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6318	07479	06317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6319	07480	06318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6320	07481	06319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6321	07483	06320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 176

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AK	AM	AN	AO	AP	AQ	AR	AS	AT	AW	AY	BAC	BE	BF	BG	BH	BI	BK
6358	07521	06357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6359	07522	06358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6360	07523	06359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6361	07524	06360	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6362	07525	06361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6363	07526	06362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6364	07527	06363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6365	07528	06364	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6366	07529	06365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6367	07530	06366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6368	07531	06367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6369	07532	06368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6370	07533	06369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6371	07534	06370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6372	07535	06371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6373	07536	06372	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6374	07537	06373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6375	07538	06374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6376	07539	06375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6377	07540	06376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6378	07541	06377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6379	07543	06378	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6380	07544	06379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6381	07545	06380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6382	07546	06381	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6383	07547	06382	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6384	07548	06383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6385	07549	06384	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6386	07550	06385	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6387	07551	06386	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6388	07552	06387	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6389	07553	06388	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6390	07554	06389	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6391	07555	06390	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6392	07556	06391	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6393	07557	06392	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
6394	07558	06393	1																			1	0	0	0	0	0	0	0	0	
6395	07559	06394	1																			1	0	0	0	0	0	0	0	0	
6396	07560	06395	1																			1	0	0	0	0	0	0	0	0	
6397	07561	06396	1																			1	0	0	0	0	0	0	0	0	
6398	07562	06397	2																			1	0	0	0	0	0	0	0	0	
6399	07563	06398	2																			1	0	0	0	0	0	0	0	0	
6400	07564	06399	1																			1	0	0	0	0	0	0	0	0	
6401	07565	06400	1																			1	0	0	0	0	0	0	0	0	
6402	07567	06401	1																			1	0	0	0	0	0	0	0	0	
6403	07568	06402	3																			1	0	0	0	0	0	0	0	0	
6404	07569	06403	3																			1	0	0	0	0	0	0	0	0	
6405	07570	06404	3																			1	0	0	0	0	0	0	0	0	
6406	07571	06405	1																			1	0	0	0	0	0	0	0	0	
6407	07572	06406	1																			1	0	0	0	0	0	0	0	0	
6408	07573	06407	1																			1	0	0	0	0	0	0	0	0	
6409	07574	06408	1																			1	0	0	0	0	0	0	0	0	
6410	07575	06409	2																			1	0	0	0	0	0	0	0	0	
6411	07576	06410	1																			1	0	0	0	0	0	0	0	0	
6412	07577	06411	1																			1	0	0	0	0	0	0	0	0	
6413	07578	06412	1																			1	0	0	0	0	0	0	0	0	
6414	07579	06413	1																			1	0	0	0	0	0	0	0	0	
6415	07580	06414	1																			1	0	0	0	0	0	0	0	0	
6416	07581	06415	1																			1	0	0	0	0	0	0	0	0	
6417	07582	06416	1																			1	0	0	0	0	0	0	0	0	
6418	07583	06417	2																			1	0	0	0	0	0	0	0	0	
6419	07584	06418	1																			1	0	0	0	0	0	0	0	0	
6420	07585	06419	1																			1	0	0	0	0	0	0	0	0	
6421	07586	06420	1																			1	0	0	0	0	0	0	0	0	
6422	07587	06421	1																			1	0	0	0	0	0	0	0	0	
6423	07588	06422	1																			1	0	0	0	0	0	0	0	0	
6424	07589	06423	1																			1	0	0	0	0	0	0	0	0	
6425	07590	06424	1																			1	0	0	0	0	0	0	0	0	
6426	07591	06425	1																			1	0	0	0	0	0	0	0	0	
6427	07592	06426	1																			1	0	0	0	0	0	0	0	0	
6428	07593	06427	1																			1	0	0	0	0	0	0	0	0	
6429	07594	06428	1																			1	0	0	0	0	0	0	0	0	

Table 179

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AK	AM	AO	AS	AW	AY	BA	BB	BE	BF	BG	BH	BI	BK
6430	07595	06429	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6431	07596	06430	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6432	07597	06431	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6433	07598	06432	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6434	07599	06433	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6435	07600	06434	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6436	07601	06435	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6437	07602	06436	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6438	07603	06437	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6439	07604	06438	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6440	07605	06439	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6441	07606	06440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6442	07607	06441	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6443	07608	06442	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6444	07609	06443	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6445	07610	06444	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6446	07611	06445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6447	07612	06446	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6448	07613	06447	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6449	07614	06448	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6450	07615	06449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6451	07616	06450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6452	07617	06451	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6453	07619	06452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6454	07620	06453	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6455	07621	06454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6456	07622	06455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6457	07623	06456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6458	07624	06457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6459	07625	06458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6460	07626	06459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6461	07627	06460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6462	07628	06461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6463	07629	06462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6464	07630	06463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6465	07631	06464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
6466	07632	06465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6467	07633	06466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6468	07634	06467	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6469	07635	06468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6470	07636	06469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6471	07637	06470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6472	07638	06471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6473	07639	06472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6474	07640	06473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6475	07641	06474	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6476	07642	06475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6477	07643	06476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6478	07644	06477	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6479	07645	06478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6480	07646	06479	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6481	07647	06480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6482	07648	06481	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6483	07649	06482	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6484	07650	06483	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6485	07651	06484	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6486	07652	06485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6487	07653	06486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6488	07655	06487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6489	07656	06488	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6490	07657	06489	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6491	07658	06490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6492	07659	06491	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6493	07660	06492	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6494	07661	06493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6495	07663	06494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6496	07664	06495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6497	07665	06496	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6498	07666	06497	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6499	07667	06498	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6500	07668	06499	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6501	07669	06500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					

Table 181

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
6502	07670	06501	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6503	07671	06502	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6504	07672	06503	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6505	07673	06504	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6506	07674	06505	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6507	07675	06506	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6508	07676	06507	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6509	07677	06508	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6510	07678	06509	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6511	07679	06510	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6512	07680	06511	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6513	07681	06512	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6514	07682	06513	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6515	07683	06514	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6516	07684	06515	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6517	07686	06516	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6518	07687	06517	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6519	07688	06518	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6520	07689	06519	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6521	07690	06520	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6522	07691	06521	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6523	07692	06522	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6524	07693	06523	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6525	07694	06524	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6526	07695	06525	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6527	07696	06526	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6528	07697	06527	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6529	07698	06528	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6530	07699	06529	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6531	07700	06530	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6532	07701	06531	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6533	07702	06532	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6534	07703	06533	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6535	07704	06534	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6536	07705	06535	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6537	07708	06536	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 182





		A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6574	07751	06573	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6575	07752	06574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6576	07753	06575	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6577	07754	06576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6578	07755	06577	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6579	07756	06578	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6580	07757	06579	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6581	07758	06580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6582	07759	06581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6583	07760	06582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6584	07761	06583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6585	07762	06584	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6586	07763	06585	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6587	07764	06586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6588	07765	06587	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6589	07766	06588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6590	07768	06589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6591	07769	06590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6592	07770	06591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6593	07771	06592	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6594	07773	06593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6595	07774	06594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6596	07775	06595	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6597	07776	06596	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6598	07777	06597	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6599	07778	06598	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6600	07779	06599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6601	07780	06600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6602	07781	06601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6603	07782	06602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6604	07783	06603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6605	07785	06604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6606	07786	06605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6607	07787	06606	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6608	07788	06607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6609	07789	06608	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 184

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	BH	BI	BK
5610	07790	06609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5611	07792	06610	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5612	07793	06611	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5613	07794	06612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5614	07795	06613	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1813
5615	07796	06614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5616	07797	06615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5617	07798	06616	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5618	07800	06617	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5619	07801	06618	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5620	07802	06619	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5621	07804	06620	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5622	07805	06621	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5623	07807	06622	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5624	07808	06623	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5625	07810	06624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5626	07811	06625	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5627	07812	06626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5628	07813	06627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5629	07814	06628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5630	07815	06629	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5631	07816	06630	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1766
5632	07817	06631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5633	07818	06632	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5634	07819	06633	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5635	07820	06634	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5636	07821	06635	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5637	07822	06636	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5638	07823	06637	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5639	07824	06638	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5640	07826	06639	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5641	07827	06640	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5642	07828	06641	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5643	07829	06642	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5644	07831	06643	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5645	07834	06644	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 185

Table 186

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AV	AY	B	BC	BE	BF	BG	BH	BI	BK
6646	07835	06645	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6647	07836	06646	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6648	07837	06647	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6649	07838	06648	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6650	07839	06649	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6651	07840	06650	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6652	07841	06651	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6653	07844	06652	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6654	07845	06653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6655	07848	06654	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6656	07849	06655	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6657	07850	06656	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6658	07852	06657	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6659	07853	06658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6660	07854	06659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6661	07855	06660	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6662	07856	06661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6663	07857	06662	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6664	07858	06663	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6665	07859	06664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6666	07860	06665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6667	07861	06666	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6668	07862	06667	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6669	07863	06668	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6670	07864	06669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6671	07865	06670	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6672	07866	06671	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6673	07868	06672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6674	07869	06673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6675	07870	06674	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6676	07871	06675	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6677	07872	06676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6678	07875	06677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6679	07876	06678	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6680	07878	06679	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6681	07879	06680	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

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A	B	C	F	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AV	AY	BA	BC	BE	BF	BG	BI	BK
6682	07880	06681	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6683	07881	06682	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6684	07882	06683	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6685	07883	06684	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6686	07884	06685	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6687	07885	06686	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6688	07886	06687	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6689	07887	06688	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6690	07889	06689	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6691	07890	06690	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6692	07891	06691	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6693	07892	06692	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6694	07893	06693	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6695	07894	06694	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6696	07895	06695	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6697	07896	06696	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6698	07897	06697	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6699	07898	06698	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6700	07900	06699	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6701	07901	06700	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6702	07902	06701	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6703	07903	06702	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6704	07904	06703	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6705	07905	06704	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6706	07909	06705	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6707	07911	06706	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6708	07912	06707	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6709	07913	06708	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6710	07915	06709	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6711	07916	06710	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6712	07917	06711	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6713	07918	06712	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6714	07919	06713	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6715	07920	06714	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6716	07921	06715	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6717	07922	06716	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 187









	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BAB	BC	BE	BF	BGBH	BI	BK	
6026	08054	06825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6827	08055	06826	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0						
6828	08056	06827	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	L13463	99.5	207	1	1139	1345
6829	08057	06828	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6830	08058	06829	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6831	08059	06830	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6832	08060	06831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6833	08061	06832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6834	08062	06833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6835	08063	06834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6836	08064	06835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6837	08065	06836	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6838	08066	06837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6839	08067	06838	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6840	08068	06839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6841	08069	06840	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6842	08070	06841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6843	08071	06842	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6844	08073	06843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6845	08074	06844	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6846	08075	06845	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6847	08076	06846	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6848	08077	06847	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6849	08078	06848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6850	08079	06849	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6851	08080	06850	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6852	08081	06851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6853	08082	06852	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6854	08083	06853	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6855	08084	06854	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6856	08085	06855	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6857	08086	06856	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6858	08087	06857	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6859	08088	06858	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6860	08089	06859	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6861	08090	06860	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

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6898	08128	06897	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6899	08129	06898	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6900	08130	06899	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6901	08131	06900	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6902	08132	06901	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6903	08133	06902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6904	08134	06903	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6905	08135	06904	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6906	08136	06905	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6907	08137	06906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6908	08138	06907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6909	08139	06908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6910	08140	06909	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6911	08141	06910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6912	08142	06911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6913	08143	06912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6914	08144	06913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6915	08145	06914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6916	08146	06915	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6917	08147	06916	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6918	08148	06917	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6919	08149	06918	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6920	08150	06919	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6921	08151	06920	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6922	08153	06921	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6923	08154	06922	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6924	08155	06923	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6925	08156	06924	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6926	08157	06925	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6927	08158	06926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6928	08159	06927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6929	08160	06928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6930	08161	06929	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6931	08162	06930	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6932	08163	06931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6933	08164	06932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BI	BK
6934	08165	06933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6935	08166	06934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6936	08167	06935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6937	08168	06936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6938	08169	06937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6939	08170	06938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6940	08172	06939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6941	08173	06940	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6942	08174	06941	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6943	08175	06942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6944	08176	06943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6945	08177	06944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6946	08178	06945	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
6947	08179	06946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6948	08180	06947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6949	08181	06948	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
6950	08182	06949	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6951	08184	06950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6952	08185	06951	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6953	08186	06952	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
6954	08188	06953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6955	08189	06954	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6956	08190	06955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6957	08191	06956	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6958	08192	06957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6959	08193	06958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6960	08194	06959	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6961	08195	06960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6962	08196	06961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6963	08197	06962	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6964	08198	06963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6965	08199	06964	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6966	08200	06965	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6967	08201	06966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
6968	08202	06967	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
6969	08203	06968	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	CA	IA	AK	AM	AO	AS	AT	AW	AY	BABC	BE	BF	BGBH	BI	BK
6970	08204	06969	1																													
6971	08205	06970	1																													
6972	08206	06971	1																													
6973	08207	06972	1																													
6974	08208	06973	1																													
6975	08209	06974	1																													
6976	08210	06975	1																													
6977	08211	06976	1																													
6978	08212	06977	1																													
6979	08213	06978	1																													
6980	08214	06979	1																													
6981	08215	06980	1																													
6982	08216	06981	1																													
6983	08217	06982	1																													
6984	08218	06983	1																													
6985	08219	06984	1																													
6986	08220	06985	1																													
6987	08221	06986	1																													
6988	08222	06987	1																													
6989	08223	06988	1																													
6990	08224	06989	2																													
6991	08225	06990	1																													
6992	08226	06991	1																													
6993	08227	06992	1																													
6994	08228	06993	1																													
6995	08229	06994	1																													
6996	08230	06995	1																													
6997	08232	06996	1																													
6998	08233	06997	1																													
6999	08234	06998	1																													
7000	08235	06999	3																													
7001	08236	07000	1																													
7002	08237	07001	2																													
7003	08238	07002	1																													
7004	08239	07003	1																													
7005	08240	07004	1																													

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AW	AY	B	ABC	BE	BF	BG	BI	BK
7006	08241	07005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7007	08242	07006	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7008	08243	07007	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7009	08244	07008	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7010	08245	07009	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7011	08246	07010	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7012	08247	07011	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7013	08248	07012	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7014	08249	07013	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7015	08250	07014	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7016	08251	07015	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7017	08252	07016	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7018	08253	07017	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7019	08254	07018	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7020	08255	07019	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7021	08256	07020	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7022	08257	07021	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7023	08258	07022	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7024	08259	07023	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7025	08260	07024	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7026	08261	07025	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7027	08262	07026	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7028	08263	07027	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7029	08264	07028	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7030	08265	07029	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7031	08266	07030	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7032	08267	07031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7033	08268	07032	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7034	08269	07033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7035	08270	07034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7036	08271	07035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7037	08272	07036	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7038	08273	07037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7039	08274	07038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7040	08275	07039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7041	08276	07040	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7042	08277	07041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7043	08278	07042	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0						
7044	08279	07043	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0						
7045	08280	07044	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7046	08281	07045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
7047	08282	07046	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7048	08283	07047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7049	08284	07048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7050	08285	07049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7051	08286	07050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7052	08287	07051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7053	08288	07052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7054	08289	07053	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7055	08290	07054	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7056	08291	07055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7057	08292	07056	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7058	08293	07057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7059	08294	07058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7060	08295	07059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7061	08296	07060	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7062	08297	07061	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0					
7063	08298	07062	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7064	08299	07063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7065	08300	07064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7066	08301	07065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7067	08302	07066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7068	08303	07067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7069	08304	07068	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7070	08305	07069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7071	08306	07070	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7072	08307	07071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7073	08308	07072	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7074	08309	07073	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7075	08310	07074	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7076	08311	07075	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
7077	08312	07076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	DE	BF	BG	BH	BI	BK
7078	08313	07077	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7079	08314	07078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7080	08315	07079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7081	08316	07080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7082	08317	07081	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7083	08318	07082	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7084	08319	07083	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7085	08320	07084	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7086	08321	07085	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7087	08322	07086	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7088	08323	07087	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7089	08324	07088	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7090	08325	07089	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7091	08326	07090	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7092	08327	07091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7093	08328	07092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7094	08329	07093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7095	08330	07094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7096	08331	07095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7097	08332	07096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7098	08333	07097	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7099	08334	07098	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7100	08335	07099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7101	08336	07100	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7102	08337	07101	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7103	08338	07102	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7104	08339	07103	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7105	08340	07104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7106	08341	07105	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7107	08342	07106	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7108	08343	07107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7109	08344	07108	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7110	08345	07109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7111	08346	07110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7112	08347	07111	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7113	08348	07112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

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[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
7150	08386	07149	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7151	08387	07150	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7152	08388	07151	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7153	08389	07152	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7154	08390	07153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7155	08391	07154	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7156	08392	07155	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7157	08393	07156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7158	08394	07157	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7159	08395	07158	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7160	08396	07159	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7161	08397	07160	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7162	08398	07161	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7163	08399	07162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7164	08400	07163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7165	08402	07164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7166	08403	07165	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7167	08404	07166	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7168	08405	07167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7169	08406	07168	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7170	08407	07169	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7171	08408	07170	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7172	08409	07171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7173	08410	07172	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7174	08411	07173	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7175	08412	07174	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7176	08413	07175	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7177	08414	07176	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7178	08415	07177	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7179	08416	07178	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7180	08417	07179	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7181	08418	07180	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7182	08419	07181	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7183	08420	07182	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7184	08421	07183	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7185	08422	07184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7186	08423	07185	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7187	08424	07186	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7188	08425	07187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7189	08426	07188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7190	08427	07189	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7191	08428	07190	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7192	08429	07191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7193	08430	07192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7194	08431	07193	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7195	08432	07194	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7196	08434	07195	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7197	08435	07196	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7198	08436	07197	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7199	08437	07198	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7200	08438	07199	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7201	08439	07200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7202	08440	07201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7203	08441	07202	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7204	08442	07203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7205	08443	07204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7206	08444	07205	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7207	08445	07206	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7208	08446	07207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7209	08447	07208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7210	08448	07209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7211	08449	07210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7212	08450	07211	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7213	08451	07212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7214	08452	07213	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7215	08453	07214	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7216	08454	07215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7217	08455	07216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7218	08456	07217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7219	08457	07218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7220	08458	07219	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7221	08459	07220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 201

Table 202

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AT	AW	AY	BABC	BE	BF	BGBH	BI	BK
7222	08460	07221	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7223	08461	07222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7224	08462	07223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7225	08463	07224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7226	08464	07225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7227	08465	07226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7228	08466	07227	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7229	08467	07228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7230	08468	07229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7231	08469	07230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7232	08470	07231	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7233	08471	07232	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7234	08472	07233	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7235	08473	07234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7236	08474	07235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7237	08475	07236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7238	08476	07237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7239	08477	07238	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7240	08478	07239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7241	08479	07240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7242	08480	07241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7243	08481	07242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7244	08482	07243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7245	08483	07244	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7246	08484	07245	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7247	08485	07246	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7248	08486	07247	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7249	08487	07248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7250	08488	07249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7251	08489	07250	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7252	08490	07251	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7253	08491	07252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7254	08492	07253	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7255	08493	07254	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7256	08494	07255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7257	08495	07256	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
7258	08496	07257	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7259	08497	07258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7260	08498	07259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7261	08499	07260	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7262	08500	07261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7263	08501	07262	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7264	08502	07263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7265	08503	07264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7266	08504	07265	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7267	08505	07266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7268	08506	07267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7269	08507	07268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7270	08508	07269	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7271	08509	07270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7272	08510	07271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7273	08511	07272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7274	08512	07273	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7275	08513	07274	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7276	08514	07275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7277	08515	07276	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7278	08516	07277	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7279	08517	07278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7280	08518	07279	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7281	08519	07280	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7282	08520	07281	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7283	08521	07282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7284	08522	07283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7285	08523	07284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7286	08524	07285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7287	08525	07286	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7288	08526	07287	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7289	08527	07288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7290	08528	07289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7291	08529	07290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7292	08530	07291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7293	08531	07292	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 203

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7294	08532	07293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7295	08533	07294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7296	08534	07295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7297	08535	07296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7298	08536	07297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7299	08537	07298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7300	08538	07299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7301	08539	07300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7302	08540	07301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7303	08541	07302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7304	08542	07303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7305	08543	07304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7306	08544	07305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7307	08545	07306	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7308	08546	07307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7309	08547	07308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7310	08548	07309	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7311	08549	07310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7312	08550	07311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7313	08551	07312	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7314	08552	07313	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7315	08553	07314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7316	08554	07315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7317	08555	07316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7318	08556	07317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7319	08557	07318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7320	08558	07319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7321	08559	07320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7322	08560	07321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7323	08561	07322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7324	08563	07323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7325	08564	07324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7326	08565	07325	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7327	08566	07326	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7328	08567	07327	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7329	08568	07328	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						

Table 204

Table 205

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AT	AW	AY	BABC	BE	BF	BGBH	BI	BK
7330	08569	07329	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7331	08570	07330	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7332	08571	07331	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7333	08572	07332	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7334	08573	07333	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7335	08574	07334	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7336	08575	07335	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7337	08576	07336	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7338	08577	07337	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7339	08578	07338	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7340	08579	07339	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7341	08580	07340	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7342	08581	07341	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7343	08582	07342	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7344	08583	07343	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7345	08584	07344	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7346	08585	07345	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7347	08586	07346	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7348	08587	07347	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7349	08588	07348	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7350	08589	07349	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7351	08591	07350	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7352	08592	07351	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7353	08593	07352	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7354	08594	07353	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7355	08595	07354	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7356	08596	07355	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7357	08597	07356	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7358	08598	07357	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7359	08599	07358	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7360	08600	07359	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7361	08601	07360	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7362	08602	07361	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7363	08603	07362	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7364	08604	07363	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7365	08605	07364	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BAB	BE	BF	BG	BH	BI	BK
7366	08606	07365	1																															
7367	08607	07366	1																															
7368	08608	07367	1																															
7369	08609	07368	1																															
7370	08610	07369	1																															
7371	08611	07370	1																															
7372	08612	07371	1																															
7373	08613	07372	1																															
7374	08614	07373	1																															
7375	08615	07374	1																															
7376	08616	07375	1																															
7377	08617	07376	1																															
7378	08618	07377	1																															
7379	08619	07378	1																															
7380	08620	07379	1																															
7381	08621	07380	1																															
7382	08622	07381	1																															
7383	08623	07382	1																															
7384	08624	07383	1																															
7385	08625	07384	1																															
7386	08626	07385	1																															
7387	08627	07386	1																															
7388	08628	07387	1																															
7389	08629	07388	1																															
7390	08630	07389	1																															



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AK	AM	AN	AO	AS	AT	AW	AY	B	ABC	BE	BF	BG	BH	BI	BK
7402	08642	07401	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7403	08643	07402	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7404	08644	07403	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7405	08645	07404	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7406	08646	07405	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7407	08647	07406	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7408	08648	07407	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7409	08649	07408	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7410	08650	07409	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7411	08651	07410	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7412	08652	07411	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7413	08653	07412	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7414	08654	07413	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7415	08655	07414	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7416	08656	07415	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7417	08657	07416	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7418	08658	07417	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7419	08659	07418	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7420	08660	07419	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7421	08661	07420	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7422	08662	07421	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7423	08663	07422	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7424	08664	07423	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	
7425	08665	07424	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7426	08666	07425	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7427	08667	07426	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7428	08668	07427	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7429	08669	07428	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7430	08670	07429	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7431	08671	07430	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7432	08673	07431	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7433	08674	07432	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7434	08675	07433	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7435	08676	07434	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7436	08677	07435	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
7437	08678	07436	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	

Table 207

[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	AI	AK	AM	AO	AS	AV	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7510	08751	07509	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7511	08752	07510	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7512	08753	07511	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7513	08754	07512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7514	08755	07513	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7515	08756	07514	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7516	08757	07515	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7517	08758	07516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7518	08759	07517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7519	08760	07518	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7520	08761	07519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7521	08762	07520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7522	08763	07521	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7523	08764	07522	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7524	08765	07523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7525	08766	07524	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7526	08768	07525	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7527	08769	07526	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7528	08770	07527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7529	08771	07528	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7530	08772	07529	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7531	08773	07530	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7532	08774	07531	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7533	08775	07532	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7534	08777	07533	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7535	08778	07534	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7536	08779	07535	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7537	08780	07536	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7538	08781	07537	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7539	08782	07538	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7540	08783	07539	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7541	08785	07540	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7542	08786	07541	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7543	08787	07542	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7544	08788	07543	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7545	08789	07544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 210

Table 211

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7546	08790	07545	1																														
7547	08791	07546	1																														
7548	08792	07547	1																														
7549	08793	07548	1																														
7550	08794	07549	1																														
7551	08795	07550	4																														
7552	08796	07551	1																														
7553	08797	07552	1																														
7554	08798	07553	1																														
7555	08799	07554	1																														
7556	08800	07555	1																														
7557	08801	07556	1																														
7558	08802	07557	1																														
7559	08803	07558	1																														
7560	08804	07559	1																														
7561	08805	07560	1																														
7562	08807	07561	1																														
7563	08808	07562	1																														
7564	08809	07563	1																														
7565	08810	07564	1																														
7566	08811	07565	1																														
7567	08812	07566	1																														
7568	08813	07567	1																														
7569	08814	07568	1																														
7570	08815	07569	1																														
7571	08816	07570	1																														
7572	08817	07571	1																														
7573	08818	07572	1																														
7574	08819	07573	1																														
7575	08820	07574	1																														
7576	08821	07575	1																														
7577	08822	07576	1																														
7578	08823	07577	1																														
7579	08824	07578	1																														
7580	08825	07579	1																														
7581	08826	07580	1																														

Table 212

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7582	08827	07581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7583	08828	07582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7584	08829	07583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7585	08830	07584	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7586	08831	07585	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0				
7587	08832	07586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7588	08833	07587	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7589	08834	07588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7590	08835	07589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7591	08836	07590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7592	08837	07591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7593	08838	07592	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7594	08839	07593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7595	08840	07594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7596	08841	07595	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7597	08842	07596	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7598	08843	07597	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7599	08844	07598	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7600	08845	07599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7601	08846	07600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7602	08848	07601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7603	08849	07602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7604	08850	07603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7605	08851	07604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7606	08852	07605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7607	08853	07606	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7608	08854	07607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7609	08855	07608	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0				
7610	08856	07609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7611	08857	07610	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7612	08858	07611	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0				
7613	08859	07612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7614	08860	07613	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7615	08861	07614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7616	08862	07615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
7654	08900	07653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7655	08901	07654	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7656	08902	07655	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7657	08903	07656	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7658	08904	07657	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7659	08905	07658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7660	08906	07659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7661	08908	07660	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7662	08909	07661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7663	08910	07662	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7664	08912	07663	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7665	08913	07664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7666	08914	07665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7667	08915	07666	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7668	08916	07667	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7669	08917	07668	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7670	08919	07669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7671	08920	07670	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7672	08921	07671	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7673	08922	07672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7674	08923	07673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7675	08924	07674	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7676	08925	07675	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7677	08926	07676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7678	08927	07677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7679	08928	07678	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7680	08929	07679	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7681	08930	07680	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7682	08931	07681	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7683	08932	07682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7684	08933	07683	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7685	08934	07684	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7686	08935	07685	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7687	08936	07686	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7688	08937	07687	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7689	08938	07688	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 214



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7690	08939	07689	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7691	08940	07690	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7692	08941	07691	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7693	08942	07692	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7694	08943	07693	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7695	08944	07694	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7696	08945	07695	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7697	08946	07696	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7698	08947	07697	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7699	08948	07698	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7700	08949	07699	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7701	08950	07700	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7702	08951	07701	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7703	08952	07702	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7704	08953	07703	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7705	08954	07704	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7706	08955	07705	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7707	08956	07706	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7708	08957	07707	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7709	08958	07708	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7710	0																														

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7726	08975	07725	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7727	08976	07726	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7728	08977	07727	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7729	08978	07728	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7730	08979	07729	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7731	08980	07730	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7732	08981	07731	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7733	08982	07732	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7734	08983	07733	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7735	08984	07734	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7736	08985	07735	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7737	08986	07736	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7738	08987	07737	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	014695	95.5359	1	1316	1860	
7739	08988	07738	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0					
7740	08989	07739	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7741	08990	07740	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7742	08991	07741	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7743	08992	07742	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7744	08993	07743	1	0	0	0	0	0																										

Table 217

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AT	AW	AY	BABC	BE	BF	BG	BH	BI	BK
7762	09011	07761	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7763	09012	07762	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7764	09013	07763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7765	09014	07764	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7766	09015	07765	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7767	09016	07766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7768	09017	07767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7769	09018	07768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7770	09019	07769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7771	09020	07770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7772	09021	07771	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7773	09022	07772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7774	09023	07773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7775	09024	07774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7776	09025	07775	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7777	09026	07776	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7778	09027	07777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7779	09028	07778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7780	09029	07779	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7781	09030	07780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7782	09031	07781	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7783	09032	07782	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7784	09033	07783	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7785	09034	07784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7786	09035	07785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7787	09036	07786	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7788	09037	07787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7789	09038	07788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7790	09039	07789	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7791	09040	07790	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7792	09041	07791	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7793	09042	07792	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7794	09043	07793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7795	09044	07794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7796	09045	07795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7797	09046	07796	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 218

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
7798	09047	07797	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	160047	95	261	1	103	1163	
7799	09048	07798	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7800	09049	07799	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7801	09050	07800	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3							
7802	09051	07801	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	100269	94	6	351	1	1268	1617
7803	09052	07802	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7804	09053	07803	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7805	09054	07804	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7806	09055	07805	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7807	09056	07806	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7808	09057	07807	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7809	09058	07808	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7810	09059	07809	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7811	09060	07810	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7812	09061	07811	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7813	09062	07812	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7814	09063	07813	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7815	09064	07814	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7816	09065	07815	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7817	09066	07816	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7818	09067	07817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7819	09068	07818	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7820	09069	07819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7821	09070	07820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7822	09071	07821	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7823	09072	07822	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7824	09073	07823	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3							
7825	09074	07824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7826	09075	07825	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2							
7827	09076	07826	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7828	09077	07827	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7829	09078	07828	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7830	09079	07829	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2							
7831	09080	07830	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2							
7832	09081	07831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							
7833	09082	07832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7834	09083	07833	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7835	09084	07834	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7836	09085	07835	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	X56976	92 287	1	3066	3419	
7837	09086	07836	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7838	09087	07837	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						

Table 219

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.  
(B) STREET: 41-8, Takada 3-chrome, Toshima-ku  
(C) CITY: Tokyo  
(E) COUNTRY: JAPAN  
(F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

(iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/ MS-DOS  
(D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: EP 95900295.7

(vi) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: PCT/JP94/01916  
(B) FILING DATE: 11. November 1994

SEQ ID NO:1

SEQUENCE LENGTH:704

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00001

SEQUENCE DESCRIPTION:

GATCTTCAAA CAAGCATCAG CGTTTCCAG GGCTTCCCAG AGGTCTGTGC GACTAGCCCG 60  
 TGTCTATCAA AAGTTATTAG AGAGGATGAA GCATTAGCTT GAAGCACTAC AGGAGGAATG 120  
 CACCACGGCA GCTCTCCGCC AATTCTCTC AGATTTCAC AGAGACTGTT TGAATGTTTT 180  
 CAAAACCAAG TATCACAATT TAATGTACAT GGGCCGCACC ATAATGAGAT GTGAGCCTTG 240  
 TGCATGTGGG GGAGGAGGGA GAGAGATGTA CTTTTTAAAT CATGTTCCC CTAACATGG 300  
 CTGTTAACCC ACTTGTCATGC AGAACTTGG GATGTCATT GCCTGACATT CACTTCCAG 360  
 GAGAGGACCC TATCCCCAAA TGTGGAATTG ACTTGCTAT GGCCAAGGTC CCTTGGNAAA 420  
 GGGAGCTTCA GTATTTGTGG GGGCNTCATA AAACCATGGN TTCAAGNCAA TCCAGCCTCA 480  
 TNGGGNNGGT CCTGGGNACA GTTTTTGGT AAAGGCCCTT GGCCAGNTG GGGGGAATGG 540  
 GCCTCCTTTT TAAGNTTGG GNTGGAATNG TCTNGCAAAT TGGGGCTCCC ATTTCNCGGG 600  
 GGTTGGGGG TTTTNGGG CCTTNCNGG NNGGAAGGGN TGGGTTGGG GGNTNGGTTN 660  
 CCNTTGGGNG GGCCTGGGN TTTGATTNA CCCGGGNCCT NGGN 704

SEQ ID NO:2

SEQUENCE LENGTH:659

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00002

SEQUENCE DESCRIPTION:

GATCTTTAAA ATACACACTC AAATCAAGAA ACTTAAGGTT ACCTTTNTTC CCAAATTTCA 60  
 TACCTATCAT CTTAAGTAGG GACTTCTGTC TTCACAACAN ATTATNACCT TACAGAAGTT 120  
 TGAATTATCC GGTGGGTTT TATTGTTTAA AATCATTTCT GCATCAGCTG CTGAAACAAC 180  
 AAATAGGAAT TGTTTTATG GAGGCTTTC ATAGATTCCC TGAGCAGGAT TTTAATCTTT 240  
 TNCTAACTGG ACTGGTCAA ATGTTGTNCT CTCTTTAAA GGGATGGCAA GATGTGGGCA 300  
 GTGATGTCAC TTAGGGCAGG GACAGGATAA GAGGGNTTAG GGAGAGAAGA TAGCAGGGCA 360  
 TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGGAGCAG GCTACTGTCA AGCTCCCCTC 420  
 GGAGGCGGNG CTGGTTCACA GCCAGCTGGC ACCAGNTTTT NTNGNGGAAG NCTTTTCAA 480  
 ACAGTCTCAG GNAATCCAAT NTGCAAAGAC TTGCTTNAG NAAAACCCAG NAGTTGAAAG 540  
 GCTCCCAAGN ATTTTAAGGG NACTTNCCAA AACGGGGCCC CNGGNCCCTT TTGGGTTTNG 600  
 GGGNTCAAAA CCCCAGAGG GTTTGGGAAG NTTTAATTG GNTTTAAAN ATNNNTNTN 659

SEQ ID NO:3

SEQUENCE LENGTH:625

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00003

SEQUENCE DESCRIPTION:

GATCTAACTG GGTACCTGAG ATATTTNACA GCTGGACCTA GTTTCACAA CTGTTGTCTC 60

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CAGCTCTGCA TATGTCTGGC CAGGGGGCTT CTAGGAAGTA GGTTCATCT ATCAAATGTC 120  
 TCCTCTGACT TCCTTTTGAA ACTTACTGCT CTTCTGTTTT ATTTTGTTTT GTTTGAAGCT 180  
 CAGAGGGAGA TGGGCAATTG ACAGGGATGC AATCCAGGGT GGGATTTCTT GAGGAAAGTTA 240  
 CAAATAAGCT TGTTACAACA TCAAGATAGA TGGAAATTGGA AGGATGCTAC CAGGAGAGTA 300  
 CTTACATAGT GCTCAGGAGT TTCTCTTCTT AAAATGTTTA CTGCTGAAAG ATGAGCAGGA 360  
 CCAGGGCGTT ATAGGCAGAG CCCTAGCCGA GAAACCTGCT GGCCTCTGCC TGTTTTTCATT 420  
 TCCCACTTTT GGTGTGTGTG GCATTACTTT CAGAATTGTC ACTTTCCTGC TTGTCATGAC 480  
 TTTTTTGCCA CACTTGCCAT GACGGGTGTT TCTGNGAACC ATGGAAGTTT TGCGGTAGTG 540  
 CCTCCAGGGG CAGGGGGNAA GGAGGNGGTG TANCTGCATT TNGTNCAAAT AAATCCNGCC 600  
 TATTGTTAAT NAACCAGTCT TTTGN 625

SEQ ID NO:4

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00004

SEQUENCE DESCRIPTION:

GATCTGCCAG GCTGGGGTGT TTTCGGTATC TGCTGTTCAC AGGTCTCCAC TGTAATCCGA 60  
 ATACTTTGCC AGTGCATAA TCTCTTTGGA GATAAAATTC ATTAGTGTGT TACTAAATGT 120  
 NAATTTTNTT TTGCGGAAAA TACAGTACCG TGTCTGANTT AATTATTAAT ATTNAAAAATA 180  
 CTTCAATCCT TAACTCTCCC TCATTTGCTT TGCCACAGC CTATTCAGTT CCTTTGTTTG 240  
 GCAGGNTTCT GCAAAA 256

SEQ ID NO:5

SEQUENCE LENGTH:616

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00005

SEQUENCE DESCRIPTION:

GATCAAGCTC AAGAATAAGC TGAAATATGG CCAGACTATC AGGCCCATTT NTCTCCCCTG 60  
 CACCGAGGGA ACAACTCGAG CTTTGAGGCT TCCTCCAACCT ACCACTTGCC AGCAACAAAA 120  
 GGAAGAGCTG CTCCCTGCAC AGGATATCAA AGCTCTGTTT GTGTCTGAGG AGGAGAAAAA 180  
 GCTGACTCGG AAGGAGGTCT ACATCAAGAA TGGGGATAAG AAAGGCAGCT GTGAGAGAGA 240  
 TGCTCAATAT GCCCAGGCT ATGACAAAGT CAAGGACATC TCAGAGGTGG TCACCCCTCG 300  
 GTTCCTTTGT ACTGGAGGAG TGAGTCCCTA TGCTGACCCC AATACTTGCA GAGGTGATTC 360  
 TGGCGGCCCC TTGATAGTTC ACAAGAGAAG TCGTTTCATT CAAAGTTGGT GTAATCAGCT 420  
 GGGGGAGTAA GTGGGATGTN TGCAAAAACC AGAAGGCGGC AAAAGCAGGT ACCTGNTTCA 480  
 NGGCCCGAAC TTTCACATCA NCTNTTCAA GGTNTNCCT GGNTGAGGNG GAACNTCCAN 540  
 GTTGGGGGTT TTGGGTTTTT TTAAGGGGTT CNTGTTNGCA AGGGGGTTGG GNTTNNTTTA 600  
 NNCCTGTTNN GNACCN 616

SEQ ID NO:6

SEQUENCE LENGTH:615

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



CLONE:HUMGS00006

SEQUENCE DESCRIPTION:

5 GATCTCTGCT ATTTTANCCC CCCAAATAAG TTATTTGTCC TTAAAGGTTG GTTACNNATA 60  
 ATACCCCTCA GTAAGATTCC AGTATTAATT TCTGGGCAGT TTGTTCTCTG TATACAATTG 120  
 CAAATGATAA GCATTTTTGT GAGTGACCAC CTTTGCAATA TGTTTGTTAA TTNTTCATGT 180  
 TGGGTTCTTT CTGAAATGTA CATCTTTACA TAAAAACCTC ACATTCTACT TGATTTACAC 240  
 TTCCTAGTCT ACATTACATG TGGTTGAAGG TTTTATACAT TCTATATGCT TTTACTAAAT 300  
 10 ATACAAGATT TACTACTAGA AATTTGGAGA AAGAACACTA ACACATGTAC TTGTGATTG 360  
 TTCATGTTAT ATTA AACCT TGAGATTGT GTATTTATGT AGGGGGGGGT ATTGNCCAGG 420  
 NCTGNTGGTT TTTTGCTCCN TGGGGCTATT NTAATAAANC NGGGGTATNG GGTGNTGGC 480  
 CTNGGTTTGG GCCTAAANTT GGATATATNT GGGGTTCCCT NGNTTTTACC AAAATNGNTT 540  
 15 TTGGTTGGTA GGGTTNTTAT TGGACCCNNT CCTGGGCCTG GGATAATNTG GCNGNTTCCC 600  
 NGGANAAAAAN NCCCN 615

SEQ ID NO:7

SEQUENCE LENGTH:608

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00007

SEQUENCE DESCRIPTION:

25 GATCAAACCA AAGGAAAAGT GTTGCTAGAG AAAATTGGGG AAAAGGTGAA AAAGAAAAAA 60  
 TGGTAGTAAT TGAGCAGAAA AAAATTAATT TATATATGTA TTGATTGGCA ACCAGATTTA 120  
 TCTAAGTAGA ACTGAATTGG CTAGGAAAAA AGAAAACTG CATGTTAATC ATTTTCCTAA 180  
 GCTGTCCTTT TGAGGCTTAG TCAGTTTATT GGGAAAATGT TTAGGATTAT TCCTTGCTAT 240  
 TAGTACTCAT TTTATGTATG TTACCCTTCA GTAAGTTCTC CCCATTTTAG TTTTCTAGGC 300  
 30 TGAAAGGATT CTTTTCTACA TTATACATGT GTGTTGTCAT ATTTGGCTTT TGCTATATAC 360  
 TTTACCTTCA TTGTTAAATT TTTGTATTGT ATAGTTNCTT TGGNGGTATC TTA AACCT 420  
 ATTTTGA AAA ACCAACCTTG GCTTTGNTAA NCATTTGGGC CGCTGGGTA NGTCCGGACC 480  
 TNNCCTTNC CCCNAGGGCC TGTCAGGAGN GCCGGNTTN CCGGGGNGTT GGNCCCGNNG 540  
 35 CCTTCCCGAT TTTTNGGGGT TGGGTCCTTN GGTTNCCGGC NTCTGTANGG GGTNCNCCTT 600  
 TTNNNCCN 608

SEQ ID NO:8

SEQUENCE LENGTH:606

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00008

SEQUENCE DESCRIPTION:

45 GATCGCTTCC TAGAAATAAG CAACACCTCT CCCAAAAAGC AGCCCACAAG GCAGGGGCCA 60  
 GCAGCCCAGC CATCACTCAT CTTNAGGAA ATNAGTTGGT AGCCTCTGTG CACTGTTTGG 120  
 TGCCACATC ANNGGTGATG TCCTGTTCAC ATACCTGCTT GTATTTAAAG CCCTCAGTCT 180  
 GTCTGTTGT GTGGGGCGAA GTGATGGACT CTGCCAGGTG GACATGCTGT GGGTGGATGT 240  
 TCCGGCGTG TGCCGGCCTG AATGGACAGG GGTCACTCA CAAGCATGTC AGGGAAAATC 300  
 50 ACTGTCACAC AATTCCAATG GATTTTGTGC TCTTTTGA AAAAAAAT TCTTTAGCGT 360  
 AAACCATGNA TTTTTTTTCA ATGTAGNCCC TTGGGGANTG AANTGAAATT TTGGGCTTCT 420

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TCANATNCGN AAAATNAAAT TTTTACCCCT GAGGGGGGGA GCCCCTTTCT GAAAGAAGGT 480  
 NTGGGCCAAA AGCCCTTTTA ATGNTTGCTG GCCNTTGNTG GTTTTNANNG TCCANTTGC 540  
 TTGGGGCGAA NGCCGNNNTG ANAAAGGTGG GTTTCNCTGG NGGNTTTAAG GNGGTGGTTT 600  
 GNTTTN 606

SEQ ID NO:9

SEQUENCE LENGTH:606

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00009

SEQUENCE DESCRIPTION:

GATCTTCANN NGTTAAGCAC TTGCTCTNAA GATTAAAATT CCTTTTCTTT TTAAGGTAA 60  
 GGGTGTGTAC GTATGGCAGT GATGTCTATG TTGAGATTAA CTTATGTATT GAGGAAAATT 120  
 TGAAGTTTAT TTTTTCGATG AATAAGGCTG TCAAATNATT TAGTATAGAT TAATGACATC 180  
 TTTTITAGAA ATATTAAAGT GAGTATTCCT CATTATGTCA TCATTTCTGA TAATTAGAGT 240  
 GCTAATTGTA ATGTTAGATA ATGNTTCCAC ATCTATACCT ATTTCTTTCT AGGGCACTTC 300  
 TGACCTGGG GCTTGGGGAT GGCCTTTAGG CACAAGTAGT GTCTGTGTTA AGTTCATAA 360  
 ATGTGTATTT AATGAGAAAC ATTCNATGT AAAAATGTGT GTATGTGAAC GTATGCNNAC 420  
 ATTGTTATTG TGCACNGTA CATTGTGAAG AAGTAGTTT GAAATTTGT AANGCACAAC 480  
 CCTTAANGNG GTGTGGAGTT ATTAAANTGN TGTAGGCNCA AATGTAATGT TTAGCCTATA 540  
 AAAGGCCCTC CTATTGTCCN TNGGCAAGGC TTTGNCNCTT GNAANTAAAN CCCGTNTTTG 600  
 TTTAAA 606

SEQ ID NO:10

SEQUENCE LENGTH:606

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00010

SEQUENCE DESCRIPTION:

GATCAGGGGA GACCCCAACT GCCAGATATA TTTTAATGTA CAAAACTGAA ACCAGATGAA 60  
 ATAATGTTCT GTCACGTGAA ATATTTAAGT ATATAGTATA TTTTACTCT AGAACATGCA 120  
 CATTTATATA TATATGTATA TGTATATATA TATAGTAACT ACTTTTATA CTCCATACAT 180  
 AACTTGATAT AGGAAGCTGT TTATTTATTC ACTGTAAGTT TATTTTTTCT ACACAGTAAA 240  
 ACTTGACTA TGTTAATACC TTGTCCTATG TCAATTTGTA TATCATGAAA CACTTCTCAT 300  
 CATATTGTAT GTAAGTAATT GCATTTCTGC TCTTCCAAAG CTCCTGCGTC TGTTTTTAAA 360  
 GAGCATGGAA AAATACTGCC TAGGAAAATG CAAAATGGAA ATAGGAGAGA GTAGGTTTTT 420  
 CAGCTTAGTT TTGAGGGGGG CCGGTTACCT TGTATATTCC CCCATTCACTA TTTGGTGTCC 480  
 ATGTGTAGGG GAAGGTAAAG GGGTGGTTCC ATAATCAAGT TCCCCGTGGG GTGTNCCCCC 540  
 TGTTAAATGT CCCTGGTTTG GTGTTACCCG GGCTTTATGG GNCCTTTCA TTATTCCGG 600  
 TNGGGN 606

SEQ ID NO:11

SEQUENCE LENGTH:598

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00011

SEQUENCE DESCRIPTION:

5 GATCAACAAA AGATAAACAA ATTTGCACGG AATACAAGTA GAATCACAGA GCTGAAGGAA 60  
 GAAATAGAAG TAAAAAAGAA ACAACTCCAA AACCTAGAAG ATGCTTGTA TGACATCATG 120  
 CTTGCAGATG ATGATTGCTT AATGATACCT TATCAAATTG GTGATGTCTT CATTAGCCAT 180  
 TCTCAAGAAG AAACGCAGAA ATGTTAGAAG AAGCAAAGAA AAATTTGCAA GAAGAAATTG 240  
 ACGCCTTAGA ATCCAGAGTG GAATCAATTC AGCGAGTGTT AGCANGATTT GAAAGTTCAG 300  
 10 TTGTATGCAA AATTCGGGAG CAACATAAAC CTTGAAGCTN GATGAAAGTT AAACATTTTA 360  
 TAATACTTTT TTTATTTGNT TTAATAANCT TGATTATTTG TTTAANATGG TAATTTTTTCC 420  
 TTCTTCANAT GCGGNNGGGT NAGCAAANCT TTCTTTTTTT AAAAAATTTT CCANTTGTGT 480  
 AATGGGGAAC TTTGCCNNTT TTCCNCATGG CNTGNTNATT NATTTTNTNT TTTTAAAGGG 540  
 15 GGGCCAGTTT TCCCCNNGG TTTTTTGNCT TNCGGTTNT TNCAGGNNTN GGGGGTCN 598

SEQ ID NO:12

SEQUENCE LENGTH:597

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS00012

SEQUENCE DESCRIPTION:

25 GATCGACAGA CCTGAAGCCA TCAGTGAAGA GAGGTTGCGA GAGATGTTTG GTTTATATGG 60  
 TCAGACAACA GGAAAGGGGA GTATATCTCT GAAAGAACTG AATGCCCGAC CCTTAGAAGT 120  
 TTTTCATGTG AGTGTGCTCA AAAGACAAGG TTACGGAGAA GGCTTCCGCT GGATGGCACA 180  
 GTACATTGAT TAACACAAAC TCACATTGGT TCCAGGTCTC AACGTTCAGG CTTACTCAGA 240  
 GATTTGATTG CTCAACATGC ATAACCTGAA TTCAATAGAC TTTTGCTNGG TTATAAAACA 300  
 GATGTTTTTT AGATTATTAA TATTAANTCA ACTTAATTTG ANTGNGAATT NGAAANCTGA 360  
 30 TTCAAGTAAG NTTTGAGTAT CACANTGTTA GCTTTCCTAA TTCCATAAAN GTACCTTGGG 420  
 TTTTTTNCAG NTTTATAAAT CTGGCCATCA NCCCCNGCGG CCTTTTNGTA AAGGGGCACC 480  
 TTTTCCNGCA GGCCATTTGG NAGCNCCTTT TTAACCACCT TGGGNTTTTT AACCCTTTTT 540  
 TNAAGGGNCN NCNTGGTTAA NTTTTTTNNT GGGCCTTNC NGGGCCTGGT NTTTAAAN 597

35 SEQ ID NO:13

SEQUENCE LENGTH:593

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00014

SEQUENCE DESCRIPTION:

45 GATCTTCCAA AGCACTATTT GTTGTAATAA CTTTTCTAAA TGTAAGTGCCT TTAAAGGAAA 60  
 AATGAACACA GGGAAGTGAC TTTGCTACAA ATAATGTTGC TGTGTTAAGT ATTCATATTA 120  
 AATACATGCC TTCTATATGG AACATGGCAG AAAGACTGAA AAATAACAGT AATTAATTGT 180  
 GTAATTCAGA ATTCATACCA ATCAGTGTTG AAACCTCAAC ATTGCAAAAG TGGGTGGCAA 240  
 TATTCAGTGC TTAACACTTT TCTAGCGTTG GTACATCTGA GAAATGAGTG CTCAGGTGGA 300  
 TTTTATCCTC GCAAGCATGT TGTTATAAGA ATTGTGGGTG TGCCTATCAT ACCANTTGTT 360  
 TTCTGTATCT TGAAAAAGTA TTCTCCACAT TTTANATGGT TTTATATTNG GGGATTCCCT 420  
 50 TAATGCCCCC TTGGNCAAAT TTATATATAT GGGCCCCATN GTTNCCNTTT NAATTTTTNG 480  
 GTTTTNGGGT GTAAGGGNCN TGCNCNTATG GTGGGGGCCT CCCAAAANTG GGANCANGNT 540

55

TTTNCCTNNG GACNCCCNT TGGTTGTTNA GGGGGGCCAA TTTTCNTNC CCN 593

SEQ ID NO:14

SEQUENCE LENGTH:574

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00015

SEQUENCE DESCRIPTION:

GATCGTNCCTG CAGTGGGAGC GTGTGACTGC GGAAGTTGTG AAGCCACGGG AAACCTCGGAG 60  
 CCTAGAGCAG CAGCTCAGCG CTTCTATGGG AAGCGGTCTC GAGCAGAAGC CCCACTGAAG 120  
 TGTCCCTGG CAGACACCCA CATGAACTCT TCCGAGAAAC TCCAGTTCTA TAAAGAGAAA 180  
 GCCCCAGATT GCCATGGGCC AGTNTTGAAA CACGAAGCTA TCTCAAGCCA GGAGTCAAAG 240  
 AAGAGCAAGA AGAGACCTTT TGAGGAGTCA GAGACAGAAC AGAATAACTC TTCACAACCT 300  
 TCAAAGCAGA AATATGTATG TTTGCTGTG GAAGACTGGG GACTTGTTAA ATTCCTATTG 360  
 ATTAAGTAGA TACAAGTTGA CCTTCTCTG GCCCCAGCT CTAGTGTGTTG AGTAAAGGGA 420  
 GACTNAGGGT GGGTTTACTT TTTTNGGTTT GNATTTANCC TATTGGCATT TAGNCATAGG 480  
 TAAGGCGGTN TTTTCNNCCT TTTNTTGGNT TTGGGNGGGG GATTNTNTNN GGGGNNNNAA 540  
 AAAANTTNCC ANGGGNTTTT TCCAAANCAT NGGN 574

SEQ ID NO:15

SEQUENCE LENGTH:573

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00016

SEQUENCE DESCRIPTION:

GATCAGCCCA GAGGAATGCT GAGAAATCAC CTGGAGGAGG GAGCAGAAAG AGAAGGTTTT 60  
 TAAGGAGGGG CTTCTGAATA CTTGGGAGAT ACGGAACGGA CCAAGGACCA CACTCCAGGG 120  
 TGCATTGCTT GCTCCCTGGG GCACCACTTC TGGATTACAG TGTGCCAGGT CCTTTGGAGG 180  
 CCCTACCCT TCCCCATTCA TTGCCACCAG TGAGAAATNG GGGTGCCCT GTGTAAAGAA 240  
 ACCTACCAA GGTTTACATT TGCACCTTAG CCTCAATAGC TACGAACCCT AGAGAAGCAG 300  
 CTAGCTGGAG CTCATGTGCA ACTCCTGATT CTCAGGAGAA AGATGGATTT TAACCNAAAA 360  
 TTATGAGTNA GCTGTAACT CTAAATGTA CTTNGGGAGA TAGGGCCAAG NGAGAGGTCA 420  
 TGGGCCAACT TAAGTGTAT CCNGTAGGAA AGNNCAGGTA NCACTGGNTT TTTTTTNNNA 480  
 GGGTTGCTNT TNCCTTNTNC TAAANGGATT TGNTANTTCC NTGGGGNTNG NATTTAAATT 540  
 GGGTTNTAAA AAGNTTNGAC GTGANAAAAA TTN 573

SEQ ID NO:16

SEQUENCE LENGTH:567

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00017

SEQUENCE DESCRIPTION:

GATCAAAACA GTCTCACCAG CACCATATCC ACATTCTAGC CCATGGAAAG GGTAAAGAAA 60  
 AGAAAGTGGA AGATATTAGT TTCCATTAA GGAAGTGACA TGGAGNTAAT ATAAGTCACC 120  
 TGTGTTTACA TTCCACTGGC AAAAATTCAG TCACAGGAAT GTACTTAGCT GCAGAGGAGG 180

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CTAGGATATG CCCTCCAAAA ACTCAGGGGG GATGTCCTAC TTGTAAAAGG AAGAAATGAA 240  
 AANTGGACAC TGAGAGGAAA TCAGCAGTCT CAGAGGTAAT ATACTTACAC AAGTTTTTTA 300  
 AAAACCATAA AATGATGCAG AATGAAGTTT CCACTCTATT CACCATCTAT CCAGTCCTCA 360  
 TGCCTCCCAN CANGNGGTAA ATNCTTTATT ATTGTGTCAT GGTATCTTTC CAGGGTTTTT 420  
 CTAAGCAATT TTGCAACNGN TTTTAATTAT GTATCCTNAT TTCCTACNTT ACCCCNTTTT 480  
 TGTCCATGNA NGGNANANTN TCCTGNGGNN TAACCTTCNT GTNTCTTTTT TTCCCCTNAT 540  
 ATTTTTTGGC GGTNCCNTNN NTTTGGN 567

SEQ ID NO:17  
 SEQUENCE LENGTH:552  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS00018  
 SEQUENCE DESCRIPTION:  
 GATCTTACCC GTGACAAAAT GTGTTCCATG GTCAAAAAAT GGCAGACAAT GATTGANGCT 60  
 CACGTTGATG TCAAGACTAC CGATGGTTAC TTGCTTCGTC TGTNCTGTGT TGGTTTTACT 120  
 AAAAAACGCA ACAATCAGAT ACGGAAGACC TCTTATGCTC AGCACCAACA GGTCCGCCAA 180  
 ATCCGGAAGA AGATGATGGA AATCATGACC CGAGANNNGC AGACAAATGN CTTGAAAGAA 240  
 GTGGTCAATA AATTGATTCC AGACAGCATT GGAAGAGACA TAGAAAAGGC TTGCCAATCT 300  
 ATTTATCCTC TCCATGGNTG TCTTCGTTAG AAAAGTAAAA ATGCTGAAGA AGCCCAAGTT 360  
 TGAATTGGGA AAGCTCATGG AGCTTCATGG TGAAGGCAGT AGTTCTGGAA AAAGCCACTT 420  
 GGGGNCCGNG ACAGGTGCTT AAAGGTTGAA CCGNGCTNGA TTGGTTNTGA ACCCACCAGT 480  
 CCCAGGAATT CTTGTTTAAA GTTCCAGNCN TTCAATTAGT TGGCAAATTA AAAANGTGCT 540  
 TTTTTGNGGA AA 552

SEQ ID NO:18  
 SEQUENCE LENGTH:581  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS00019  
 SEQUENCE DESCRIPTION:  
 GATCGCCGTT CTGGTAAAAA GCTGGAAGAT GGCCCTAAAT TCTTGAAGTC TGGTGATGCT 60  
 GCCATTGTTG ATATGGTTCC TGGCAAGCCC ATGTGTGTTG AGAGCTTCTC AGACTATCCA 120  
 CCTTTGGGTC GCTTTGCTGT TCGTGATATN AGACAGACAG TTGCGGTGGG TGTCATCAAA 180  
 GCAGTGGACA AGAAGGCTGC TGGAGCTGGC AAGGTCACCA AGTCTNCCCA GAAAGCTCAG 240  
 AAGGCTAAAT CGAATATTAT CCCTAATACC TGCCACCCCA CTCTTAATCA GTGGTGGAAG 300  
 AACGGGTCTC AGAACTGTTT GTTTCAATTG GCCATTAAAG TTTTAGTAGT AAAAGACTGG 360  
 TTTAATGATA ACAATGCATC GTAAAACCTT CANGAAGGGN AANGGAGGAA TGNTTTTGTG 420  
 GGCCCACTTT GGGTTTTNCT TTTTNCGGT GTNNGCAGTT TTTAAGGTIN TTAAGTTTTT 480  
 TNAATATNCA GGACCTTTTT TAANTGGNAA CCAACTTTGG CCCAAAAATT TTGTCACCAG 540  
 ATTTTTTNGG GCCCCNTTA AAAANGTNTT NATNNGGAA A 581

SEQ ID NO:19  
 SEQUENCE LENGTH:556  
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00020

SEQUENCE DESCRIPTION:

5 GATCAGCAGG GTTCTTTGTA AATAGTATTT TGAGACACTA AGATGTTTCT ACTGCTACGG 60  
 AATGTATTTT AAACACATAT CGTTTCTTTT TCTTGGA AAAA AAAGTTGATT AGGACCACAG 120  
 NNNNGGTTTA GAAAGGGTAA TATTTTGA AA TACTACAAGG TTTAGACAGT CCATGAAATC 180  
 GACCTGTTTA ATAATTTACC ATCCTGAAAG TCCAGAATTA AAATATGGAA GCAAGAACTA 240  
 10 TATAATTGAT TAGGATGCTT GGTAGGTTTT TTTCAATTGT CAAATATTCA TTGCACAGTG 300  
 GATTGTTTTG ATTAGTTAGT ATGCTTTTTT TTTAATTAAT TCAGTCTTCT GTTAATTTTT 360  
 AAGNTTGGT TAGTGCCACA AGGAATTTNA CTTNTTGATT TGTATAATNG GAACCTGACC 420  
 TNGGGATTNG TAGCGGGGNT TTGAAGGGTG GGGACCTNCC CNCAAAATAA GGGGGAGGTT 480  
 TCCAAANNTT CCNCTGGCCG NCCNNNNATC CCAGGTAAAG GGGGTNGAAA TANTNNGGGN 540  
 15 NCCCCCAGG GGAAAN 555

SEQ ID NO:20

SEQUENCE LENGTH:555

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00021

SEQUENCE DESCRIPTION:

25 GATCTGGTAC GAGTGTGTGA AAACATCCCC ATTGTGTTGT GTGGCAACAA AGNGGATATT 60  
 AAGGACAGGA ANATGAAGGC GAAATCCATT GTCTCCACC GAAAGAAGAA TCTTCAGTAC 120  
 TACGACATTT CTGCCAAAAG TAACTACAAC TTTGAAAAGC CCTTCCTCTG GCTTNCTAGG 180  
 AAGCTCATTG GAGACCCTAA CTTGGAATTT GTTGCCATGC CTGCTCTCGC CCCACCAGAA 240  
 GTTGTCAATG ACCCAGCTTT GGCAGCACAG TATGAGCAGC ACTTAGAGGT TGCTCAGACA 300  
 30 ACTGCTCTCC CGGATGAGGA TGATGACCTG TGAGAATGAA GCTGGAGCCC AGCGTCAAGA 360  
 AGTCTAGTTT TATAGGGAAG TTGTCCTGTG ATGTCAGCGG TNCAGCGTGT GTNCCACNTC 420  
 ATTATTATCT AGCTAAGCGG ACATGTNTTC ATCTGTGGGN TCTTAAGGAG NTGAGTNGNN 480  
 TNGGNGTNAT NTGGANTTAA AAATAACTTC ATNTTNGGC CNNATATTTA NGTNTTTTNG 540  
 CCCGNTTNNT CCTN 555

SEQ ID NO:21

SEQUENCE LENGTH:544

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00023

SEQUENCE DESCRIPTION:

45 GATCGATACA TGCAAATTTA ATGTAGTAAC TCACTTTTCC ATATATTTTN AATGTATATT 60  
 TCTATTTATG AATACCAATT TATAAAAAAT AATTACACAG AAAAAATGG AATAGGAAAA 120  
 ATTATGCATC TAGCACATTT AAACGTGCA AATATGAAAA TTTTTCGAGG ATTACATTTT 180  
 NTNNNTAGGC TGCATATTTT AACTGGCTTT AAACTGTAA CACATCACAT AAAAGTACTT 240  
 TACCCGGTAT GTATTGCATT ATATCATTGC AATAATTATT GGAGTCTAGA TATCGAGCCA 300  
 TCCCAGGTGT TGGGCGGGGG GAGGGTTGTG GCAAGTTGTC TTTTCAATT NGNGNGTTTT 360  
 50 CCTGTNGCTC CAGGGCAAGT ACCGGGTTGG AAAGCTGCCT GTAAGCGTTG GCACCTTCAT 420  
 AGNGTAGTGT TTNGGTGNCT TTTTTNTCG GTTCTTGTA ATTNGGTNCG GTNGGTGGTG 480

55

TTCAGATGNT TTTTNCNCT NGTTCAGCAA CTTNCCCNNT NNCTTGTCTT GATAGGGNAC 540  
NTCN 544

5 SEQ ID NO:22

SEQUENCE LENGTH:538

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10 CLONE:HUMGS00026

SEQUENCE DESCRIPTION:

5 60  
GATCTCTATC CAGTTGGACA CTTAATTGCT TTCTTCATTC AGAAAGATAG TCATGTTTAC  
TGGTATATTT GGTCACTCTT AGAACCTGTC CTTACATAT GTTTTTTATG GGACCCATGA 120  
15 ATGGTTAGCC TTTCTGTACT ATTGTAGAAG GAAATAAATA GGCGTAAAAA GACCATTGTA 180  
GTAAATAAGT TCAAGGGGAA CTTGGGACCA GAAACCACTG GTATGTACAA AAAAGCTGGC 240  
AATTTGAATA ACCTCAAGTT TGACAATAAT TTTTAAATTT GAACAGTTAT GATAAATTTT 300  
AGTAGTTTTA TACTACTAGAT GTGCCTAGAT GGTTCTCAAG GCTTATAGGA CTGGCTCACA 360  
GTTCAACCATT TCTAGTGGCT TTTCTTGCCT TTGGGCTCTGG GGGGCTGGGG GCAATGGGCT 420  
20 TTTTTCCTTG GGTGCGCAAT CGGTTTCTCT GGTGGTCTAG TTCCAATCC TTNGGGGGGT 480  
CNTTGTGNTN TTNNCNGCCC NGNNNGGTNN GTCCNGGGTG TTNGCCGGGN NCNTTTTN 538

25 SEQ ID NO:23

SEQUENCE LENGTH:535

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS00028

SEQUENCE DESCRIPTION:

5 60  
GATCCTGGAA TATGTCGAGG TTATATTACC AGGTATTTTT ATAACAATCN GACAAAACAG  
TGTGAACGTT TCAAGTATGG TGGATGCCTG GGCAATATGA ACAATTTTNA GACTCTGGAA 120  
GAATGCAAGA NCATTGTNA AGATGGTCCG AATGGTTTCC AGGTGGATAA TTATGGAACC 180  
CAGCTCAATG CTGTGAATAA CTCCCTGACT CCGCAATCAA CCAAGGTTCC CAGCCTTTTT 240  
35 GAATTTACAG GTCCCTCATG GTGTCTCACT CCAGCAGACA GAGGATTGTG TCGTGCCAAT 300  
NNGAACAGAT TCTACTACAA TTCAGTCATT GGGAAATGCC GCCCATTTAA GTACAGTGGA 360  
TGTGGGGGGA AATGAAAACA ATTTTACTTC CAAACAAGGA ATGTCTGAGG GGCATGTAAA 420  
AAAGGGTTTC ATCCAAAGGA TTTCANAAGG GNGGCTNATT TAAAACCANA NGGAANNGGN 480  
40 AGGAGGCNGG NNGTGAATTT GNNTTTTGGN GGAANTTTTT GNTTNAANNT TNTGN 535

45 SEQ ID NO:24

SEQUENCE LENGTH:528

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS00029

SEQUENCE DESCRIPTION:

5 60  
GATCTACACT TGGATGGATG CAACTTTGAA AGAACTGACA AGTTTAGTAA AAGAAGTCTA  
CCCAGAAGCT AGAAAGAAGG GCACTCACTT CAATTTTNC ATCGTTTTTA CAGATGTATA 120  
50 AAGACCTGCG TATCGAGTTA AGGAGATTGG CAGCACCATG TCTGGCAGAA AGGGGACTGA 180  
TGATTCCATG ACCCTGCAGT CGCAGAAGTT CCAGATAGGA GATTACTTGG ACATAGCAAT 240

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TACCCCTTCCA AATCGGGCAC CACCTCCTTC AGGGCGCATG AGACCATATT AAATTCTATT 300  
TACTATTTGT TGAATTTATT TTTCCGTCAG TTATGTAAAA TAAACATACT CTNCCTTCCT 360  
CCCCCTGGATT TATTGCCATT TAAGGCTTTT AAAATTCTAA TCAANNTTTG TNANTGCAAT 420  
CATCTGTTTN GGGNGTTNNG TTTTGGGATG TGCTTTTGN NTGGNTTNCG GNTTAGNCTT 480  
GGNTTGTTTT AATGGCCNTT CNNGTNANAT TTGGNGGNAA NGNGCTTN 528

SEQ ID NO:25

SEQUENCE LENGTH:528

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00030

SEQUENCE DESCRIPTION:

GATCAAGGTA TAATGGAAAA ATATACCTAT TCTTGAAGTA GTTTATTATN GTTTTCAAAT 60  
TGATTTATAC CATTATTAAC CTGATGTGGT CTGCTTAAAA AATGAATATA TCAGTATTTA 120  
GAAATAAATT GCAAAGGTGG GAATATATAC TTAATAATT TGTCTTAAGT AAATTAGCAT 180  
TTGGTAGTCT GANATGGTGA CAGATTACTT GTTAAAATTG TGAAANCTCT GTGTGTCTCT 240  
CTCTNCCTAC ATTTGTCCCT GAGAGTNTC CACGATTACT AGGTTCTTGA TTCCCTTATA 300  
TGGCAATCAG GCAGAGGCGT TCCTTAAGCA TTAGAGAGTT CTGAAGCTTA AGATTTGTTT 360  
TGGTTGGATG AANGTCCTTA GTACAGTTGA AAANCAGAGC ATTAAAGNCT ANTCANTTTG 420  
TTTTGNCTC ACCAGTCATT TTAATAATNG TNGGAATNCT TTTNNCTCA GTGCTTAAAN 480  
NTTCCNTTG TTCAANCTG NNGGGGGTTN GGATTAAACC AGGCCNCN 528

SEQ ID NO:26

SEQUENCE LENGTH:527

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00031

SEQUENCE DESCRIPTION:

GATCAGAATG CCCCTCCACT CATGAGACTC TTCATTTTGT CCACTTTGAC AGGAAAAGTG 60  
GGAATGTATG CAGAGCTCTC AAAAGAAACA AAAAAGGCCA AAACGGTGCC TTCAGCCACA 120  
TCCTCTGAAT TGGCCCTGAC TTGGACTAAA TGCACAAATG CAAAATCCCT TGACAAAAGC 180  
GCATAGGTTA TTTCAAACCA GCATTGTTTT TTATGTAACC TGTTTACCG CATCTTCTCA 240  
GCAGCTTCTG ACCACTGCTC AATTTTCTCC TTTACAGCCA TTGTTCTGGT GGACAAATAA 300  
CCTAGGTACT CCAAATCCTG GCAGGAAAAA TATACAGCAT TATGAANCAG CACTCANGTA 360  
ATCCTAAAAT GGATTTCCAA AGCTGGTTAC ACATGGCCCT GGNAANGTCN TATTGANTTT 420  
ANANGGGCTT TCTTCNTTTC AGGAGTTTNG GTCAACGGTG GCAAATCCNT GGGGTNNTTA 480  
ANTGGNNNGG TTNNTTAANT TNTGNTANTT TCNTNGGGGC CANAGGN 527

SEQ ID NO:27

SEQUENCE LENGTH:520

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00033

SEQUENCE DESCRIPTION:

GATCAAAATG GTTGGTGAAC CTCCACATGT CCAGTTCTGT TGCCAAACTT TCCATTCAGA 60



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5 GTATTTGGTG GAGTTTGAAT TTGAGCAAAC TAAATGCCTT CATCTTAGGT AGAAAGGGCC 120  
 TGAATCTTCC ATTTTATATT CAAACCTCAT TGTTATTTGG CCTAAGTAAA AAGTCAGATT 180  
 TCATTTCAT TTACCTGAGT TCGCTTTAAA GAGCTTTTCA AAGAGAGCTT TATAGACACC 240  
 CACAATTGTC CCCAATCTCT TCATGATGTT GCATTAATAG TTGTTTTTGT CCCTTTCCTG 300  
 GAAATGTTAA TGCCAAAGNT TGCCTGAACA TTNGGGCGGG TTTTCTTAAA TTTGAANGTN 360  
 TAAAAATTTT NTAANGGGGG AATTNCCAAA NGGGTATTTA AAAGGGTTNG TTTTAACCAG 420  
 GTATTGTNGT GGGGGGATGG TCCAATAATC CTCNNGGGGG AGGGCTTTCA AGGGAAATCC 480  
 10 CTTTTTNGGG GAAATAAAAA NNGGGTTAAA ANNNNTTTTN 520

SEQ ID NO:28  
 SEQUENCE LENGTH:514  
 SEQUENCE TYPE:nucleic acid  
 15 TOPOLOGY:linear  
 CLONE:HUMGS00034  
 SEQUENCE DESCRIPTION:  
 GATCAGCGAG GCCGACAAGA AGAAGGTGCT GGACAAGTGT CAAGAGGTCA TCTCGTGGCT 60  
 20 GGACGCCAAC ACCTTGGCCG AGAAGGACGA GTTTAAGCAC AAGAGGAAGG AGCTGGAGCA 120  
 GGTGTGTAAC CCCATCATCA GCGGACTGTA CCAGGGTGCC GGTGGTCCCG GGCCTGGGGG 180  
 CTTCGGGGCT CAGGGTCCCA AGGNAGGGTC TGGGTCAGGC CCCACCATTG AGGAGGTAGA 240  
 TTAGGGGCCT TTCCAAGATT GCTGTTTTTN TTTTGAGCT TCAAGACTTT GCATTTCTTA 300  
 25 GTATTTCTGT TTGTNAGTTC TCAATTCCT GTGTTTGCAA TGTTGAAATT TTTTGGTGGA 360  
 AGTACTGAAC TTGCTTTTTT TCCGGTTTCT ACATGCAAGA GATGAATTTA TACTGCCATC 420  
 TTACCGGCTA TTTCTTCTTT TTTAATCCA CTAACTCAG GCCATTTTTT AAAGTTGGGT 480  
 ACTTGCAAAG TAAAATAAAC TTTAAAAATT CAAA 514

30 SEQ ID NO:29  
 SEQUENCE LENGTH:513  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 35 CLONE:HUMGS00036  
 SEQUENCE DESCRIPTION:  
 GATCATCATT CTTCTGACTC TAGATGGGAC ACTTGACAGT GACTTGAAAC ATTTGCATAT 60  
 TCAGGAATGC ATGAGATTTC AAGAGAGCCT ACAGTATGAA ATCATTTTCA CAAAATAAGC 120  
 AGCTTGCTTC TGAAATGCTG TCTTTCCAG TAGCTACTCA CCTGCCTCTG GTGGCTGGGA 180  
 40 TTCAGATGCC ACAAACACTGT CAGTATCTAT AGACCAGGTC TGTGCCACCT CCTCTCTCCT 240  
 CTGTGCTCAG TGAGGAGGCA GTAAATGAAG TTACAGGCTA GCACAATACC TAACTCATGT 300  
 TTCCAGTAC ACCTGTTGGA TATTNNCTGT NCCTTTTAAT GGTCTCAAG GGANTTAGGT 360  
 TTTGNCCTG TTTCCAGNGG TTTCCAGGTT TTCTTTGGGT NCTTTTTNAA TTTTNAANTT 420  
 45 CCNAGGGGGG GGGNNTTTTG GGNAAGGGGG GGGCAAAGGG GNTTTTTTTT TTNTTGGGCC 480  
 NNGNTTTTGG GGGGGAAANC CTTTNNGGTN NCN 513

SEQ ID NO:30  
 SEQUENCE LENGTH:512  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

55

CLONE:HUMGS00037

## SEQUENCE DESCRIPTION:

5 GATCTAAATT GTTACATTTT ACCATTTTCAT TCCGAAGTTG GTTTTACTTT ATTAATGAA 60  
 GATTTAGTTT TCATATCGTA TACATAGCTG TATAGATTTC AAAATNAGGT TGTTAATTTG 120  
 TGTCACCTAC TATTTTGTG TTGGTAATGC TTTAAATGCA TACTTAAAAA TGAAGTACTG 180  
 TTATCTAAGC TACTGTGTTT AGAAAATGTT AAGAATGAGC AGAAATTTT ATAGAAAAGT 240  
 10 ATAACCGGAA GANGAGAGAA GATACTGCCA ATAGGCCCTC AANCTTAAAA NAGAAAAACC 300  
 TTTGCCAGTT TTANGGACAT ATTTTGATTG TTTTCNGTATT CTTAACACCT TTTTAAACAA 360  
 NGTTCCTGAT AGTACCCACT ATTATTGGGT TTGTTTATG CCATTATTG ATTCTTGGAT 420  
 ATTCAAGCAT TTNCAATGTG GCATATTNG NTTCCNNTN NCCTTNCNTT TTTTNGGNCN 480  
 NCNTTACCCT TTCNTTGA AAGNCANTN GN 512

SEQ ID NO:31

SEQUENCE LENGTH:510

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00038

## SEQUENCE DESCRIPTION:

20 GATCAGCCAG GCACAGAATC TCCAGAACAA CCTAGAGAGT GAATGCTAAT TTGTAGAGCG 60  
 AACTTCCATT TGGCCCATNA TTTGTAAGT TGTAAGTCT CCAAGTGCCA GANTGCTTAC 120  
 25 ACGTTAAAGC AGCACCTTTC CATTTGCCCA CATATTCTTC TTGCACACCC CTTCCATTAC 180  
 TGCTGAATAG GACATTGCAT GGGAAGAGTA CAGAGGTGGC AGANTGANGC TAGAGTGGGC 240  
 AGGNCTAAAG ACTGAGCCCC AGAGTGCTCC CAGCAACCGC CACGTACANG GTCTGNAATG 300  
 NCANGGGCAN GNGTGAGATT GGAANCTGTG TGTGAANGGT AAGCCCTTGC AGTNTTCTG 360  
 CCTCCCTTTC TTTCTGCCTT TCACCCCNCT TANTTGTNTG GTTNTTGGTT TGCCCGTTCT 420  
 30 TCTCTTGGTG GNTGCNCATT TGTTANATGG TGTTAGGGGT GTGGGGNTGA GGTTTTCCCC 480  
 TTTGATGTGG GNTTNTTCN TTGGGTTTAN 510

SEQ ID NO:32

SEQUENCE LENGTH:507

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00039

## SEQUENCE DESCRIPTION:

40 GATCGTGAAG CCCAATGGCG AGAAGCCGGA CGAGTTCGAG TCCGGCATCT CNCAGGCTCT 60  
 TCTGGAGCTG GAGATGAACT CGGACCTCAA GGCTCAGCTC AGGGAGCTGA ATATTACGGC 120  
 AGCTAAGGAA ATTNAAGTTG GTGGTGGTCG GAAAGCTATC ATAATCTTTG TNCCCGTTCC 180  
 TCAACTGAAA TCTTCCAGA AAATCCAAGT CCGGCTAGTA CGCGAATTGG AGAAAAAGTT 240  
 45 CAGTGGGAAG CATGTCGTCT TTATCGTCA GAGGAGAATT CTGCCTAAGC CAACTCGAAA 300  
 AAGCCGTACA AAAAATAAGC AAAAGNGTCC CAGGAGCCGT ACTCTGACAG CTGTGCACGA 360  
 TGCCATCCTT GAGGGACTTG GTCTTTCCNA AGCGGAAATT NTNGGCAAGA GGANTCCNGN 420  
 GTCAAACCTT GNTTGGCANG NCGGGCTCAT AAANGGTTCA TTTTGGNNCA ANNGACNAGN 480  
 50 AGGNCCAATT NTGGGNCAAA NAGGNTN 507

SEQ ID NO:33

SEQUENCE LENGTH:508

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00040

SEQUENCE DESCRIPTION:

GATCAGAAAC TCACCCTAAA TCTNAACGGG TGCCGCTATA ATTNGTNACA TCTGGCAAGA 60  
 TTTCCCTTTA TGTATATATT TAAACAATCC GCTTGGACAC GAACAAAGCC ACACTTCTAA 120  
 CTGCTTCTGG CGAACTGATT TAATTTTNAA TTTTNTNCAA TAAAGATATT CTTAGATACT 180  
 GAAAGAAATA GTTAATGAGT TTNCATTTGT CCTTGAGAAA ATTTGGCTCA AGTCCATTG 240  
 GCTGTAGTGT CAACGATGTT TCCAGTAGTG TTTAGGATTT GGTGTCTTCA AAGGTAGTTG 300  
 ATTAAACCAA GTGTGTCTTT AATATCTTGT ATCAGAATAA CTTTGTATGT TACCAACTTA 360  
 AATTGCTAGA ATAAGGGTAA ATTGGATACA CAACTGCTGA TTTTAAATTT AGGANCTTTG 420  
 ACCNNATTTT GGGGTTTTCA AANCCGTTTT TGGNTGCTNT GTATCCTTAT GCTGTTTGGT 480  
 TNATTTCCAN TAAAAANTTC ACNCGNGN 508

SEQ ID NO:34

SEQUENCE LENGTH:505

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00041

SEQUENCE DESCRIPTION:

GATCTGTAAG TAACTTCACA TAAAAAATG AAATATTTTT TAATTTAAAG CTTACTCTGT 60  
 CCATTTATCC ACAGGAAAGT GTTATTTTTA AAGNNAGGTT CATGTAGAGA AAAGCACACT 120  
 TGTAGGATAA GTGAAATGGA TACTACATCT TTAAACAGTA TTTCATTGCC TGTGTATGGA 180  
 AAANCCATTT GAAGTGTAAC TGTGTACATA ACTCTGTAAA ANCACTGAAA ANTTATACTA 240  
 ACTTATTTAT GTTAAAAGAT TTTTTTTAAT CTAGACAATA TACAAGCCAA AGTGGCATGT 300  
 TTTGTGCATT TGTAATGCT GTGTTGGGTA GANTAGGTTT TCCCCTCTTT TGTTAAATAA 360  
 TATGGCTATG CTTAAANGGT TGCATACTGG GGCCAAGTAT AATTTTTNTG GTAATGTGTG 420  
 GNAAAGGATG NCCAGTTATT GGTACCNCCT TTANGNNATC CNNTAANGGG AACCTTCCCC 480  
 TNGGTTAAAA NCANGNNGTA NANNN 505

SEQ ID NO:35

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00042

SEQUENCE DESCRIPTION:

GATCTGGAAG GAGCTGTTTT GGATGAATGC AGTATAAAAT GTAAAANCCC TGCTAAATGA 60  
 AA 62

SEQ ID NO:36

SEQUENCE LENGTH:503

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00043

## SEQUENCE DESCRIPTION:

GATCGAAAAG CACTCCATGA GCTAAACTG GAAGAGTGGA AAGGCAGACT ACAAGTTACT 60  
 GAGCACCTCC CTGAGAAAAT TGAAAGTAGT TTACAGGAAG ATGAACCTGA GAATGNTGCT 120  
 AAGAAAATTG AAGCACTGCT AAACCTTCCT AGAAACCCTT CAGTAATAGA TAAACAAGAC 180  
 AAGGACTGAA AGTGCTCTGA ACTTGAACT CACTGGAGAG CTGAAGGGAG CTGCCATGTC 240  
 CGATGAATGC CAACAGACAG GCCACTCTTT GGTCAGCCTG CTGACAAATT TAAGTGCTGG 300  
 TACCTGTGGT GGCAGTGGCT TGCTCTTGTN TTNTTCTNGN CTNTTAACT AAGAATGGGG 360  
 CTGTTGTA CTCACTTTAC TNATCCNTAA ATNTAAATAC ATACTGATGN TTTGTATTAA 420  
 TCGNTCCAAT ATATGNNTAC ATGNANTATA TCNACNCNCC TTNGATNTT AAGCANGTAA 480  
 ATAAAACCAT TNNGCAATGG AAA 503

SEQ ID NO:37

SEQUENCE LENGTH:497

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00044

## SEQUENCE DESCRIPTION:

GATCGATAAA GAATTGGCTA GTGGTGAATA CTTTTGAAG GCAAATCAGA AGAAGCGGCA 60  
 /GAAAATGGAA GCAATAAAGG CTAAACAAGC AGAAGCCATC AGTAAGAGAC AAGAGGAAAG 120  
 AAACAAAGCA TTTATTCCAC CTAAGGAAAA ACCAATTGTG AAACCTAAGG AAGCTTCTAC 180  
 TGAAACTAAA ATTGATGTGG CCAGCATCAA GGAAAAGGTT AAGAAAGCAA AGAATAAGAA 240  
 ACTGGGAGCT CTTACAGCTG AAGAAATTGC ACTTAAGATG GAGGCAGATG AAANGAAAAAN 300  
 GANGAAAAAN NAGTANCATA CCCAAANCTC CTTGNCTNGG ACCTATCTCC TTTTNGTAA 360  
 AGGGGTTTTT TGGGGTTTTT AGGCCTTTAG GTTNCCCTTT TTTTGNNGGA AANTTTTTNTT 420  
 GGGGGGGTTT TTTNNCTTT TTTNGGGGGG GGNGGGGGTT TTNNTCCTTG GGNGGGGTTT 480  
 TCTTTNAAA AATTTN 497

SEQ ID NO:38

SEQUENCE LENGTH:498

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00045

## SEQUENCE DESCRIPTION:

GATCTTATGG ATGCTGAGCA TGTTCTGCAC TGGTGCTAAT GTCTAATATA ATNTTATATT 60  
 TACACACATA CGTGCTACCC AGAGATTAAT TTAGTCCATA TGAACATTG ACCCATTGTT 120  
 CATTGAGACA GCAACATACG CACTCCTAAA TCAGTGTGTT TAGACTTTTC AAGTATCTAA 180  
 CTCATTTCCA AACATGTACC ATGTTTTATA AACCTCTTGA TTTCCAGCAA CATACTATAG 240  
 AAAACACCTG CTAACAAAA CACAACCTCT CAGTGTCATC CATTGCTGTC GTGAGAGACA 300  
 ACATAGCAAT ATCTGGTATG TTTGCAAGCT TTCAAGATAG CCTGAACTTA AAANGTTGGT 360  
 GCATTAGTTG TATCTGATGG NTATAAATTT TGCCTCCTAG GTTCACTTTG GTGTCCAGGN 420  
 GCTAAACCTG TGGANCCTAA CTTTCCCTN ATTGGGGGGG GAATAACCTG GAAAATAAAG 480  
 GGTTTTTTTC CAGGGNTN 498

SEQ ID NO:39

SEQUENCE LENGTH:494

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00046

SEQUENCE DESCRIPTION:

GATCTGTGCT GTAGAAAAAC ATTAACCCCTT GTTCAAAAAA GAAATGGATA ANCTTGGCCT 60  
 TTCTAAGTGG TAAGAATGAC CTGTCACTAT AATATACTGT ATGTTTACAT TTNATTTAAA 120  
 TTTAATCTCT TATGTATAGG GTGATAACCT TCCCAGAAA CAACAGTGAT TGCNATTGTT 180  
 TTCTAGAAAC TNCTTTAAAG TGCCACATTT GGCAGTACAA ATGAGTCTGA GTGTAATAGC 240  
 CCAGAGATTT ATATATAGTT GAATGTCTAA NATGGTAAAA TGTGCCACTG TGCAAGTTA 300  
 CAGTGGCTTA TGTTTTTCAT AGTAATTCAN ATGANCTTCC TATTTTTGNT AGTAAATGGC 360  
 CATTTAATAG NATTCCTTGG CCATTTGAGG CTCACTGGCA AATTTTAGGT GCNGGGGGNG 420  
 GAANCCANTT TTTTANATGG NAATCCTTGG GTTTTNNCCN CCNTNNTNCC TGGNCCNTTC 480  
 CCCCCAAAAN CCTN 494

SEQ ID NO:40

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00047

SEQUENCE DESCRIPTION:

GATCAGTTGA CAGTGGCAAT TAAACTGTAA ATAACCTGCC CTGGGGGCCT TTTTTTAAAA 60  
 AACAAAAACC ACAAAAATTC CCAAACCATA CTTGTCTAAA ATNCTGGTAA GTATGTGCTT 120  
 TTNTGTGGGG GTGGGATTTG GAAGGGGGGT TGGGTGGGC TGGATATCTT TGTAGATGTG 180  
 GACCACCAAG GGGTGTGTA AACTAATTG TATTAAATGT CTTTGTATAA GCCTTCTGCT 240  
 CAAA 244

SEQ ID NO:41

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00048

SEQUENCE DESCRIPTION:

GATCACTGTA AATGAACCTC CCTGTTGGCC GCTCTGTGGA TGANACTTTA AGACTAGTTC 60  
 AGGCCTTCCA GTTCACTGAC AAACATGGGG AAGTGTGCCC AGCTGGCTGG AACCTGGCA 120  
 GTGATACCAT CAAGCCTGAT GTCCAAAAGA GCAAAGAATA TTTCTCCAAG CAGAAGTGAG 180  
 CGCTGGGCTG TTTTAGTGCC AGGCTGCGGT GGGCAGCCAT GAGAACAAAA CCTCTTCTGT 240  
 ATTTTTTTTT NCCATTAGTA AANCACAAGA CTTCAGATTC AAA 283

SEQ ID NO:42

SEQUENCE LENGTH:486

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00049

SEQUENCE DESCRIPTION:

GATCAGTTTT CNTTGTAAAC CTGGGTTTAA TCTGAATGGC GCTGATTCTN CCAAGTGCAC 60

# EP 0 679 716 A1

5 TGAGGAAGGA AAATGGAGCC CGGAGCTTCC TGTCTGTNCT CCCATCATCT GCCCTCCACC 120  
 ATCCATACCT ACGTTTGCAA CACTTCGTGT TTATAAGCCA TCAGCTGGAA ACAATTCCCT 180  
 CTATCGGGAC ACAGCAGTTT TTNAATGTTT GCCACAACAT GCGATGTTTG GAAATNATAC 240  
 AATTACCTGC ACGACACATG GAAATTGGAC TAANTTACCA GGAATGCAAG GGAAGTAAAA 300  
 TGCCCATTCC CATCAAGACC AGNCAATGGA TTTGTGGNAC TATCCTGCAA ANCCCAACAC 360  
 TNTNTTTCCT AAGGNTTAAA GGCCACATTT TGGGTTGGCC ATTGGTNGGG TTATTNTCT 420  
 TGGGAGTTGG GCGCCGGANG GAANTTTGNN TNTGTTNCCN NAANCTTGGG GAACCCTTGG 480  
 10 GTTTNN 486

SEQ ID NO:43  
 SEQUENCE LENGTH:470  
 SEQUENCE TYPE:nucleic acid  
 15 TOPOLOGY:linear  
 CLONE:HUMGS00050  
 SEQUENCE DESCRIPTION:  
 GATCCACCAG CTGAGAATTC GTCCGCTCCC GAGGCTGAGC AGGGCGGGGC TGAGTAAATG 60  
 20 CCGGCTTACC ATCTCTACCA TCATCCGGTT TAGTCATCCA ACAAGAAGAA ATATGAAATT 120  
 CCAGCAATAA GAAATGAACA AAAGATTGGA GCTGAAGACC TAAAGTGCTT GCTTTTGGCC 180  
 CGTTGACCAG ATAAATAGAA CTATCTGCAT TATCTATGCA GCATGGGGTT TTTATTATTT 240  
 TTACCTAAAG ACGTCTCTTT TTGGTAATAA CAAACGTGTT TTTTAAAAA GCCTGNGTTT 300  
 25 TTCTCAATAC GCCTTTAAAG GTTTTTAAAT TGTTTCATAT CTGGTCAAGT TGAGATTTTT 360  
 AAGNCCTTCA TTTTAAATTT GTAATAAAN GTTTACCACC TTGGATTTTT TCAANAAAGG 420  
 TCAACCAANC TGCAANGCAC CTGTTAATAA NGGGTCTTTA ANTAATTAAA 470

30 SEQ ID NO:44  
 SEQUENCE LENGTH:479  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00051  
 SEQUENCE DESCRIPTION:  
 35 GATCTGTAAG TAACTTCACA TTAATAAATG AAATATTTTT TAATTAAAG CTTACTCTGT 60  
 CCATTTATCC ACAGGAAAGT GTTATTNTNA AAGGAAGGTT CATGTAGAGA AAAGCACACT 120  
 TGTAGGATAA GTGAAATGGA TACTACATCT TTAANCAGTA TTTCATTGCC TGTGTATGGA 180  
 AAANCCATTT GANGTGTACC TGTGTACATA ACTCTGTAAA ANCACTGAAA AATTATNCTA 240  
 40 ACTTATTAT GTTAANNGAT TTTTTTAAT CTAGACAATA TACAAGCCAA AGTGGCATGT 300  
 TTTGTGCATT TGTAAATNCT GTGTTGGGTA GAATAGGTTT TCCCCTCTTT TTGTTAANTA 360  
 ATATGGCTAT NCTTTAANGG GTTGCNTACT GGGCCAGGTN TAATTTTTTG TAATGGNGTG 420  
 AAAGGGTGCC ATTTTTTGT CNCACTTNGG GGGTCTCANT GGGGGGNTTC TNNCNGGGN 479

45 SEQ ID NO:45  
 SEQUENCE LENGTH:477  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 50 CLONE:HUMGS00053  
 SEQUENCE DESCRIPTION:

55

GATCTCTAAG GAACTCCTGT TGCTAAATAT GAAGAGTATG GAACATTCAT ATAGTCTCTG 60  
 TGAAGCATGG GGGGAGGGAA GACATTCTT TTTCTTATAG GCTTTATGCT CAAATGTCAT 120  
 AGTCTCCTTT CAAAGAATTG TGTTCATTT TAAATGCACC CAGCTTAAGT AGAAGACATT 180  
 GAAGGATGCA TTAATTTTCA GGAACATTT TGAATTATGA AAAGATTCCC AATTGAAAAA 240  
 NTTATTCAAC AAGTAAAAGC TAAGAAATTT CATTGAAATC ATAAGGCAGT TTAAGCATAA 300  
 NTTGATAAAA ATAGCTGTGT ACTACTAATT AATAGAAAAT CATTCAACCA AGAGANGAGT 360  
 CANGTGAATA TCGTTTGTGTT ATTTGCTAGT GAGTTTCTTT GTAACGTTGG ATTTTATTAA 420  
 NTGGTTAATN TTTGGTTAGG TATGTCCTAT GTTANTNAAA ANTGGNCCAA NTTTAAA 477

SEQ ID NO:46

SEQUENCE LENGTH:476

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00055

SEQUENCE DESCRIPTION:

GATCACCATT AGCAAATGGA AATNACATTT GAAAGCCATT AGACTTATAG GTGATGCAAG 60  
 CATCTAAGAG AGAGGTTAAT CACACTATAG AGGCATAAGT GGTATCAGTT TTCATTTTCN 120  
 TAATTGTTTA ANCTGTGTTT TATACCAGTN TTTGCAAGTA ATTGGGTGTT AGCTTGAGAT 180  
 GGTAAAGGT GGTTCGGGA GGGACTTCGT TGTAATGGTT TTCCTGTAAA ANATGTTTCC 240  
 AACTCCNCTG AAATGTTGCT GAAAAGCATG GTGCTGGTAA CAGTTCAACA ATCCCGTGGC 300  
 TGCTCATTCT TGGCCTACTT TTA CTCTCCC ACTTGNAGC AGGTTAGCGT TTGAAGGGTG 360  
 GTATGGGAAA AGCCTNGCAT TGCCCTGGGC AAATTCCTTT TGGGGTTCTN CTCCTTCCC 420  
 CNCTTCNCCN TNTCCTTCTT TCCCCCNTN ANGTCNNCC NCTTNCNTTA GGTTCN 476

SEQ ID NO:47

SEQUENCE LENGTH:472

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00056

SEQUENCE DESCRIPTION:

GATCAAATCT GCACTGTGTC TACATATAGG AAAGGTCCTG GTGTGTGCTA ATGTTCCCAA 60  
 TGCAGGACTT GAGGAAGAGC TCTGTTATAT GTTTCATTT CTCTTTATCA AAGATAACCA 120  
 AACCTTATGG CCCTTATAAC AATGGAGGCA CTGGCTGCCT CTTAATTTTC AATCATGGAC 180  
 CTAAAGAAGT ACTCTGAAGG GTCTCAACAA TGCCAGGTGG GGACAGATAT ACTCAGAGAT 240  
 TATCCAGGTC TGCCTCCCAG CGAGCCTGGA GTACACCAGA CCCTCCTAGA GAAATCTGTT 300  
 ATAATTTACC ACCCACTTAT CCACCTTTAA ACTTGGGGAA GGNNGCNTTT CAAATTAAAT 360  
 TTAATCNTNG GGGGNTTTTA AACTTTAACC CTTTNCNT TNTNGGGGTN GGNANTTGNC 420  
 CCCNTTAAAG GGGGNCCCC TNCNNGGGG AATAAAACAA NTTNNTTTT TN 472

SEQ ID NO:48

SEQUENCE LENGTH:472

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00057

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCAAANCT GCACTGTGTC TACANATAGG AAAGGTCCTG GTGTGTGCTA ANGTTCCCAA 60  
TGCAGGACTT GAGGAAGAGC TCTGTTATAT GTTTCATTT CTCTTTATCA AAGATAACCA 120  
AACCTTATGG CCCNTATAAC AATGGAGGCA CTGGCTGCCT CTTAATTTTC AATCATGGAC 180  
CTAAAGNNGT ACTCTGAAGG GTCTCAACAA TGCCAGGTGG GGACAGATAT ACTCAGAGAT 240  
TATCCAGGTC TGCTCCAG CGAGCCTGGA GTACACCAGA CCCTCCTAGA GAAATCTGTT 300  
NTANTTTAGC AACCCAGTTA TCCNCNTTAA NNCTGNGGAG AGTGGTCTTT ACATCTTAAT 360  
TTTATTCNTG TGGTGGTTNT TACCTTTAAC CCGGTTTCTT ATTTTGGGT TTGTTATTGG 420  
CCCTTTTATG GGGTGGTCCC TTTCCNGGT TGGNTTCCC TTTTTTGTG TN 472

SEQ ID NO:49

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00060

SEQUENCE DESCRIPTION:

GATCTCATGG TCCGGAATGA CACCCCTGT GGAACCACCA TTGGACCTAT CTTGGCTTCT 60  
CGGCTGGGGC TGCGGGTGCT GGATTTAGGC AGCCCNNAAC TGGCCATGCA CTCTATCCGG 120  
GAGATGGCCT GCACCACAGG AGTCCTCCAG ACCCTCACCC TCTTCAAGGG CTTCTTTGAG 180  
CTGTTCCCTT CTCTAAGCCA TAATCTCTTA GTGGATTGAG CCCTCTGGA AAGACTTCTC 240  
TGCCATCCCT TTGCACCTGA GAGGGGAAGT TCTCAGCTGA GCTGAAGCTG GATTATTAAA 300  
GTGGATTGTC ACTCAGAAA 319

SEQ ID NO:50

SEQUENCE LENGTH:461

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00061

SEQUENCE DESCRIPTION:

GATCTTCCTC TAATTGACAG CCTCATTACG GGTCTTACAA AATATGGAAC AGTGTGAGAA 60  
AAAACCAGAG AACTCGGCAG AGTCTAACAC AGAGGAAACC TAAAAGGACT GATTTAACCC 120  
AAGATGATTT CCACTTGAAA ATCTTAAAGG ATATTTTATG TGAATTTCTT TCTAATATTT 180  
TTCAGGCATT AACAAAGGAG ACGGTGGCTC AGGGAGTAAA GGAAGGCCAG TTGAGCAAAC 240  
AGAAGTGTTT CTCTGCATTT CAAAACCTTC TTCCTTTCTA TAGCCCTGTG GTGGAAGATT 300  
TTATTGAAAA TCCTACGGTG AAGTTGATAA GCGGCTTTGC TGGATGGGCT TGGGATAAAA 360  
ACCCTTTCCC AAGTTTTAAA GGGTTTCAGG TCTTTAAATC CCTGAAATTT TGGGATTTCT 420  
TTCTTGTTCC AGGTTGTTA AACCTTTTAT TTTTCTCTCC N 461

SEQ ID NO:51

SEQUENCE LENGTH:458

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00062

SEQUENCE DESCRIPTION:

GATCTAGCAT ATTTCACTAT TCTGTGGATG AATACATAGT TTGTGGGGAA AACAAACGTT 60  
CAGCTAGGGG CAAAAAGCAT GACTGCTTTT CCCTGTCTGG CATGGAATCA CGCAGTCACC 120



EP 0 679 716 A1

TTGGGCATTT AGTTTACTAG AAATNCTTTA CCTTAAGCAG CACACACATT TACTACACAC 180  
ACAGNCCTAA CAAAGCACTG TGCTTAGAGG GTAAAAAGGA ATCACAAAAC AAGAATCTTT 240  
CCAAAGTTGT CTCATTCAGC AATGTTAAGG CATCTGTATC AAATTATTTT GGATGTAAAG 300  
ATTCTGTGT CTCATAATAT GAATGTATTT TTTGATATAC AAGGAACTG GCCATAAAAA 360  
TGGTGNNGNA ANCCGCCCN TAATTTTNCC CCTGGGGCCC CAATTGGTNN NNTCNANTCT 420  
NGGNTTNAGC NTTGTCTCTC AAATGGGATN CANTNNNN 458

SEQ ID NO:52  
SEQUENCE LENGTH:459  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00064

SEQUENCE DESCRIPTION:  
GATCTATCAC CCAAACATCG ACGAAAAGGG GCAGGTCTGT CTGCCAGTAA TNAGTGCCGA 60  
AAACTGGAAG CCAGCAACCA AAACCGACCA AGTAATCCAG TCCCTCATAG CACTGGTGAA 120  
TNACCCCCAG CCTGAGCACC CGCTTCGGGC TGACCTAGCT GAAGAATACT CTAAGGACCG 180  
TAAAAAATTC TGTAAGAATG CTGAAGAGTT TACAAAGAAA TATGGGAAA AGCGACCTGT 240  
GGACTAAAAT CTGCCACGAT TGGTTCCAGC AAGTGTGAGC AGAGACCCCG TGCAGTGCAT 300  
TCAGACACCC CGCAAAGCAG GACTCTGTGG AAATTGGCAC GTGCCACCGN CTGGCGTTCG 360  
NTTGTGGCAG TTAATACTT TTCTACAGTT TTCTTAATCA AAAGTGGTCT TAGGTAANCC 420  
TGTAAGGNA AGGGGTTTAN NAATTTTANG GTTGGTCTN 459

SEQ ID NO:53  
SEQUENCE LENGTH:458  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00065

SEQUENCE DESCRIPTION:  
GATCAGCTGG CCAACTCAGC CAATCCGCAC ATTTAGCTCT CCAACTACCA TACAACGTGC 60  
TTGGTTTAGG TCGGAGCGCA AATNTNCTTG ACCATCTCTA CGTTGGTATT CCCCGTCCAT 120  
CTGGAGAAAA ATCTATACGA AANCAAGAGT GGACTGCAAT NATTCCAAAT NCCCAGCTAA 180  
TTGTCATTCC ATACCCTCAC AATGTCCCTC GAAGTTGGAG TGCCAAACTG TATCTTACAC 240  
CAAGTAATAT TGTNCTGCTT ACTGCTATAG CTCTCATCGG TGTCTGTGTT TTCAATCTTT 300  
GGCAATAAAT TGGCATTTTA CCATTTGNCA GGGAAAAGGA AAGGCNGGTT GGNTTGGGGG 360  
GAAAACCGGC CAAGGGANGG CCCCCCGGG TTTTCNATTT TTGGNGGGNT TNTTGGGNNT 420  
TTTGCTTTT TAAANTTTT CCNAANAAAN NGGGANTN 458

SEQ ID NO:54  
SEQUENCE LENGTH:454  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00066

SEQUENCE DESCRIPTION:  
GATCAGTTNC GTGTCCGCNG GAGCAGGCCT TGCTGAGTGA AGACACTGGN ACTAGCTGGG 60  
TCCTGGGGTG ACTTGGAGGC TTTGGGCCTA AAAGGGCAGC CTGAACCTGG AGTCTTATCT 120

CCCCCAGGAG CCGAAAGCAC TTTTCTTGAT TTCCCCCAGG AAATCAAGCG CTGCTTCTCA 180  
 GCTCCTGTGG TTTTAGTATT TATATATCTG TATCTTCTTT GTAGAAATTT ATTTATTTTT 240  
 GAATAAGAAT ACCTGCCTGG AAAAAATTA AAAGGACGGG AGGGCGAANT GCAAGGGAAG 300  
 GCCTCTCCTA TGCCGNCCCA GAGNAGCACT GTACCAATTT CATGTGATTG CTTAACTCTG 360  
 TTTAAGGAAG CTCTGAAACT GTCATTTCTT TTGCAGATTG TTNTGAACCT GGAAACCCNG 420  
 AATTTATNGN TAANNCTCAN TTNCCACCNG GAAA 454

SEQ ID NO:55

SEQUENCE LENGTH:505

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00067

SEQUENCE DESCRIPTION:

GATCGTTGGG GAACCCAGCC CCTTGGAAC TGAAGACCC GTGTTTCCTG GACCGCGAAT 60  
 CAGTGTGTTG GGCATCAGTG TTTTCTGCAA GGGTTGTGAC CTGAAACTTT TAAAAACCA 120  
 CCCACCTTGG GGAAGCATT TCTGAATTA TCCATCACCA ACCATTTCTT CTGGATACC 180  
 ATCAAGTAAC AGCTATTATT TGCCAAGTGG AGCTGTCATT TAATTGATG CACCTCTGGN 240  
 TTCAGATGAA ACATTAAATT GTCTTCCTCG ATTCTCCATC GGGTGTAGAG TTTTAAACT 300  
 ATCANTGGCA TTTCAAGTCT TCTGANACAA CATGGCTGTA TGTGCGTGGT CCATAGCACA 360  
 GTACATGCAG CATCTAATAA GNGTTTCCAT TTGTAGAATT NTTTTCNCA NACTTNTAGT 420  
 TAAANNCAAA ATTTTTTAAT TTGNAAANAA GNGTNGTGT GGTATTTNN GNTGTTNTTT 480  
 GTNTNTGGTT GNTNTGTTTA TTNTN 505

SEQ ID NO:56

SEQUENCE LENGTH:450

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00068

SEQUENCE DESCRIPTION:

GATCAGAGAC TGGAGAGGTG GAGTGAGAAG TCTCCGCTGC TCGGGCCCTC CTGGGGAGCC 60  
 CCCGCTCCAG GGCTCGCTCC AGGACCTTCT TCACAAGATG ACTTGCTCGC TGTTACCTGC 120  
 TTCCCCAGTC TTTTCTGAAA AACTACAAAT TAGGGTGGGA AAAGCTCTGT ATTGAGAAGG 180  
 GTCATATTGG CTTTCTAGGA GGTGTTGTTG TTTGCCTGTT AGTTTGTAGG AGCAGGAAGC 240  
 TCATGGGGGC TTCTGTAGCC CCTCTCAAAA GGAGTCTTTA TTCTGAGAAT TTGAAGCTGA 300  
 AACCTCTTTA AATCTTCAGA ATGATTTTAT TGAAGAGGGC CGCAAGCCCC AAATGGAAAA 360  
 CTGTTTTTAG AAAATATGAT GATTTTTGAT TGCTTTTGTA TTTAATTCTG CAGGTGTTCA 420  
 AGTCTTAAAA AATAANGATT TNTANCAGGN 450

SEQ ID NO:57

SEQUENCE LENGTH:447

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00069

SEQUENCE DESCRIPTION:

GATCTTTGAT AGTNGAGAAA ATTATGCAAA GTTCCTCAGA AGTNGGTTAT NATGCTATGG 60

CTGGNGATTT TGTGAATATG GTGGAAAAAG GAATCATTGA CCCAACAAAG GTTGTGAGAN 120  
 CTGCTTTATT GGATGCTGCT GGTGTGGCCT CTCTGTAAAC TACAGCAGAA GTTGTAGTCA 180  
 CAGAAATTCC TAAAGANGAG AAGGACCCTG GAATGGGTGC AATGGGTGGA ATGGGAGGTG 240  
 GTATGGGAGG TGGCATGTNC TAACTCCTAG ACTAGTGCTT TACCTTTATT AATGANCTGT 300  
 GACAGGAAGC CCAAGGCAGT GTTCCTCACC AATAACTTCA GAGAANGTCA GTTGGAGAAA 360  
 AATGANGAAA AAGGGCTGGC TTGAAANTCA CTNTTAACCN NTTANGGTG CTTGGGTTTC 420  
 ANGTTGGCCA NAGTTTTNNN TNNTGGN 447

SEQ ID NO:58  
 SEQUENCE LENGTH:445  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00070

## SEQUENCE DESCRIPTION:

GATCACTGAG CAGTTTCCCAT AGAGCTCCAT GGGAAAGGCAA GCTCTCCCTC CCAATGGGAG 60  
 CCCCACTGTC ACTAACTGTA AACTCAGGCT CAGGCTTCAN CTGCCTACCC CCATCCTCAT 120  
 ATTTCTGTCT GTCCCAGCAC CTCAGGAGCA TTCTCATTGT GGCCGGCTAA CTCCGCCTGG 180  
 ATGTGAACAG GCAAGCACAG TGGGAAATNA GTCACGTACT TGTATTGCAC AGTGGACACC 240  
 TCTAGAGGTC CATTGGTTTA AAGGGATAGG GAAGGAGGAG GGATGAGACC ATCTCCCCCT 300  
 CCCAGGAAGT AAATCTAAGT ATCTAAGGTT TTCTTTATNG CCTTNGAGTC AAANTANTAA 360  
 CTGGCTAGTA CGGGAGGTGT NTGCTNGGTT TTTTCGGGT GGTTTTTTCC TAATGNAATA 420  
 AACTTCATT NTGCTNGT TGGNN 445

SEQ ID NO:59  
 SEQUENCE LENGTH:459  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00071

## SEQUENCE DESCRIPTION:

GATCTTCGGT GGCCTCATGT AAACGTGGCA GCCAGCCTCT TCTAGAACCC TAGCCCAGGG 60  
 ACTGGAGCAG GAAAGGGACC TTCAAAGTGA AGACTGCCTT GTCCCGCAGC TCCTTCTGGC 120  
 TTAGATTGAA ACATGGGCTT CCTAATGGGT TAAATCCTTT AAAACAAGGA GTTGTGGGGG 180  
 AAGGGTGTCTG TGCACTCCTA GAGAAAGGTA CACAGTTGCC CGGTTGGGAA TGTGCTTGGC 240  
 GCTGACCCTG CGGGCATCTG ACTGGTCTTC CAGCTCAGGA AAAAGAATTT GAAAGAGGCT 300  
 TAGCGTGAAG GGGAAATCAA GAGGAGGTTG TNATTNGGT CGAAGGTGCC TTGTTTAAAG 360  
 TCCTNGTAAT TTGTNCTTAT TAATTTTTTT TNATATAATA TNATTTNTT GGGGGGTAAA 420  
 CCATTTTAA ATTAAACCAA CCATTTGTCT TNCTNGAAA 459

SEQ ID NO:60  
 SEQUENCE LENGTH:441  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00072

## SEQUENCE DESCRIPTION:

GATCAGACAC TTCAAGGTCT AGGCTAGACA TGGCAGAGAT GAGGAGGTTT GGCACAGAAA 60

ACATAGCCAC CATT TTTTCC AAGCCTGGGC ATGGGTGGGG GGCCTTGTCT GCTGGCCACG 120  
 CAAGTTCACA TGCNATCTAC ATTAATATCA AGTCTTGA CTCTACTTCC CGTCATTCCCT 180  
 CACAGGACAG AAGCAGAGTG GGTGGTGGTT ATGTTTGACA GAAGGCATTA GGTGACAAC 240  
 TTGTCATGAT TTTNACGGTA AGCCACCATG ATTGTTTTCT CTGGCCTCTG GGTGACCTT 300  
 AAAAAACCC ATTTGGA CT TGNNGACTTT GAAANGGTGC TCTTTGCTTA AGGCTTTNAT 360  
 ATNGNGCCTT GTTTAATTGG GANGGTCNCT TNAAGGCC NTTTCCTTA NTTAANGNG 420  
 GGGTTNTTAN GGNTGTAGAA A 441

SEQ ID NO:61

SEQUENCE LENGTH:436

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00073

SEQUENCE DESCRIPTION:

GATCCGTCAC TCTTCCTTGT GGTAATCCCT AGACTGGGAG CTCAGGTACT CTTTAGTCA 60  
 TCTTTGTATG TCTTTAGCAG AGTTCTTGAC ATGTGGTAGG TGCTTAATAA ATNTTGTG 120  
 TTTATCAAT TTTATGGTAG GGAGAGTAAG TCAGCATCGG TATAAATCG CTTACTCCAC 180  
 GTAACCTTC TTCTGATAGG GTTTGATTTT CTATTAGAAG CTCAATTTTA GTTTTTTTC 240  
 ATATTATAAC TAAATATGTT TCCTGAGAGA TAAGAGAAAT AATGTCCTA CAATAGTTGT 300  
 ATGTATCTAA GATAAGACAT ATAGATGCTT AAGACATTTT GTTTCACCTG CTATTCATA 360  
 GTGTA CTGA ACCATGGTCA TTTTAGCCC TTTTCCTAGG GACCATGCTT ATTTCTCAAT 420  
 AAGGAAATAC CTTCCN 436

SEQ ID NO:62

SEQUENCE LENGTH:434

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00074

SEQUENCE DESCRIPTION:

GATCTTTTTC CATCCAGCAG TGGAGTTTAG TACTTAAGAG TTTGTNCCCT TAAACCAGAC 60  
 TCCCTGGATT AATGCTGTGT ACCCGTGGGC AAGGTGCCTG AATTCTCTAT ACACCTATT 120  
 CCTCATCTGT AAAATGGCAA TAATAGTAAT AGTACCTAAT GTGTGGGGTT GTTATAAGCA 180  
 TTGAGTAAGA TAAATANTAT AAAGCACTTA GAACAGTGCC TGGANCATAA AAACACTTAN 240  
 TAATAGCTCA TAGCTAACAT TTCCTATTTA CANTTCTTCT AGAAATAGCC AGTATTTTGT 300  
 TGGAGTGCCT ACNATGTTAG TTCCTNTTAC TAGTTGCTT ACATGGATTA TCTTNATATC 360  
 CTGTTTTAAA GNTTNTTAC AGGTACCAGG TTTTCATGGA ATTTTCCTTT NANTAAANG 420  
 GGAGGNNAN GNTN 434

SEQ ID NO:63

SEQUENCE LENGTH:433

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00075

SEQUENCE DESCRIPTION:

GATCTGTGAA TCTTGGCTGG GACTTCCTCT GAGTGATGCC TGAGGGTCAG CTCCTCTAGA 60

CATTGACTGC AAGAGAATCT CTGCAACCTC CTATATAAAA GCATTTCTGT TAATTCATTG 120  
 AGAATCCATT CTTTACAATA TGCAGTGAGA TGGGCTTAAG TTTGGGCTAG AGTTTGACTT 180  
 TATGAAGGAG GTCATTGAAA AAGAGAACAG TGACGTAGGC AAATGTTTCA AGCACTTTAG 240  
 AAACAGTACT TTTCCTATAA TTAGTTGATA TACTAATGAG AAAATATACT AGCCTGGCCA 300  
 TGCCAATAAG GTTCCTGCTG TGTCTGGTTA GGCAGCATTN CTTTGTATGC AAATTTCCCTA 360  
 TTGGNCCCTN TTTTNTCCA AAAAGGTAAA TGNCTTNNAT TNCCCGGTTA AAAAATNNNT 420  
 CCCNGGNNAT TTN 433

SEQ ID NO:64  
 SEQUENCE LENGTH:432  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00076

SEQUENCE DESCRIPTION:  
 GATCCTGGAG GTCTTTTCTA GTCTGAGCTT CTTTAGCTAG GCTAAAACAC CTTGGCTTGT 60  
 TATTGCCTCT ACTTTGATTG TNATAATGCT CACTTGGTCC TACCTATNAT CCTTCTACTT 120  
 GTCCAGTTCA AATAAGAAAT AAGGACAAGC CTAACCTCAT AGAAACCTCT CTATTTTTAA 180  
 TCAGTTGTTT AATAATTTAC AGGTTCTTAG GCTCCATCCT GTTGTATGA AATTATAATC 240  
 TGTGGATTGG CTTTAAGCC TGCATTCTTA ACAAACCTTT CAGTTAATTC TTAGATNCAC 300  
 TAAAANTCTG AGGAACTCTA CATGTAACTA TTTCTCAGA GTTGTGCATA TACTGNTTGG 360  
 CATCTGAATG GCTACTCAGC ATTTGGTTAA CATTNNGTA AATTGGAAT AAANTTCCCC 420  
 AGTAAGCCAT TN 432

SEQ ID NO:65  
 SEQUENCE LENGTH:459  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00077

SEQUENCE DESCRIPTION:  
 GATCCATCGC AGAGTCCTAA AGAAGAACCC ACTGAAAAAC TTGAGAATCA TGTGAAGCT 60  
 AAACCCATAT GCAAAGACCA TGCGCCGGA CACCATTCTT CGCCAGGCCA GGAATCACAA 120  
 GCTCCGGGTG GATAAGGCAG CTGCTGCAGC ANCGGCACTA CAAGCCAAAT CAGATGAGAA 180  
 GGCGGCGGTT GCAGGCAAGA AGCCTGTGGT AGGTAAGAAA GGAAAGAAGG CTGCTGTTGG 240  
 TGTTAAGAAG CAGAAGAAGC CTCTGGTGGG AAAAAAGGCA GCAGCTACCA AGAAACCAGC 300  
 CCCTGAAAAG AAGCCTGCAG AGAAGAAACC TACTACAGAG GAGAAGAAGC CTGCTGCATA 360  
 AACTCTTAAA TTTGNTTATT CCATAAAGGT CAAATCATTT TGGNCAGCTT CTTTTTTGAA 420  
 TAAAAGNCCT GNTTATACC AGGGCAGTGA GGAACCAA 459

SEQ ID NO:66  
 SEQUENCE LENGTH:626  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00078

SEQUENCE DESCRIPTION:  
 GATCTACAAA GGCCATGGGA AAAATTCAGA GAGTTAGGAA GGAAAAACCA ATAGCTTTAA 60

AACCTGTGTG CCATTTTAAG AGTTACTTAA TGTTTGGTAA CTTTNATGCC TTCACTTTAC 120  
 AAATTCANGC CTTAGATAAA AGAACCGAGC ANTTTTNTGC TAAAAAGTCC TTGATTTAGC 180  
 ACTATTTACA TACAGGCCAT ACTTTACAAA GTATTGCTG AATGGGGACC TTTTGAGTTG 240  
 AATTTATTTT ATTATNCCC G TTTNGTTTAA TGTCTGGTGC TNNCTATCAC CTCTTCTAAT 300  
 CTTTTAATGT ATTTGTTTGC AATTTTGGGG TAAGACTTTT TTATGAGTAC TTTTCTTTG 360  
 AAGTTTTAGC GGTCAATTTG CCTTTTAAAT GANCATGTGA AGTTATACTG TGGGCTATGC 420  
 ACCAGCTCTC ACCTACNGGG GGNCTTACCT TGGGGGTAGN GNCCATACCA GNCCACTGTA 480  
 TGTTTACTTC CTCACCCATT TGGNGTTGCC CCANCTTGGT TNAACACTNG GGCANCATTN 540  
 TGGTTTNAGG GGNCTTAGG GTTNACCAGN TCNTTTTAAAC NGGNTATTTN CCCGGGGTTT 600  
 TTTNAAANTG GCCCAAAATN CTAA 626

SEQ ID NO:67

SEQUENCE LENGTH:534

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00079

SEQUENCE DESCRIPTION:

GATCAACAGT TCTAGTACTC TTCTTTGTCA GTATATCAAC CTACAGCTAT TGAATGCAAA 60  
 GCCACAAGAG TGTTTAATGG GGACAGTGGG CACTCTCCTG CTTGAAAACC CACTTGGGCA 120  
 GAATGGACTC ACCCACAAG GTCTTCTGTA TGAAGCAGCC AAGGTGTTTG GCCTTCGGAG 180  
 CAGGAAGCTA AAGCTGTTTC TGAATGAGAC CCAAACGCAG GAAATTACAG AAGACATCCC 240  
 CGTGAAGACT TTGAATATGA AGACTGTGTA TGTTCCTGTG TTACCAACAA CAGCAGACTT 300  
 CTAGCATGTA CTTATCAATG TTGTTCTGGTC AGCCCTTCCC TAATTACACC TATCCCCTAC 360  
 ACATACATGC ACATAGNCAC ACACATGNAC AACTTGAAG GTATTCCTT CAAGGTGTGT 420  
 GTAAAAATAT GCTGCTTGGN TTTGAATTCA AATGGGGTTG NTTAGGTCAA GTACTTTGNG 480  
 GCCTNANAGG NATCTTCACA CTTAACCTTA GGCACTTTGT ANGCAATTGTT GGGN 534

SEQ ID NO:68

SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00080

SEQUENCE DESCRIPTION:

GATCTTAGTT GATATTTTGG GCTTGGGGCA GTGAGGGCTT AGGACACCCC AAGTGGTTTG 60  
 GNAAAGNAGG AGGGGAGTGG TGGGTTTATA GGGGGAGGAG GAGGCAGGTG GTCTAAGTCC 120  
 TGAATGGCTA CGTAGTTCNG GGCAAATCCT CAAAAGGGA AAGGGAGGAT TTCCTTAGAA 180  
 GGATGGCGCT CCCAGTGAAT ACTTTTGGAC TTCTGTTTGT NTTACGCTTC TCTCAGGGAA 240  
 AAACATGCAG GTCCTCTAGT GTTTCATGTA CATNCTGTNG GGGGGTGACA CCTTGGTTCT 300  
 GGTAAACAAA GCTGTACTTT TAATAGCTGT TNCAGGAAGG GTTAAGGCCA ACTACAAATT 360  
 AATGTTGGTT GCAAATGTAG TGTGGTTCCT TAACTTTNCG GGGTTTTCCT GAGGAAA 417

SEQ ID NO:69

SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00081

SEQUENCE DESCRIPTION:

5 GATCTGCCCTG CCCACCAACT GGTGATGGAA GGTACAAGT GGCACCTCAA TGAGACGGTG 60  
 CTCACGTGTGT GGTCCGGCACC AACTACTGCT ACCGTGTGGG AATGTGGCAG CATCTTGGAG 120  
 CTGGACGAGC ATCTCCAGAA AGATTTTCATC ATCTTTGAGC TGCTCCCAAG AGCACGGGGC 180  
 ATCCCTCCAA GAGCCGTGCC GCTATTCCTG TGACCCGCCG GCCTGCCCTC ACCTTTGGCT 240  
 CGACATGTGC TTGCATTTCT AGCGAGCTGG CGTGGGGGCT GTCTGGTTGT GTCCCAAGAG 300  
 10 GTGTTGAGGT AGGTNTTGAG AGCTGAGACT AGTCATGTCT CTCTTTCCAT TACATGAGTT 360  
 CATATTTTNN TTTTCTNNTT TGTGTTAGTA ATTTGGAAAT GAAATTATAA GGAATGN 417

SEQ ID NO:70

SEQUENCE LENGTH:415

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00082

SEQUENCE DESCRIPTION:

20 GATCTTTCTG GGAACACAGC CCNGCTGGCG GCTAACCTGC TGTTTGAGAT GCTATGTGCT 60  
 CTCCCCAAAG TGACAACCGT CTGAGTCTTG TGCTCTTCAA GACAAAACAG ATTGCGTCGC 120  
 TGACAAGTTC TCAAGAAGAA CTTATGAGTA AGCAGTCTGA GAACTAAAGA GTTTATGCCA 180  
 AGAAAACTTT CTGCTGAAAG TGTCAATTGCT GGCTGTGAAG TCGGGATAAT CAGTAGAATT 240  
 25 CTCACCCAAA CAGCAACATT TCTAAGGAAC TTGGATTAAT TGGGGGAAAA AAAANGGGGT 300  
 ACTTGACTG CTTTGATTG TTTTCCTTTG GNTGAAAAGN TGGGGGGTTA AANGGGGGAT 360  
 NGTGAGGGGG ANTTTNCCTN TNNAGGGNTT TTTTNTNANC CCATTTNGGN NTNCN 415

SEQ ID NO:71

SEQUENCE LENGTH:415

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00083

SEQUENCE DESCRIPTION:

35 GATCAGAATC ATTAAAAAAT ATTTTGTGTT AGTAAGTTTG AAGATTTCNN GCTTTNAGGC 60  
 CTTTCCTATT TTGTCCCAT TATTTTNNCA GGCAATCTTT TCCATGGAGG GCAGGGTATC 120  
 CATTCCTTAC CATGGGTGTA CCTGCTTAGG TTAAAAATCA TACCAAGGCC TCATACTTCC 180  
 AGGTTTCATG TTGCGTCTTG TTGAGGGAGG GAGAGCAGGT TACTTGGCAA CCATATTGTC 240  
 40 ACCTGTNCCT GTCACACATC TTGAAAAATA AAACGATAAT AGANCTAGTG ACTAATTTNC 300  
 CTTACAGTT CCTGCTTGGN CCCACCCNAC TGNGGGTNGG CTCCATTGGT NNGTTCCGGG 360  
 GCCGTNNNTT AGGGGGNANT TGGGGGNTCG GTTAGGCCTN TNGGTTTGGG GAAAN 415

SEQ ID NO:72

SEQUENCE LENGTH:410

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00084

SEQUENCE DESCRIPTION:

50 GATCTCCCN CTCTAGGGGT CAGGCTCCAT TAGGATTTGC CCCTTCCAN CTCTTCTAC 60

EP 0 679 716 A1

CCAACCACTC AAATNAATCT TTCTTTACCT GAGACCAGTT GGGAGCACTG GAGTGCAGGG 120  
 AGGAGAGGGG AAGGGCCAGT CTGGGCTGCC GGGTTCTAGT CTCCTTTGCA CTGAGGGCCA 180  
 CACTATTACC ATGAGAAGAG GGCCTGTGGG AGCCTGCAAA CTCACTGCTC AAGAAGACAT 240  
 5 GGAGACTCCT GCCCTGTTGT GTATAGATGC AAGATATTTA TATATATTTT TGGTTGTCAA 300  
 TATTAAATAC AGACACTAAG TTATAGTATA TCTGGACAAG CCAACTTGTA AATACACCAC 360  
 CTCACTCCTG TTACTTACCT AAACAGATAT AAATGGCTGG TTTTGTAGAAA 410

SEQ ID NO:73  
 SEQUENCE LENGTH:406  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00085

SEQUENCE DESCRIPTION:  
 GATCGTGACG CTGAATAAAT GTCTTTTTTT TAATGTGCTG TGTAAGTTA GTCTACTCTT 60  
 AAGCCATCTT GGTAATTTTC CCCAACAGTG TGAAGTTAGA ATTCCTTCAG GGTGATGCCA 120  
 GGTTCATATTT GGAATTTATA TACAACNCGC TTGGGTGGAG AAGCCATTGT CTTCGGAAAC 180  
 20 CTTGGTGTAG TTGAACTGAT AGTTACTGTT GTGACCTGAA GTTCACCATT AAAAGGGATT 240  
 ACCCAAGCAA AATCATGGAA TGGTTATAAA AGTGATTGTT GGCACATCCT ATGCAATATA 300  
 TCTAAATTGA ATAATGGTAC CAGATAAANT TATAGATGGG AATGAAGCTT GTGTATCCAT 360  
 TATCATGNGT AATCAATAAA CGGNTTNAAT TCNCTTGGAN TGGAAA 406

SEQ ID NO:74  
 SEQUENCE LENGTH:408  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00086

SEQUENCE DESCRIPTION:  
 GATCACATTG TAAACTATG GATGGTCTGA TAAGGCTTTN ACTGACCCCA CTGACTTCAG 60  
 AGTTATACTC TGTTTGCNAC ATCATAATGC TGGTTTTCCT GACTTTTTGT NTTTTAATAT 120  
 ATTTATAAAA AAAGAAAAAG TTGGTGATTG CATTTGGGAA TTCCCAGGGT ATTACTGGAC 180  
 35 CTATGTGGTG TATTGTTAAA CCAGTGCCT TGTNATACTG TTGCTCTTGA TGTTCTGAT 240  
 ACAGGTAAGG ANGCAATTGG TCAACTCTNA TACAAAGTAT ATATACAGTT CAGTATTGTC 300  
 TCTGTTTATT TTGTTTAAAT TTCATTGGNC AAANTCAANC CAGCATTCCC CATTTGTGTA 360  
 AATAAATGAT TTTCTGGAA TAAAAGGNAA AGGNCTNAA ATTCCAAA 408

SEQ ID NO:75  
 SEQUENCE LENGTH:407  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00087

SEQUENCE DESCRIPTION:  
 GATCAAACTA GTCAGGCCA AACTTTAAGT TCATACCTGA GCTAAGAAGG ATAATTGTCT 60  
 TTTGGTAACT AGGTCTACAG GTTNCATTT TTCTGTGTTA CACTCAAGGA TAAAGGCAAA 120  
 50 ATCAATTTTG TAATTTGTTT AGAAGCCAGA GTTTATCTTT NCTATAAGTT TACAGCCTTT 180  
 TNCTTATATA TACAGTTATT GCCACCTTTG TGAACATGGC AAGGGACTTT TTTACAATTT 240



TNATTTTATT TTCTAGGTAC CAGCCTAGGG GATTTCGGGT TAGGTACTCA TTTTGTATTC 300  
 ACTGTCACTT TTTCCTCATG GTCCTAATTA TAAATNGNCC CAAAATCAAG GNTTGCCTNA 360  
 AAAAGGGGGN AAAATGGTTG GCCCCNNGGT TTTTNGNNNC CCCNGTN 407

SEQ ID NO:76

SEQUENCE LENGTH:413

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00088

SEQUENCE DESCRIPTION:

GATCTACCGA CTCACTTCTG AGAATATTTT TNACAGATTA TCTTTGGGCC TTTCCATTAG 60  
 AAAGCTGTTT GTTGTCCCC CTGTTGGTAC ATTTGGTTAC CTCATTTTGC CGTTTCAAAT 120  
 TGTAAGGCT CACAGGGGTG TTTTGGAA TCATTGCTG AGTCATTTTC TCAAATCATA 180  
 TTCCATTGTA TCAGTTAACA TATAGTTTAA AATGTATGTA TTATAAATNT CTGTANCCAA 240  
 ATCATTGAA GGCTTGATAA ATTTNTAACA ANGTTTGTAC ATTTNTCATG AAAGTCACTA 300  
 GTAATGCTNG GNGNGGTAGT GCAATGGANT TTTCCNTTTT TCNTCCCTGT GCCCATTTTG 360  
 GAGTTGAGAG GGTGTNGGT AATNAACTGT ATGGTGTACA NTGNANCCNA NNN 413

SEQ ID NO:77

SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00089

SEQUENCE DESCRIPTION:

GATCGGCAAG CCNCNCACTG TCCCTTGCAA GGTGACAGGC CGCTGCGGCT CTGTNCTGGT 60  
 ACGCCTCATC CCTGCACCCA GGGGCACTGG CATCGTCTCC GCACCTGTGC CTAAGAAGCT 120  
 GCTCATGATG GCTGGTATCG ATGACTGCTA CACCTCAGCC CGGGGCTGCA CTGCCACCCT 180  
 GGGCAACTTC GCCAAGGNCA CCTTTGATGC CATTTCTAAG ACCTACAGCT ACCTGACCCC 240  
 CGACCTCTGG AAGGAGACTG TATTCACCAA GTNTCCCTAT CAGGGAGTTC ACTGACCACC 300  
 TCGTCAAAGA CCCACACCAG AGGTCTCCGT GCAGNGGACT TCAGGNTNCA GNTTGTGGTT 360  
 ACAACATAGG GGNTTTTAT ACAANGGAAA NGTAAAGGTG NNNTTAAAGN GGTGAAA 417

SEQ ID NO:78

SEQUENCE LENGTH:404

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00090

SEQUENCE DESCRIPTION:

GATCAGAAGA AACACTCCAA AAATTGAGAT GAAATGTTGG TGCAGCCAGT TATAAGTAAT 60  
 ATAGTTAACA AGCAAAAAA GTGCTGCCAC CTTTATGAT GATTTTCTAA ATGGAGAAAC 120  
 ATTTGGCTGC ATCCACATAG ACCTTTATGT TTTGTTTCA GTTGAAAAC TGCCTCCTTT 180  
 GGCAACATTC GTAAATNAAG CAGAATTTT TTTTCTCTT TTTCCAAATA TGTTAGTTT 240  
 GTNCTTGTA GATGTATCAT GGGTATTGGT GCTGTGTAAT GAACAACGAA TTTTAATTAG 300  
 CATGTGGTTC AGAATATNCA ATGTTAGGTT TTTAAAAAG TATCTTGATG GTTCTTNTTC 360  
 TATTTATAAT TTCNGACTTT CATAANGTGT ACCCANGANT TTCN 404

SEQ ID NO:79

SEQUENCE LENGTH:622

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00091

SEQUENCE DESCRIPTION:

GATCCCCGCA ACTCGCTTGT CCTTGGGTCA CCCTGCATTG CATAGCCATG TGCTTGTCCTC 60  
TGTGCTCCCA CGGTTCCAG GGGCCAGGCT GGGAGCCAC AGCCACCCCA CTATGCCGCA 120  
GCGGCCCTAC CCACCTTCAG GCAGCCTATG GGACGCAGGG CCCCATCTGT CCCTCGGTCTG 180  
CCGTGTGGCC AGAGTGGGTC CGTCGTCCCC AACACTCGTG CTCGCTCAGA CACTTTGGCA 240  
GGATGTCTGG GGCCTCACCA GCAGGAGCGC GTGCAAGCCG GGCAGGCGGT CCACCTAGAC 300  
CCACAGCCCC TCGGGAGCAC CNCACCTCTG TGTGTGATGT AGCTTTCTCT CCCTNAGCTG 360  
CAAGGGTCCC GATTTTGCCA TCGGAAAAAG ACAACCTCTA CTTTTTNTCT TTTGTATTTT 420  
TGATAAACAN TTGAAGNTTG GAGCNTGTTA AAATTTATTN TTTGGGGGGA AACCTNAAGA 480  
ACTGGGNCTT AATTTNGGNG TTCGTGGGAC CCTNTTANNT GGTTTTNAAT NAANCGGTGA 540  
NGGAATTAAA CTGTTTTGGA ANANTTGGTT TAAAGNTTAA AAATTTTGGG AAAAAAGGG 600  
GCTTTTAA TTTTTGGGT TN 622

SEQ ID NO:80

SEQUENCE LENGTH:400

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00092

SEQUENCE DESCRIPTION:

GATCTTCCTT TTTCTNTGA ATNGGCTCTG TTGNCTTTTT CTCTTTTTTC TCATGTGTTC 60  
TTCCCTCCAC CTCCACCCTT TTCTTTCTTT CTCTCTCTGA TTGAGAGGCA TTNAATTACG 120  
TTTTCAGTAG TACAGGCTTC TTGCCGATAT GAAGGGAAGT TTTCAGAAAG AGACCTACTC 180  
TGGGTCAATT AATTTTGAAT ACAGTTTCA ATCGTTCAAG TTTTGNNNG NTTATATCTA 240  
ATGTGTGTTT CATTTTTTGG GAAAGCTATA TTTGTATT AGGAAATGGT ATACTATTTT 300  
GCTATTTGTA CTGAGTGAGT ACATTGGCAT AAATATAGAA ATTTATATAT ATACATATAT 360  
ATAACTGTGC TNNTTGGCCT TTTTNTGNG GGAAATTGGN 400

SEQ ID NO:81

SEQUENCE LENGTH:396

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00093

SEQUENCE DESCRIPTION:

GATCAGACTG TGGCATTGTA AATGTCAACA TTCCAACAAG TGGGGCTGAG ATTGGAGGTG 60  
CCTTTGGAGG AGAAAAGCAC ACTGGTGGTG GCAGGGAGTC TGGCAGTGAT GCCTGGAAAC 120  
AGTACATGAG AAGGTCTACT TGTACTATCA ACTACAGTAA AGACCTTCCT CTGGCCCAAG 180  
GAATCAAGTT TCAGTAAAGG TGTTTTAGAT GAACATCCCN NAATTTGAGG GTGTTCCAGC 240  
AGCTGTTTTT GGAGAAGACA AAGAAAATTA AAGTTTTCCC TGAATAAATG CATTATTATG 300  
ACTGTGACAG TGACTAATCC CCCTATGACC NNAAGNCCT GATTAAATCA AGAGATTTCCT 360

TTTTTAAAAA TCAANTAAAA TTGTNACACC ATAAAA

396

SEQ ID NO:82

SEQUENCE LENGTH:400

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00094

SEQUENCE DESCRIPTION:

10 GATCGATGGT TGACAATCCA GAGTGGTGAA CAGCCCTACA AGATGGCTGG TCGATGCCAT 60  
 GCTTTTAAAA AAGAATGGAT AGAATGTGCA CATGGAATNG GTTATACTCG GGCAGAGAAA 120  
 GAGTGCAAGA TAGAATATGA TGATTTCGTA GAGTGTTCG TCGGCAGAA AACGATGAGA 180  
 CGTGCAGGTA CCATCAGGAA GCAGCGGGAT AAGCTGATAA AGGAAGGAAA GTACACCCCT 240  
 15 CCACCTCACC ACATTGGCAA GGGGGAGCCT CGGCCCTGAA CAGAGCAGCT GCTGATGTCT 300  
 GGAGGCTGAT TTTCTGTTC TCTGTTCTCC ACTGGAAAGG TTGTTTACGA CAAACCTCCT 360  
 TGTCAAAGTN TGTAATAATA AAGGATTGCT CCATCCTAAA 400

SEQ ID NO:83

SEQUENCE LENGTH:397

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00095

SEQUENCE DESCRIPTION:

25 GATCTGGGCA CTGTACTTNA GCCTGGGCGA CAGAGAGACC CATCTCAAAN AAAAAATTGG 60  
 AACCTGAGAA GGGGGTCGTG GGGTCCCCGG GGCCACCGT CTGCACTGG NATCTNAAGT 120  
 CGGGGTGGNC TTGTGGGACT NACCCNTTAC CCTGTGGGTT CTGTACTAGC TCCGGGNAAT 180  
 TGGTGACAGA NTCGAGTTAA ATTGTAGGAC ATCGCGTTGG TGTCTGAGAG GGAGTTGGAG 240  
 30 AGCTGGTTGG TGTGGAGGGA AAGGNTTACA CACATGTNAT TTCAGAAGCG TTCTGTGGGT 300  
 AGAGGAATCG TTTTCTCTTT GAGACTGTTA TGAGTATGTA CAAATTTTAT TTCCTGTAAA 360  
 AATATTTNCA TTTTTTAAAN TGTTATTTT CTAGAAA 397

SEQ ID NO:84

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00096

SEQUENCE DESCRIPTION:

40 GATCGAAGAT TTATCCCAGC AAGCACAAC AGCAGCTGCT GAGAAATTCA AAGTTCAAGG 60  
 TGAAGCTGTC TCAAACATTC AAGAAAACAC ACAGACTCCA ACTGTACAAG AGGAGAGTGA 120  
 AGAGGAAGAG GTCGATGAAA CAGGTGTAGA AGTTAAGGAC ATAGAATTGG TCATGTCACA 180  
 45 AGCAAAATGTG TCGAGAGCAA AGGCAGTCCG AGCCCTGAAG ANCAACAGTA ATGATATTGT 240  
 AAATNCGATT ATGGAATTAA CAATGTAACC ATATGGANGC AACTTTTTTT TGGTGTCTCA 300  
 NAGGNGTAAC TGCAGCTTGG TTTGAAANTT TGTTACCTTG TTTCTTATCA TAAATNAAAN 360  
 NGTTATTNGC TTCCTTTTTT GGNTTGGAAG 390

SEQ ID NO:85

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00097

SEQUENCE DESCRIPTION:

GATCACTTTC ACTNTCAATT ATTTGCCAGG NCTCACAGAA CTCAGAAAAG CTCAGANCAC 60  
 TCATGGTTAC TATTTAGTAA AGCAAAAAGA CACAAATNAA AATNAGCAAG TTTGGCCGGG 120  
 ATTGCAGGCA TGAGCCACTG AGCCCGGCC CCAACTGTTA CATCAAAATA TTATTTGAGA 180  
 GTATATGTGT CCTCACGTCC CTAAAACACT AGAAACTGTC AANCTTTTAA TCTTTGTCAA 240  
 ACTCTCAAAA GTAGTATCTC TGCATTTGCA TGCCTTTGNG TNCTAATAAG GTTGAGTACT 300  
 GCTTTAAAAG TTTGCTGGNC ATCTNNTTGN TTTTTTTAAG GACCTGCGGT GGNNAGGCCC 360  
 NTTCAANANA TTNTTTCNTT AATTNGGGCC TN 392

SEQ ID NO:86

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00098

SEQUENCE DESCRIPTION:

GATCAGTCTG GCTGGTGGTT TAACAGGTGT CACTCTGCAA ACCTGAATGG TGTATACTAC 60  
 AGCGGGCCCT ACACGGCTAA AACAGACAAT GGGATTGTCT NGNACACCTG GCATGGGTGG 120  
 TGGTATTCTC TGAAATCTGT GGTATGAAA ATTAGGCCAA ATGATTTTAT TCCAAATGTA 180  
 ATTTAATTGC TGCTGTTGGG CTTTCGTTTC TGCAATTCAG CTTTGTTTAA AGTGATTTGA 240  
 AAAATACTCA TTCTGAACAT ATCCATGCGC AATCATGATA ACTGGTTGTG AGNAGTGCTT 300  
 TTCATTCTTC TCACTTGCTT TTGTTACTTA ATGTGCTTTC AGGACAGCAG ATATGCAATA 360  
 TTCACCAAAT AAATGTAGGC TGGTGGTAAT AAA 393

SEQ ID NO:87

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00099

SEQUENCE DESCRIPTION:

GATCCAGAAA TACTTAACAC GTGAATATTT TGCTAAAAAA GCATATATAA CTATTTNAAA 60  
 TATCCATTTA TCTTTTGTAT ATCTAAGACT CATCCTGATT TTAACATCA CACATGAATA 120  
 AAGCCTTTGT ATCTTTCTTT CTCTAATGTT GTATCATACT CTNCTAAAAC TTGAGTGGCT 180  
 GTCTTAAAAG ATATAAGGGG AAAGATAATA TTGTCTGTCT CTATATTGCT TAGTAAGTAT 240  
 TTCCATAGTC AATGATGGTT TAATAGGTAA ACCAAACCCT ATAANCCTGA CCTCCTTTAT 300  
 GGTTAATACT ATTTANGCAA GGANTGCGT ACAGATTTGG NTACAGTACG GATTTGNCCA 360  
 AATAANTTCA NTAAAAGCCT TAAAGCTGAA A 391

SEQ ID NO:88

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00100

SEQUENCE DESCRIPTION:

5 GATCAACCCA CAGAACAAAG CGGATTTCCT AGGCATCTCC CCAGAGCGAG CCTTTGCTGA 60  
 TTTTCTCTTT GCCAGCACCA TCCTGCACCT TGTTGTCTATG AACTTTGTG GCTGACTCAT 120  
 TCTCATTTAC TTAATTGAGG AGTAGGAGAC TAAAAGAATG TTCACTCTTT GAATTCCTG 180  
 GATAAGAGTT CTGGAGATGG CAGCTTATTG GACACATGGA TTTTCTTCAG ATTTGCACTT 240  
 ACTGCTAGCT CTGCTTTTGA TGCAGGAGAA AAGCCCAGAG TTCACTGTGT GTCAGAACAA 300  
 10 CTTTCTAACA AACATTTATT AATCCAGCCT CTGCCTTTCA TTAAATGTAA CCTTTTGCCT 360  
 TCCAAATTAA GGACTCCATG CCACTCCTCN 390

SEQ ID NO:89

SEQUENCE LENGTH:390

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00101

SEQUENCE DESCRIPTION:

20 GATCTTTCTN AATGTGTATT GATTGGTCTT TTCAGCTACT CTGAACAGAT TACTAAGGCC 60  
 ATCTCCTCAT CTCTAAGGGA GAAAAATAGT CTGTAGATGA ATAATGTAAG GTAAAGAGTT 120  
 GCATGTCACT CTTTGTAAATN ATTTACACTT TAACCTTCTC CAGAACTCAG ACATGATTTC 180  
 AACATGGTGT TAGATTTGTG CATTNATTT TCCTGACCAC CTCATTCCAG CCAATGTATG 240  
 25 GTTATCCACT CTGTGTGCNA AANCCAATCA TGCNTTTCAC GGCCCTTTAG TTCAGAGAAG 300  
 TTCTGCACTG ATTTTGTAGT TCTTGATGTC TCAATCTTAC ATGTATACCA ATCACAATGG 360  
 AATAAAAAGT GTTTGAGGTT GTACTGTGGN 390

SEQ ID NO:90

SEQUENCE LENGTH:391

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00102

SEQUENCE DESCRIPTION:

35 GATCCGAGGA GGCGGAACAA GTCCACGGAG TCCCNNGCAG GCCAACGTGC AGCGGCTGAA 60  
 GGAGTACCGC TCCAAACTCA TCCTCTTCCC CAGGAAGCCC TCGGCCCCCA AGAAGGGAGA 120  
 CAGTTCTGCT GAAGAACTGA AACTGGCCAC CCAGCTGACC GGACCGGTCA TGCCCGTCCG 180  
 GAACGTCTAT AAGAAGGAGA AAGCTCGAGT NATCACTGAG GAAGAGAAGA ATTTCAAAGC 240  
 40 CTTGCTAGT CTCCGTATGG CCCGTGCCAA CGCCCGGNTC TTCGGCATA GGGCAAAAAG 300  
 AGCCANGNAN GCCGCAGANC AGGATGTTNG TAAGGAAANN ATTTANAGCC CCTCCTGGGN 360  
 GACCTTTGGG ATTCAGTCGN CAGTCAATAA A 391

SEQ ID NO:91

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00103

SEQUENCE DESCRIPTION:

50 GATCTGTGCC AAGCTCAGGG TGTAGCGCTG CAAACGATGA AGCAAGAGAT TCTCATTAAC 60

55

CTTGTGAAGC AAAAGCCACA AATAACAGAG GAACAACCTG AGGCTGTCAT TGCAGATTTT 120  
 TCAGGCCTGT TGGAGAAATG CTGCCAAGGC CAGGAACAGG AAGTCTGCTT TGCTGAAGAG 180  
 5 GGACAAAAAC TGGNGNCAAA AACTCGTGCT GCTTTGGGAG TTTAAATTAC TTCAGGGGAA 240  
 GAGAAGACAA AACGAGTCTT TCATTCGGTG TGAACCTTTC TCTTTAATTT TAACTGATTT 300  
 AACACTNTTT GGTGAATTAA TGAAATGNTA AAGACTTTTT ATGTGAGATT TTCCTTATCA 360  
 CAGAAATNAA NTNTCCTCCA AATGTTAATA N 391

SEQ ID NO:92

SEQUENCE LENGTH:385

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00104

SEQUENCE DESCRIPTION:

GATCTTTTCC CCTGGCCAAA GGGAAAGTTGT ATTAGTCTGT GACATCTTGT GATGCTGTTT 60  
 ATCTTGGTTT GACATTGGAG ATACGCTAGT AACTGTGATA CCATACTATA AAACAGAAGA 120  
 ATTTTCTGCT ACTAAAACT GCCTTTTAC AAAATGACTG TAAATATTTG TAAAAATAAA 180  
 20 TAACACTAAA CTTTAAGCCC AAAAGGAGAG ATAGAGCCAT GTGTTCAGTT GTGGACCTGT 240  
 CCGTGGGGCA CAGTGCCACC CCATCACAGT GTTGCTGTCA TCAGGCAAAN GTGAATGTTT 300  
 GTTTATGGCA AATTCGNCTT TTGCGAATGG CTTANTTCTG ACACTACCTT TCTGGGAAAT 360  
 GTTAATANAT TTTTAATTNT TCAAA 385

SEQ ID NO:93

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00105

SEQUENCE DESCRIPTION:

GATCTTTGAT AGTTTTGGTG AACTCTCTAA AATACATTCA CTGTGGGTCC GACGCAATTT 60  
 ATAAAAATNA TGTACTCAAG AAGGGAGACC TGTTTGTTTC ATTTCTCATC TGTTTGGGAG 120  
 ATGATTTTAG AGCACTAGAA AGGCACTGGG GAGATTCTCA GCTTAAACA TCCAGCAGTT 180  
 35 TGAAGTATGA TTAGGTACAT CAGGGCTGCA TTGTCAATNT TCTCTTTAAG TCTTTTAAACA 240  
 TTTATAGCAA TTTTTTTTTT CCCGGAGAGT TTAGGTTGCA AGTTTTGGGT TTCTTGTTTG 300  
 TTTTGTGTTT GCTTCCTGCT TTAATNCTTN AATTTCAGT CATTACTGGT ATTGAAAAAT 360  
 AAAATATCTT TAAANCANNG N 381

SEQ ID NO:94

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00106

SEQUENCE DESCRIPTION:

GATCTAAGAG ACTCAAGAGC TGGGTTTCTT TCAGCACTCT GTACTGTCCC AAATAGCAAA 60  
 CAAATNACTT TGTAGCCAGA TTTCTGAATG GAAATNAGAA ATTGAATTCT CCATGGACTT 120  
 50 TTAGGTTTAT GGGGGAGTTT TAGCTGTGTT TCTTGTTTTT ATTCAGCCA AACATGCTCTG 180  
 CTTTTGATTT TTTTTTAAAA GTATAAGTGG TCTATATATA TGTTACACCTT TTAAATGTAA 240

ATGTTTAAAA AGTAAGCATT TATGTGTTTC CATAACTGAC ATCTGATGCA GACCTCATT 300  
 TCTCCCCCTC TTCTACCCTC CTCTTTTCCC CTTTTTCAAT ACTCTTGAT TGGGTTCTAA 360  
 TAAAATGGGT TGCTTTTCN 380

SEQ ID NO:95  
 SEQUENCE LENGTH:379  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00107

SEQUENCE DESCRIPTION:  
 GATCCATACT TGGATGATAT TGATGATGAG ATGGACCCAG AGATAGAAGA AGCTTATGAA 60  
 AAGTTTTGTT TGGAAATCAGA GCGTAANGNA NAACAGTAAA GTTAAATTTT AGCATATCAG 120  
 TTTTATAAAG CAGTTTAGGT ATGGTGATT AGCAGAACAC AAGAGAGCAA GAAAATGTGT 180  
 CACATCTATA CCAAATTGAG GATGTTGAGT TATGTTACTA ATGTATGCAA CTTTAATTTT 240  
 GTTTAACT ATCTGCCAAA ATAACTTTA TTCCCTATAA CTTAAAATGT GTATATATAT 300  
 ATAATAGTTT ATTATGTACA GTTAATTCTA CTGTTTGGC TGCAATAAAA TCGATTTTGG 360  
 AAATAAATGG AATGTTGGN 379

SEQ ID NO:96  
 SEQUENCE LENGTH:384  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00108

SEQUENCE DESCRIPTION:  
 GATCTTTGCT GGCAAGCAGC TGGAAGATGG ACGTACTTTG TCTGACTACA ATATTCAAAA 60  
 GGAGTCTACT CTTTCTCTTG TGTGAGACT TCGTGGTGGT GCTAAGAAAA GGAAGAAGAA 120  
 GTCTTACACC ACTCCCAAGA NGAATAAGCA CAAGAGAAAG AAGGTTAAGC TGGCTGTCCT 180  
 GAAATATTAT AAGGTGGATG AGAATGGCAA AATTAGTCGC CTCGTCGAG AGTGCCCTTC 240  
 TGATGAATGT GGTGCTGGGG TGTATATGGC AAGTCACTTT NGNCAGACAT TATTGTGGCA 300  
 NATNTTGTCT GACTTACTGG TTNCAACAAN CCCAGAAGNC ANGTTNACTG TNTGANGTTN 360  
 ATNAAAAGNC ATGTNCTGAA CAAA 384

SEQ ID NO:97  
 SEQUENCE LENGTH:583  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00109

SEQUENCE DESCRIPTION:  
 GATCCTCATG AATGACTATC CTAAATTTAA GTATGCAGTT CTNTTTTTC TGGGTTTATT 60  
 CGTGCTGGTT CATCGNGAGT NAGANGCCTG CCTTGCTGTT CCTGGGAAGA TGCCATAGTT 120  
 TTCGTTACTG GATGTTTGA GTAGATACTG GTCTGTNATT GGTGGAATGG AGAACACACG 180  
 TGTTGGTGCT TCTGGGTAGC ACTGGTTTGC ATTAGTTTAT GTTCCATGC CAGAGTTTGT 240  
 GTGGGCGGGC GCATGTCCAC CACAGAGTGC ACTCGAGGGG ACTTTCAGTC ACAGGATTTT 300  
 ATAATTGTNA TTGTCACACT TTCAAATTTT TGTACATCAG TGAATTTTTT TTATATTAAA 360  
 AGGTTGAGCC AAAGCCCCCA GTGTTTTGTA TTTTGAAGCC AAGCTTCACT TCTAAAAGTG 420

CCTACAGAGG ACTTGTA AAA TGGAAATGC AGCTCTGCAC GGAGTTTGAA ACCGTCATAC 480  
CTCCTTCTAT TAGGGAATNG GCATATACTG AGGGTGGTCC GGAAGNNNTT AACTTCCTAA 540  
AATTTTAA TAAAAGGCCT TTGCACCATT GGACCCNTT AAA 583

SEQ ID NO:98

SEQUENCE LENGTH:370

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00110

SEQUENCE DESCRIPTION:

GATCAAGAAA AGCAACTTAT GGAAACAAC TACAGAATTTA CAAAAAGGA TACTCAAACC 60  
AAAAGTATTA TTTCAGAGAC CAGTAATAAA ATTGACGCTG AAATTGCTTC CTTAAAAACA 120  
CTGATGGAAT CTAACAAACT TGAGACAATT CGTTATCTTG CAGCTTCAGT GTTACTTGC 180  
CTGGCAATAG CATTGGGATT TTATAGATTC TGGAAAGTAG ATTAATGCTC ATCCTGCTGT 240  
GGCTGTTGGC TTCTTAGAAC ACCAAACCGG GAGAGATTTA CTTGAACAT TGTCAGTTGC 300  
AGCAAAAATT TACTACACAA GATTATTCGA AGTGTATACG GACTAAAAGA GGAAGTGTG 360  
TAGAATGAAA 370

SEQ ID NO:99

SEQUENCE LENGTH:384

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00111

SEQUENCE DESCRIPTION:

GATCTGAAGA GCGTCCTGGG TCAACTGGGC ATCACTAAGG TCTTCAGCAA TGGGGCTGAC 60  
CTCTCCGGGG TCACAGAGGA GGCACCCCTG AAGCTCTCCA AGGCCGTGCA TAAGGCTGTG 120  
CTGACCATCG ACGAGAAAGG GACTGAAGCT GCTGGGGCCA TGTTTTTAGA GGCCATACCC 180  
ATGTCTATCC CCCCCGAGGT CAAGTTCAAC AAACCCTTG TCTTCTTAAT GATTGNCCAN 240  
AATACCAAGT CTNCCCTCTT CATGGGAAAA GTGGTGAATT CCACCNA AAA ATAAGTGNCT 300  
GTNGGTNCTC AACCCCTTNC NNTTCATCCN TGGGCCCNTN GGCTTGGATN GANAATTAAA 360  
AGAAGGGGTT GNGGCTNGGG NAAA 384

SEQ ID NO:100

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00113

SEQUENCE DESCRIPTION:

GATCTTTGAA ACCTTGGTCC CGTAACTTA CTAGTCACAT TGACCAATGT TTTATAGAAA 60  
TGCCTAGAAT TTTGAGACTA ATNGTAGTTA TCCATTAACA TTCCAAAAGT TTTGTNCTTT 120  
TNAAAATTTG TTTGGTAAT TATCACATTT NTNCTCTTA CCTTCCTTA AATGGCCACA 180  
GTGTGTACTG CTGGANTGTN CCATCCAAAA GATGTAGCTT CAGANGCACA GTGATTGCCC 240  
CAGGGTCCAT GAGATATTGT TTGTATTATG ANGTTGGAGT GCTGTCTACT GAAATTATAC 300  
TCTTAAATAA NTATGTATGT NGTGTGTAAT ATTCCTAAT AAATNCTTN GATAAACTAA 360  
AAAACNNNG CTNN 374



SEQ ID NO:101  
SEQUENCE LENGTH:382  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00114

## SEQUENCE DESCRIPTION:

GATCTGTGCA AGGTATTAAC GTGTCAGGGC TGAGTGTTCT GGGATTTCTC TAGAGGCTGG 60  
CAAGAACCAG TTGTTTTGTC TTGCGGGTCT GTCAGGGTTG GAAAGTCCAA GCCGTAGACC 120  
CAGTTTCCTT TCTTAGCTGA TGTCTTTGGC CAGAACACCG TGGGCTGTTA CTTGCTTTGA 180  
GTTGGAAGCG GTTTGCATT AC GGCTGTAA ATGTATCAT TCTTAATT TA TGAAGGTTT 240  
TTTTTTGTAC GCAATTCTCG GATTCTTTG AAGNAGATGA CAACAAATTT NGGTTTTCTA 300  
CTTGTTATGT GAAGACCATT AAGGCCCAA GCAACAAGNC AATTNTGTAA GGGAAANTNA 360  
AAGTTCCTTG CNGTAANCCA AA 382

SEQ ID NO:102  
SEQUENCE LENGTH:368  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00115

## SEQUENCE DESCRIPTION:

GATCTGTCTC TGCTGTTTAA CTTCAATTGGA TTAATCAGCT GGTTCAACT CTA CTGCGAA 60  
ACAAAAATAG CTCCTTAAAA GTACTGTTCT CCTTCAGTGG CATGTAGTTA TCTAATCAAG 120  
ACACCTCATT CAAACAAAAC CTGCCTTAGG AAAATTTAAT ATATTTNAAA TNATTTTAAA 180  
AGAAATACAA CATCTTATTC TTTAGCTTTC TTAATCGGTG CTTTATGGAG GCCAGTGTA 240  
CGNTACATGA CTCGTTGAGA AAGTTGAGGA ATTTCTCTA CCACCTTTGT TGCTTGAAGA 300  
AAAACATGTC TTTTCAAAT GAGAGGCTTT CATTGAAGAA AAGAAAAAAA CAACAGTTAA 360  
AAGCTAAA 368

SEQ ID NO:103  
SEQUENCE LENGTH:367  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00116

## SEQUENCE DESCRIPTION:

GATCTCGGAT GACCAAACCA GCCTTCGGAG CGTTCTCTGT CCTACTTCTN ACTTTACTTG 60  
TGGTGTGACC ATGTTTCATNA TAATCTCAA GGAGAAAAA AACCTTGTA AAAAGCAAA 120  
AATGACAACA GAAAANCAAT CTTATTCCGA GCATTCCAGT AACTTTTTTG TGTATGTNCT 180  
TAGCTGTACT ATAAGTAGTT GGTTGTATG AGATGGTTAA AAAGGCCAAA GATAAAAGGT 240  
TTCTTTTTTT TCCCTTTTT GTCTATGAAG TTGCTGTTA TTTTTTGGG CCTGTTTGAT 300  
GTATGTGTGA AACANTTGTN GTCCAACATT AANCAGGANT TTTATTTTNC NGAGTNGTNC 360  
TANCAAA 367

SEQ ID NO:104  
SEQUENCE LENGTH:366

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00117

SEQUENCE DESCRIPTION:

GATCTTAGTA ACTATGNATG AAGATGGTGC TTGGCCTGTN CTTCTTGATG AATTTGTTGA 60  
 GTGGCAAAAA GTCCGTCAGA CATCATAGCA AGAACTATGT GAAGAAAATG CAAACCTTTC 120  
 AATTCCCACG TGTATACAAG CTAATGTGAT GAGGGGGAAA AAAATCCAAC GGGTGCATTT 180  
 TCATTCATAT GAAAGACTTC TCATAGTACT TTTTTTCCN TTTTTTAAAA GGAGGTTTTT 240  
 CTTGTTACAT GTGATGGGCA TTGAGCCACA CCNNTCTTA GACTGAATAT NGAAGTTTTT 300  
 GTTTTGAGTT ATGTTTATAA CATTTATTTC AGAACANTAA TGATTCAGAT TTGTGACAAA 360  
 GGCAAA 366

SEQ ID NO:105

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00118

SEQUENCE DESCRIPTION:

GATCCCCGAA ATTGGTGGGC TTGACCTCCT GGCAAATTGC TCGGTCTTTC CACTTGCTGT 60  
 TCAGGACCAC TAAATGCTGA AATNTGGATG CATACCGAAA TAAAAGNAAT TCATTGTGTA 120  
 AA 122

SEQ ID NO:106

SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00119

SEQUENCE DESCRIPTION:

GATCTTCAAT ATGAAGACAT GAGCTTTTCT CGCAGGAAAT TTTCTTTTTC ACAGAACTGG 60  
 TGTCAGGAAT CACTGAAGGG CTAACCGTGA TAGTCCTTGC AAGTAAGTCA AGGTTTTATC 120  
 CTGATTGGAA ATAGAAGACA TTTCCGGTTG AGAGAACAGA TTCGTTGGAA GCTTAACTTT 180  
 TGTGCTCTCT TAACGCCACC AAATTTTAGG GTAATTTGAT TATGAAAGAG TGAATTTTTC 240  
 TGGACAGAAA AGGGAGAGCT ACCAAATTGT TTTTTTCTTT TTAAGGAA GTTTAATGTC 300  
 CGTTGTATCA CAAATCAGTG TTAACACACC AGAACTTTAG CCAAAATAAA TGTCTTACAT 360  
 TACN 364

SEQ ID NO:107

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00120

SEQUENCE DESCRIPTION:

GATCAGCAGG GAGTTTATTT GAGGACATCA GTCACCTTTG GGGTTGCCAT GTACAATNAG 60  
 ATTTATAATC ATNATACTCT TCGGTGGTAG TTTCAAAGA CACTACTAAT ACGCAGGAAG 120  
 CGTTCCAGCT ATTTAATGCT GGCAACTACT GTTTAATGGT CAGTTAAATC TGTGATAATG 180

EP 0 679 716 A1

GTTGGAAGTG GGTGGGGTTA TGAAATTGTA GATGTTTTTA GAAAAACTTG TGAATGAAAA 240  
TGAATCCAAG TGTTTCATGT GAAGATGTTG AGCCATTGCT ATCATGCATT CCTGTCTCAT 300  
GGCAGAAAAAT TTTGAAGATT AAAAAATAAA ATAATCAAAA TGTTTCCTCT TTNCTAAA 358

SEQ ID NO:108

SEQUENCE LENGTH:430

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00121

SEQUENCE DESCRIPTION:

GATCTGTCTC TGGGGTCCCN CATAACAGAGA AATGCATCTT GCTGAACAAG TGACCAATAA 60  
TCTTAAAGAA CTTGCACAGC AAGTAACTCC AGGTGATATC GTAAGCACGT ATGGAGTTCG 120  
AAAAGCAATG GGGATTTCCTTTCCTCCCG CGTCATGGAA AACAACCTTN TGGATTGAC 180  
AGANGNNCT GAAGAACCTA AAAAGACGGA TGTGCTGAG TGTGGACCTG GTGGAAGTTG 240  
AGGCTGCCTG GTATTTGATT ATATATTATG TACATACTTT TTCATTCTTA ACTTAGAAAT 300  
GCTTTTCAGA AGATATTAAA TATTTGTAAA TTGTNTTTT AATTAACTT TGGAAACAGCG 360  
AATTTGGNTG TTCCAGAGGT TGGGCCTTGT ATTAGGGAAA TAAAAGCTTG GACCTGGGGC 420  
CTCGTGGAAA 430

SEQ ID NO:109

SEQUENCE LENGTH:357

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00122

SEQUENCE DESCRIPTION:

GATCACTNGA TATTTTAGTC ATTCTGCTTC TCATCTAAAT ATTTCCATAT NCTGTATTAG 60  
GAGAAAATNA CCCTCCCAGC ACCAGCCCC CTCTCAANCC CCCAACCCTA AACCAAGCAT 120  
TTTGGGAATGA GTCTCCTTTA GTTTCAGAGT GTGGATTGTA TAACCCATAT ACTCTTCGAT 180  
GTACTTGTTC GGTTGGTAT TAATTNGACT GTGCATGNCA GCGGCAATCT TTTCTTTGGT 240  
CAAAGTTTC TGTTATTTT GCTTGTCTATA TTCGATGTAC TTTAAGGGTG TCTTTTATGA 300  
AGGTTTGCTA TTCTTGGCAN TTAAGNTTTT TTAGGNCTTT TTAAANGNGN ANNNAAA 357

SEQ ID NO:110

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00123

SEQUENCE DESCRIPTION:

GATCAAGGGA CGGCTGAACA GACTTCCCGC TGCTGGTGTG GGTGACATGG TGATGGCCAC 60  
AGTCAAGAAA GGCAACCAG AGCTCAGAAA AAAGGTACAT CCAGCAGTGG TCATTGACA 120  
ACGAAAGTCA TACCGTAGAA AAGATGGCGT GTTCTTTTAT TTTGAAGATA ATGCAGGAGT 180  
CATAGTGAAC AATAAAGGCG AGATGAAAGG TTCTGCCATT ACAGGNCCAG TAGCAAAGGA 240  
GTGTGCAGAC TTGTGGCCCC GGATTGCATC CAATGCTGGC AGATTGCATG ATTCTCCAGT 300  
ATATTTGTAA AAANTAAAAA AAAGCTAAAC CCATTAATAA GTATTTGTTT TGCAAA 356

SEQ ID NO:111

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00124

SEQUENCE DESCRIPTION:

GATCCTACCT ATCAAGCACT AAAAAGTTGA ACCATTATAC TTTATATCTG TAATGATACT 60  
 GATTATGAAA TGTCCCCTCA AACTCATTGC AGCAGATAAC TTTTTTGAGT CATTGACTTC 120  
 ATTTTATATT TAAAAAATTA TGGAATATCA TCTGTCATTA TATTCTANTT AANGTTGTGC 180  
 ATAATGCTTT GGAANAATGG GTCTTTTATA GGAAAAAACC TGGGATAACT GATTTCATG 240  
 GCTTTCAAAG CTNAAATATN TAATATACTA AACCANCTCT AATATTGCTT CTTGTGTTTT 300  
 ACTGTCAGNT TAANTTACAG CTTTATGGG TGGTTAACTT TTCGTNCATT TTCAAAAAAN 360  
 CCNGGGGNNN NNNNN 375

SEQ ID NO:112

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00125

SEQUENCE DESCRIPTION:

GATCTCTGTT TTGTTGTTGA AAATTCATTT GTATACTTTT GTTTTNATCT AGGACTTCAT 60  
 GTTTTTTNAA AGCACTGGCA GCCAGGAACA AAAATCAGGA GTGTGGTAGT GGATTAGTGA 120  
 AAGTCTCCTC AGGAAATCTG AAGTCTGTAT ATTGATTGAN ACTATCTAAN CTCATACCTG 180  
 TATGANTTAA GCTGTAAGGC CTGTAGCTCT GGTGTATAC TTTTCCTTTT CAAATTATAG 240  
 TTTATCTNCT GTATAACTGA TTTATAAAGG TTTTGTACA TTTNTNAATA CTCATTGTCA 300  
 ATTTGAGAAA AAGGACATAT GAGTTTTTNC ATTTATTAAT GNAACTNCCT TTGAAA 356

SEQ ID NO:113

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00127

SEQUENCE DESCRIPTION:

GATCACATTA TNATAAATAA ATGAAAAAAT GATTTAATCT GTAATAAACT GGTTTATTGT 60  
 GCAGTGACTG TAATATACTA GAGTTATAAT AAATTGTTTA CTCTGCCTCA CCAAACACAT 120  
 GCTAGGATAT AACCCCAAA ATAAGTATTT AACTTTGCAT TAGGTATAAA GGAGACTGGG 180  
 TGCTATAATN AGATTATTTT GAGGCAGACA GAGAGCTGTT ATCCTAACTG ATTTAGTATG 240  
 TTCTGTAAAT GAGAAAAATGT TCACCAAAATN ATACTTTTTTA GTGATTTACA TGTACATTTT 300  
 ATAGGGGACA TGTCTGTGT ATAGCGAATA AATAACTTTT ATAGTATCAC N 351

SEQ ID NO:114

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00128

## SEQUENCE DESCRIPTION:

GATCTTGAAC CTGGTGCTCC ATCCATGGNA GCNNAAAGCC TTTGCATCCC CTTCAAACCA 60  
 CTCTGTGAAC TGCAGCCTGG AGCCAAATNT GTCTGTGGCA AGAACCCCTGC CAAGTACTAC 120  
 ACCTTATTTG GTCGCAGCTA CTGNGGGATG NACGAAAGCC CCCTCTTCAA CTCCTCTCAC 180  
 TTTTAAAGC ATTGATATTA GTATCTTCTC AGATACAGAC CGTTTTATGA TTTTAAAAA 240  
 AGTAAAGTT CTAAATGAA GTCACACAGG ACAATTATTC TTATGCCTAA GTTAACAGTG 300  
 GATAAAGAC TTTCTGTAA ACAACTCCAG TAATAATAT CATGNACTNA AA 352

SEQ ID NO:115

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00129

## SEQUENCE DESCRIPTION:

GATCAAGTCG TGCTCCTGGC AGGCGCGCCC CTGGAGGATG AGGCCACTCT GGGCCAGTGC 60  
 GNGGTGGAGG CCCTGACTAC CCTGGAAGTA GCAGGCCGCA TGCTTGGAGG TAAAGTCCAT 120  
 GGTTCCCTGG CCCGTGCTGG AAAAGTGAGA GGTCAGNNTN NTNAGGTGGC CAAACAGGAG 180  
 AAGAAGAAGA AGAAGACAGG TCGGGCTAAG CGGCGGATGC AGTACAACCG GCGNTTTGTC 240  
 AACGTTGTGC CCACCTTTGG CAAGAAGAAG GGCCCCAATG CCAACTCTTA AGTCTTTTGT 300  
 AATTCTGGGC TTTCTTCTAA TAAAAAGCC ACTTNAGTTC AAGTCAA 348

SEQ ID NO:116

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00130

## SEQUENCE DESCRIPTION:

GATCTCCAC AATTAATTTA TCTTTTGACA AAGGGGATAA AGAGTTTCAG TTTAGCTCCT 60  
 TTTGATTGTA TATNATTTT TCCTTTTNA TTGTGAAAAG AGGTAGGTTT TATTTGTGGA 120  
 GAGAGAGTTG AAGATTAGG AACCAGTGAT TTTAATTATG CTACTTTTCC TTCTAAGAGA 180  
 TAAATTGATA TATCATTCAG TGTCATGAAA AACATGAATG TNGTACAATT TTCTNCCTCA 240  
 AAAAATTTT TAAATGTAAG TATCCTTATT TNNTTTTAA AAGAGCACAA TGTAGGTGTA 300  
 TTTGGGTATT TCCAAGAAAA GANTAAANCC ATTAATGCAG TAAA 344

SEQ ID NO:117

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00131

## SEQUENCE DESCRIPTION:

GATCTGGGCT CCAAGCCAGG AAAGGTGAAC AGAAACCACA AGTNTCCAGC CCTCGGTGCT 60  
 GGAGTGGACG TTAATTGTNA GCCACCAGAC TGTCCCGCA CCTACAGAGA ATGTTTCACA 120  
 GTTCTGGCAT TTAAATCCTT TGATAGTGGA TTGTGCTGCT GTTAGCCTTA GTTTCAGTGC 180  
 TTTACAAGTC TCGCTTATNA TCTCATTGGT ATTTAGGTAT AAAAAACAGT TGATTATTCA 240  
 CCACGCCAAT ATCTGGGTCT CTGTATCTCA TGTAGAACAT AAGAAAATGG GAACTAATAG 300

GGAAATTTAT TTATAGCATG AAAATAAACC TGGTGGCTGG AGTCTGCTAA A 351

SEQ ID NO:118

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00132

SEQUENCE DESCRIPTION:

GATCCTAAGG CAATAAAGA ATAAGGAGAT TTGGAAAACC ATTGTCTGTA ATCTCTGAAG 60  
 AAAAGTGGAC ATTAGGGGAG TCAGTTGAAA AGCAAAGCTA TCACCATTTT CTAAAGAGGA 120  
 AAAAGGTGAA CCTCACAAC TATAGACCAA AAAAATAGGA CATCGAGAGA AAGAATATGA 180  
 AGCTAGCATA GGTTCACAAA GAATGAGTCA AATCAAAACA CATGCATTTT TTATTTATAA 240  
 AGCATGACTT GTTCATTGTC AATTCATGTT AGCTTAATCA TTAGGCATTA ATGCCATCAC 300  
 TGCAATGCAT ATGTCAGCAA TAAATAATCA AGGCCCGGCT TCN 343

SEQ ID NO:119

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00133

SEQUENCE DESCRIPTION:

GATCTTCCCA CAACACCACA GGAAGTGCAGG GTGCACAAC CCCCTGCCAA GGAAAACCAT 60  
 GCAGTCTCC CCTCCCTGGT CTCCTGCTTC AGCTCTGTAC AACGAGGGCA AAGATGCTAA 120  
 ATCTTGCTTT GCATTCAGTA AAGTGTCAAG TGATTAAGTG TGTATTTGTA CCCTAGATGA 180  
 TATGAACCAG CAGTCTTGTT TTGGCATCAT CCTCATCATG TTGTATTCCA GCTTCTTAAG 240  
 TGGAAGGAAA AGAGTGCTGA GAAATGGCTC TGTATAATCT ATGGCTATCC GAATTCTCTG 300  
 AAAAANTANT AAAAGTCCCC TCTNTTATAT GAGCCTGTAC AGAAA 345

SEQ ID NO:120

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00134

SEQUENCE DESCRIPTION:

GATCCCCCT CTCGAGGGCG ATGAGGATGC GTCTCGCATG GAAGAAGTCG ATTAGGTTAG 60  
 GAGTTCATAG TTGGAAAAC TGTGCCCTTG TATAGTGTCC CCATGGGCTC CCACTGCAGC 120  
 CTCGAGTGCC CCTGTCCCAC CTGGCTCCCC CTGCTGGTGT CTAGTGTTTT TTNCCCTCTC 180  
 CTGTCTTGT GTTGAAGGCA GTAAACTAAG GGTGTCAAGC CCCATTCCCT CTCTACTCTT 240  
 GACAGCAGGA TTGGNTGTTG TGTATTGTGG TTTATTTGAA TTNCCTTCAT TTTGTTCTGA 300  
 AATTAAGAGT ATGCAANAAT AAAAGAATTA TGCCCNNTTT TNATACAANA NNAANAAA 358

SEQ ID NO:121

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00135

SEQUENCE DESCRIPTION:

5 GATCTTCATG CCCTGGGTTT TGCCCGNACG GACCCNCATC TCTGTGACTT CCTGGGAGACT 60  
 CACTTCCTAG ATGAGGAAGT GAAGCTTNTC AAGAAGATGG GTGACCACCT GACCAACCTC 120  
 CACAGGCTGG GTGGCCCGGA GCTGGGCTGG GCGAGTATCT CTTCGAAAGG CTCACTCTCA 180  
 AGCACGACTA AGAGCCTTCT GAGCCCANCG ACTTCTGAAG GGCCCNNTGC AAAGTAATAG 240  
 GGCTTCTGNC TAAGGCTCTG CCTNCAGNCA ATAGGNANGC TTTTAAACN ATCCTAACAN 300  
 10 GGNTTGGGAC CAAATGGNAA TAAAGNTTGT TNGATGCAGG AGATATGAAA 350

SEQ ID NO:122

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00136

SEQUENCE DESCRIPTION:

20 GATCTGAGCT GAATTTGAAG ACTATTAATA AGTTATGTTT GGAAGTTTGA ACTTCAATGA 60  
 AGTAATTATT TGCTGTGAAA GAAACAAACA TTGAATTACT AAACAAAGAT GGTGCAATAT 120  
 CTTTGTTTTT TTTTATGAG GCTCCTGAGA ATCAACCCAA CTGAAGCATT TCAATTCAC 180  
 TGAATGAGAA ACGTGTCTAG TATCAAAAGA GCCCAAGAAG ACACTGGTGT GAAAGGTACA 240  
 NTCTCAGAGG TTGGTCAATT ACCGTGGCAC ANTTTCTGGT CACTTTGTAC AATGTAGATT 300  
 25 TGAAGTACAG TGGTGAAGAC ATTAATGTG ACATTTGN 338

SEQ ID NO:123

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS00137

SEQUENCE DESCRIPTION:

35 GATCAAAAAA CATGAGGNAG AAGAAGCCAA AGCTGAGCGT GAGAAGAAGA NAAAAAGAAC 60  
 AGAAAGAAAA GGATAAATAG AATCAGAGAT TTTATTACTC ATTTGGGGCA CCATTCAGT 120  
 GTAAAAGCAG TCCTACTCTT CCACACTAGG AAGGCTTTAC TTTTNAAC TGGTGCAGTG 180  
 GGAAAATAGG ACATTACATA CTGAATTGGG TCCTTGTCAT TTCTGTCCAA TTGAATACTT 240  
 TATTGTAACG ATGATGGTTA CCCTTCATGG ACGTCTTAAT CTTCCACACA CATCCCCTTT 300  
 40 TTTTGAATAA AAATTTGGAA AATGGAAATN AAGGAAA 337

SEQ ID NO:124

SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS00138

SEQUENCE DESCRIPTION:

50 GATCACCATT TGAGATACGC GGCTTAACGC ACATGTGAGT GTAGCTTGCT ACATGAAAAT 60  
 GCTAGGCTCT AGGGCATGTA AAACATGAAT ACAGAATACT AGATTGTTCT AAGTAATGTC 120  
 ATTCGGTTT GTGANTTTGA TTTTCCCTT CATTTTCATG CATATTGNAA ATGCAAACAA 180  
 ACTGCTCTCA AGAACACCCA GAAGCTATCT GTGTTACCAG ATGTGTTGTG NAACTCTAC 240

55

TNTTTTTCAT AGGTGCTACC TGGNAATATA TGTCCATTGT AGTGGTGGNG NGGGNCTNGA 300  
CTCTNTCAGG CTCTTNTCTN GCCAGNTGNC TNCNGN 336

5 SEQ ID NO:125  
SEQUENCE LENGTH:338  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS00139  
SEQUENCE DESCRIPTION:  
GATCTGGGCT GCAGGAGCTG GGGCCACCCA CAGCCCCCT ACCGACCTGG TGTGGAAGGC 60  
ACAGAACACC TGGGGCTGCG GGAACAGCCT GCGTACGGCT CTCATCAACT CCACTGGGGA 120  
15 AGAAGTGGCC ATGCGCAAGT TGGTGCCTC AGTACTGTG GTTGAGGACG ACGAGGATGA 180  
GGATGGAGAT GACCTGTCTC ATCACCACCA CGTGAGTGTA AGCCGCCGTT GAGGCCGAGC 240  
CTGCACTGGG GCCACCNAGC CAGGCCTGGG GGNAGCNTTT CCCNAGNNTN CNNGTGCCAA 300  
AANTTTTTTN ATTAAAAGAT TGTTTGGGA ACTTTAAA 338

20 SEQ ID NO:126  
SEQUENCE LENGTH:347  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

25 CLONE:HUMGS00140  
SEQUENCE DESCRIPTION:  
GATCAAGCAG ATTCCACGAA TCCTNCGGAC CAGGTTTAAA TANGGCAGGA AAGTTCCTT 60  
CCCTGCTCAC ACACAACGAA AACATGGTGG CCAAAGTGGA TGAGGTGAAG TCCACAATCA 120  
AGTTCCAAAT NAAGAAGGTG TTATGTCTGG CTGTAGCTGT TGGTCACGTG AAGATGNCAG 180  
30 ACGATGAGCT TGTGTATAAC ATTACCTGG CTGTCAACTT CTTGGTGTCA TTGCTCAAGG 240  
AAANCTGGCA GANTGTCCGG GCCTTATATA TCANNNGCA CCATGGGCAA NGCCCCAGCG 300  
GCTTATATTT AAGGCACATT TTNNATAAAT TCTATTNACC CGGTAAA 347

35 SEQ ID NO:127  
SEQUENCE LENGTH:335  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00141

40 SEQUENCE DESCRIPTION:  
GATCAGTTGT AATCAGAATA CAACTGNGTC TTGTAGTTGT AATATGTTCT ATCTTAACCA 60  
CCACTTTCGT ACCAGGAACC TGCTCAGGTT TGTTCTCTAG AAGCTCCCAA CATAGATAGT 120  
CTACATTCA GACTACTAAG TTATTAACAA ACCCTTTGGG CCCATGTTCA CTTTAGGGTT 180  
45 GAGCATAGTG TGAGGAGATG TAAATTAAAT TATAATCCTA TATGTGTGTG TAATAAATAT 240  
TAAAGTGTAT AAATTAAACA GCAGATTCTA AGTATCCAAC AAGAGTCAAA TAAATGATAC 300  
AAAGTCACCA AATAAATAAT ATTTAATCTC ATCTN 335

50 SEQ ID NO:128  
SEQUENCE LENGTH:356  
SEQUENCE TYPE:nucleic acid



TOPOLOGY:linear

CLONE:HUMGS00142

SEQUENCE DESCRIPTION:

5 GATCTAGTTA AAGTTATTCA ACAGGAGTCT TACACATATA AAGACCCAAT TACAGAATTT 60  
 GTTGAATGTT TATATGTTAA CTTTGACTTT GATGGGGCTC AGAAAAAGCT GAGGGAATGT 120  
 GAATCAGTGC TTGTGAATGA CTTCTTCTTG GTGGCTTGTC TTGAGGNNNN CATTGAAAAT 180  
 GCCCGTCTCT TCATATTTGA GACTTTCTGT CGCATCCACC AGTGTATCAG CATTAAACATG 240  
 TTGGCAGATA AATTGAACAT GACTCCAGAA GAAGCTGAAA GGTGGATTGT AAATTTGATT 300  
 10 AGAAATGCAA GACTGGATGC CAAGATTGAT TCTAAATTNA GGTCATGTGG TTATGN 356

SEQ ID NO:129

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

15

TOPOLOGY:linear

CLONE:HUMGS00143

SEQUENCE DESCRIPTION:

20 GATCAAAGNA CTCTGACTGC AGAACTGCCG CTCTCAGTGG ACAGGGCATC TNTNACCCTG 60  
 AGACCTGTGG CAGACACGTC TTGTTTTCAT TTNATTTTGT TTAAGAGTGC AGTATTGCAG 120  
 AGTCTAGAGG AATTTNNNTT TCCTTGATTA ACATGCTTTT CCTGGTTGTN ACATCCAGGG 180  
 CATGGCAGTG GCCTCAGCCT TAAACTTTTG TNCCTACTCC CACCCTCAGC GAACTGGGCA 240  
 GCACGGGGAG GGTTGGCTA CCCNTGCCCA TCCNTGAGCC AGGTACCACC ATTGTAAGGA 300  
 25 AACACTNCA GAANTTCAGC TGGTTCCTCC AAA 333

SEQ ID NO:130

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear

CLONE:HUMGS00144

SEQUENCE DESCRIPTION:

35 GATCTCTGTA GATATTCTGT TTTATTTTGG TCATCTTTAG AAGTTATCAG GAATGTGTTT 60  
 AAAACAAGAA GAGAACTTTT CTAAGGAATG ATACATAGAA AAGATTTTAT TTTAAAATGA 120  
 GTTGTAAGC TTGTTTTTCT TTGTTGCTGC AANTATCTGC CCAAGTTAAT GCAAAATGGAC 180  
 ACATTTTTTA TGTGAGAAAA ACACACACAC ACACACACAC ACACACACAC ACACACNCGC 240  
 GNNACACAGN GANAAAAGTG CTTGNGCTTN NNCTCNCTNC CCCTTGCGT CTGTTGTGTG 300  
 40 CGCAGCCTGT TTAINTCTCT NNTATTGTGT CN 332

SEQ ID NO:131

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

45

TOPOLOGY:linear

CLONE:HUMGS00145

SEQUENCE DESCRIPTION:

50 GATCTGTGAC CTTACCCCA AACCTGTNCT CTCTGAAACA TGTGCTGTGT CCACTCAGGG 60  
 TTAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGTTAAA CAGATGCTTG AAGGCAGCAT 120  
 GCTCCTTAAG AGTCATCACC ACTCCCTAAT CTCAAGTATC CAGGGAGACA AACACTGCGG 180

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AAGGCCGCAG GGTCTCTGC CTAGGAAAAC CAGAGACCTT TGTTCACCTG TTTCTTTGTT 240  
CACTTGTTTA TCTGCTGACC TTCCCTCCAC TATTGTCCTA TGACCCTGCC AAATCCCCNT 300  
NTGATGAAAA ACACCCAAGN ATANTCANTA AA 332

SEQ ID NO:132

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00146

SEQUENCE DESCRIPTION:

GATCGAGGTT GTTTGCAACG ACCGTCTGGG GAAGAAGGTC CGCNTTAAAT GCAACACGGA 60  
TGATACCATC GGGGACCTTA AGAAGCTGAT TGCAGCCCAA ACTGGTACCC GTTGAACAA 120  
GATTGTCCTG AAGAAGTGGT ACACGATTTT NAAGGACCAC GTGTCTCTGG GGGACTATGA 180  
AATCCACGAT GGGATGAACC TGGAGCTTTA TTATCAATAG ATGAGAATCC TCATCTTNCT 240  
GCCCCGCTNT CCNCTNCCA TCCTCATCCC CCACANTNGG GATAGATGCT TNGTTTGTA 300  
AAACTCANCN NAATAAAGAC TTAGATGTTG AAA 333

SEQ ID NO:133

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00147

SEQUENCE DESCRIPTION:

GATCAGGTCT GTAAATGTGT ACTAAAAAAA TNAGAGTTTA TTTATAAACA AAATAGTTTA 60  
TTTAAAGAGA AGGTCTCTTC CTTATTGATA TCATGGTATG CATTAAATCC ATTTGTTACT 120  
ATTGTGCACA AAAGCCCTGT TCACAGGGGA ATGGTGTAAT CATTATACT GTTTTGTTCA 180  
CTGTATTAG TAGACATAAC TGTTGAATAG TTAGTGAATC ATGATGTAAA GAATATGTGA 240  
CCATCTTCAG GTATGGGATT TCTGAACGTT TCAAATTTCA ATCAATGAGC ACTGTCAACA 300  
CCCACAGGNG AGAATAAAAT TACCTGTGCN 330

SEQ ID NO:134

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00148

SEQUENCE DESCRIPTION:

GATCGAACCA CTGCACTCCA GCCTNGGTGA CAGAGAGAGA CACTGCCTTN GAAAAAAAAA 60  
GAATCTCACT CACTATCTAG AGAGGATTGT CAGANTATTC ACGATTCAGN TCTTGAAACT 120  
TTGATTATGC AAAAGAGGTA TATATAAATA TTTTATTATG ATTCAGGTTT TAGGCTTTGC 180  
AGCTTCTATA AGGTGTTCTC AGGTGGCCCT TGTACNNCTN AAAGCATCCT TTAGGAAATN 240  
CTTTAAGGNG GGCTTTNTAT AAGGAATAGG NGGNTGTTGA ATTTTACAG GGGGGTTTGG 300  
GTCATTNAGN CCCCATTNT GTANGN 326

SEQ ID NO:135

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00149

SEQUENCE DESCRIPTION:

GATCATGANC TCTGAAAAA AGAGAAACCT TATCTTTNCT TTGTGGTTCC TTAAACACA 60  
 CTCACACACA CTTGGTCAGA GATGCTGTGC TTCTTGAAG CAAGGNTCA AAGGCAAGGT 120  
 GCACGCAGAG GGACGTTTGA GTCTGGGATG AAGCATGTNC GTATTATTTA TATGATGGAA 180  
 TTTCACGTTT TTATGTNAAG CNTGACAACA CCAGGCAGGT ATGAGAGGAA AGCAAGGCC 240  
 GTCCATNGCT GTCCGTACNC TTACGGNTTG CTTGTNGGAG NCATTNNGT ATTGTTTGT 300  
 GTAANANCCA AAANGGGCTT TGGNN 325

SEQ ID NO:136

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00150

SEQUENCE DESCRIPTION:

GATCNACGCT GTGCCTTGGC AGGGCACAAT GACCTTGTCG AAATCCACCT GTCAGGACGC 60  
 CTAGGGGTCT GTACCGGGCT GGCCTGTGCC TATNACCTCT NATGCACACC TCCCACCCCC 120  
 TGTATTCCCA CCCCTGGACT GGTGGCCCCCT GCCTTGGGA AGGTCTCCCC ATGTGCCTGC 180  
 ACCAGGAGAC AGACAGAGAA GGCAGCAGGC GGCCTTTGTT GCTCAGCAAG GGGCTCTGCC 240  
 CTCCCTCCTT CTTCTTGCT TCTNATAGCC CCGGTGTGCG GTGCATACAC CCNCACCTCC 300  
 TGCAATAAAA TAGTAGCATC GGCAAA 326

SEQ ID NO:137

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00151

SEQUENCE DESCRIPTION:

GATCAAGNNG CCCTGGAGGC GGTGGGCGGC ACCGTGGTTC TGGAGTAGCC TCCAGCTCGG 60  
 AGGACTTGTN TNCAGGGGTC CTGGGCCCCG GNCAAGGTCC CGCCCTCCCG TGGTCACTGG 120  
 CTCCGCCCCA GCACCAGGCG CCCAGTGGAG CCGTTTGGAA GAATTGCCTG CNGCACGAGC 180  
 GGGGCCGGAC AGGCGCACAG ACCTACTGTN GCGGGAGGAA GGGGCGGCTG CTGCCTGGTG 240  
 ACGGCACCCG GANGCCACC AGGACGCGCC ACCGGTNAAT GTNNCTCTNG TGGCTGCTGA 300  
 GAAAAATACA CTGTGCAAGT CAAA 324

SEQ ID NO:138

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00152

SEQUENCE DESCRIPTION:

GATCTCAGCT TTTGGTTTCC CATGATACCA TCTCTAGGGG TAGCAGCTGG CTATAATAAC 60  
 TAATGTCTGG ATTATCTAA CTCTCTGTT TGTNCTTCA GGTATTTAA AATGTTGTGA 120

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CTAATTGGCT TCCATTATTT CCCTAGAGTA GGTTCGTGTA TNACCCTGGA ATATGTTTGT 180  
AATAGAGTGG GCTATTACAA TCATCTAGGA TAAAGATAAT CGTGGCTTGG AATAAGGGTG 240  
GTAGCAATGG AAGTGATGAG AAGTCATTAG ATGCAGAATA TATTTTATAG ATGGANTGTG 300  
ATAAANTAAA AAATAAACTG GGN 323

SEQ ID NO:139

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00153

SEQUENCE DESCRIPTION:

GATCCATTCT CGGAATTCAC AGAATTTTNA TAACATCTNA CTCTCAGGGG GCATGAAGTG 60  
CATAATCTTC CCTAGATTAC AAAAAACATA TAGATGACGG GTTTCCTAT NAAACTTCAG 120  
TACTACAAGA AACATAAAAT ATTTAAATAT ATGANATTTA AATATATTTA AAATTATTAA 180  
AGTAATATAA ACATTTTTTNA GTGACTGTGT TATGTTTTTC TGGTTATTTT GTTTTCTACT 240  
AGTATATTTT TCTGTAAAAA TTGTAAAACT ATATCAGCAA TTTCTAATGC CAANAANGTA 300  
AAACCTNGTG TGTATAAATG CN 322

SEQ ID NO:140

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00154

SEQUENCE DESCRIPTION:

GATCAGAGGC ACAAGTNCAG AGGCTGTGGT CATGCGGAAC ACTCTGTTAT TTAAGATGGC 60  
TATCCAGATA ATCCTGAACA CTGTGTATTT ATTTAATTTA GACTACCAGC AAAGATTAAA 120  
GCATGAAATG TAAAACATCT GATAAACTT ACAGCCCCCT ACACCAAGAG TGTATCTGTG 180  
AAAGAGCTCC TACACTTTGA AACTTAAGA NTCCCTTNTC ATGAAGTTTG CCTGTNCTAG 240  
AATTGTAAGA TTGTTAATTT CCNTCAATCT CTAGTGACAA CACTTAATTT CTTTNCTAAT 300  
ANAAAAAGCC TNGTNGGTGN AAA 323

SEQ ID NO:141

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00155

SEQUENCE DESCRIPTION:

GATCAAGTTT AAATGACTGT GCTGCCCTT TCACATCAA GAACTACTGA CAACGAAGGC 60  
CGCGCCTGCC TTTCCCATCT GTCTATCTAT CTGGCTGGCA GGAAGGAAA GAACTTGCAT 120  
GTTGGTGAAG GAAGAAGTGG GGTGGAAGAA GTGGNGTGGG ACGACAGTGA AATCTAGAGT 180  
AAANCCAAGC TGGCCAAGG TGCCTGCAG GCTGTAATGC AGNTTAATCA GAGTGCCATT 240  
TTTTTTTTTG GGTTCAAANG NTTTTAATT TNTTNGGAAT NGNNCCANTT TTTTNAATTT 300  
NGCAANTAAA AANGTTTAAA ANCTTAAA 328

SEQ ID NO:142

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00156

SEQUENCE DESCRIPTION:

GATCTCTGGC AGTGGAGGAA GTCTCTTTAA GAAAATAGTT TAAACAATTT GTTAAAAAAT 60  
 TTNCCGTCTT ATTTCAATTC TGTAACAGTT GATATCTGGC TGTCTTTTT ATAATGCAGA 120  
 GTGAGAACTT TCCCTACCGT GTTTGATAAA TGTNGTCCAG GTTCTATTGC CAAGAATGTG 180  
 TTGTCCAAAA TGCCTGTTTA GTTTTTAAAG ATGGAAGTCC ACCCTTTGCT TGGTTTTAAG 240  
 TATGTATGGA ATGTTATGAT AGGACATAGT AGTAGCGGTG GTCAGACATG GAAATGGTGG 300  
 GGAGACAAAA TTATACATGT GAAATAAACC TCAGTATNTT AATAAAGTAG CACGGNTTCT 360  
 ATTTGNAAA 369

SEQ ID NO:143

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00157

SEQUENCE DESCRIPTION:

GATCATGAAG GAACACATAG CACCAAGAGA GGCCATGCTA AATCTCGCCC TGTCAGANNN 60  
 NTCCACACTT CTCCTTTGGG GAAGNCTTCC CTGTCCCCCT AGACTAAGTT AAATATTTCT 120  
 GCACAGTGTT CCCATGGCCC CTTGCATTC CTTCTTAACT CTCTGTTACA CGTCATTGAA 180  
 ACTACACTTT TTTGGTCTGT TTTTGTGCTA GACTGTAAGT TCCTTGGGGA CAGGGCCTTT 240  
 GTCTGTCTCA TCTCTGTATT CCCAAATGNC TAACAGTACA GAGCCATGAC TCAATAAATA 300  
 CATGTTAAAA TGGGATGAAT GAAA 324

SEQ ID NO:144

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00158

SEQUENCE DESCRIPTION:

GATCATTGAA CGAGACAGAA AGCGACCATC CTGGTTCACC CAGAATTGAC ACCAAAGATG 60  
 TTAAAAGGAT AACTTCACAG TAAATCATTT CTCCTGAAAT AGAGGAAGAT TCTTTACGTT 120  
 GTTGTNCTTG TTTTAAATC ATCAGTATAG TTAAACACAT TCTTTCTAAG CAGTTTGTG 180  
 TGGGATAATT TGAAGAATAT ATTATGAGTA ANCTCCGAAA ATTTTGTTTA TCCAAAGGCT 240  
 CANTGGATTA TGTTTCTATT ATNTACAAGG TTTTAAGTAA ACATANNNTT TCCNGNNCNG 300  
 AGNTTANAGN NATTTN 316

SEQ ID NO:145

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00159

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTTCATT TTATTGCATT AGTTCATGTA GATGGGCATC TCTATGAATT AGATGGGCGG 60  
 AAGCATTTCC AATNAACCAT GGTGAAACTA GTGATGAAAC TTTATNAGAG GATGCCATAG 120  
 AAGTTTGCAA GAAGTTTATG GAGCGCGACC CTGATGAACT AAGATTTAAT GCGATTGCTC 180  
 TTTCTGCAGC ATAGCTTGTC AATAATGGAA ACACCAAAAA CTGTATTATT TGCAACTAAA 240  
 TTTTCTCTGC CATACTAA CTCAAAAATT TTGATATTTT CATTAACTTG ATGATTAAAC 300  
 TTTATGTGAG TTAANCTTG AAA 323

SEQ ID NO:146  
 SEQUENCE LENGTH:319  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00160

SEQUENCE DESCRIPTION:  
 GATCTTACTG CTTGTNACTT GAATCCCGTG ATTGTNATAC ATCTCTGGTA TAAGCAACAT 60  
 TTGATTTTTG AAGTGTGTAG ACCATCTCTT CATATTTTCA AGATGTAATT TTACATTNCT 120  
 GCATTTTTTAA AACAGTTTGG CCATAATCCT AGATGCACGC TTCTAATTCA TGTACCTGCA 180  
 CATGTGACCT TTGTGAACAG NAATTTGCAT GNATAATNG TGTTTACTTG TAACTNCTG 240  
 GTTATATACT GCTTATATCT GTGGATTCAA GTTACTGAAG TGGANTNCCA ATAGAAAGNA 300  
 ANCCCTAGGC CATGTTAAA 319

SEQ ID NO:147  
 SEQUENCE LENGTH:316  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00161

SEQUENCE DESCRIPTION:  
 GATCTCTGAT TACCAGCCTG ACATCAACAA ATCCCCTCAG TTACAACGTA TAGGTTAAAC 60  
 AAAGCTTTTA AAAGCTCATG TGGTATGACC TCAAGGTTGC TAACCTGGTC ACTCATGGTA 120  
 ATNAGAAACT CTGATTGGCA GCTTTGTATT TCTTGACTAA AAACCTAAAT AAAGTGATTA 180  
 GGTTTTAGGC GTTCTTTCAA AGAGGTTCTT GAGAAGATTG AGAACTATCC TATTTGGTGC 240  
 TTAGTGAAAA GATTTTGAAT TACTGTACGT ACCAGTTGTT GCCATTTCTT TATTAAATTC 300  
 AGAAGTTTTT TTGCCN 316

SEQ ID NO:148  
 SEQUENCE LENGTH:319  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00162

SEQUENCE DESCRIPTION:  
 GATCTTGGAC AGCNTGGGTA TCGAGGCGGA CGACGACCGG CTCAACAAGG TTATCAGTGA 60  
 GCTGAATGGA AAAACATTG AAGACGTCAT TGCCCAGGGT ATTGGCAAGC TTGCCAGTGT 120  
 ACCTGCTGGT GGGGCTGTAG CCGTCTCTNC TGCCCCAGGC TCTGCAGCCC CTGCTGCTGG 180  
 TTCTGCCCT GCTGCAGCAG AGGAGAAGAA AGATGAGAAG AAGTAGGAGT CTNAAGAGTC 240  
 AGNTGNTGNC ATGGGATTTG GCCTTTTTTG GTTAAATTCC TGNTNCNCTG CAAATAAAGG 300  
 CTTTTTTTAC AGANGTAAA 319

SEQ ID NO:149  
SEQUENCE LENGTH:313  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS00163

SEQUENCE DESCRIPTION:

GATCAATGCC CTCATTAAAG CAGCCGGTGT AAATATTGAG CCTTTTGGC CTGGCTTGTT 60  
TGCANAGGCC CTGGNCAACG TCAACATTGG GAGCCTCATC TGCAATGTAG GGGCCGGTGG 120  
ACCTGCTCCA GCAGCTGGTG CTGCACCAGC AGGAGGTCTT GGGCCCTCCA CTGCTGCTGC 180  
TCCAGCTGAG GAGAAGAAAG TGAAGCAAA GAAAGAAGAA TCCGAGGAGT CTGATGATGA 240  
CATGGGCTTT GGNCTGTTTG ACTAAAACCT CTTTATAAC ATNGTNCANT AAAAAGGCTG 300  
GAGCTTTAAT AAA 313

SEQ ID NO:150  
SEQUENCE LENGTH:313  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS00164

SEQUENCE DESCRIPTION:

GATCCAGAAT CCACGGGGTC TGGAGCATAA GGTATTATCTC AAGTNTCAAT TGANCTGCCT 60  
CCTCTTGTTA GGCAGGGACA ACTGGGAGGA TGAGCCCCAA GAGCCTCAAG AACCCAAACA 120  
GGTGCCCTA GAAGACACAG AGACAGATGA NCTTTGGGCA TCCTTGAGG CAGCTGCCAA 180  
GCGGANAGCT CTCGGGTTTG GAGCAGCCCC AAGGAGCTCT CCAAACGAGA CGGAGAAAGA 240  
AGAAGCGGCC TGGGTCCACC AGCCCCTGAC GCCCCTGTNN CCACTTTGTA AATAAACTTG 300  
CTGAACACCC AAA 313

SEQ ID NO:151  
SEQUENCE LENGTH:313  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS00165

SEQUENCE DESCRIPTION:

GATCATCAAC AAAGAAAGTC TGAGAAATTG TCCCGGAATA AAGGGGCCTA AGGAGACATA 60  
ACATCTAAAT GTAATGTAGT ATCCTGGATG GACTCCTGCA ACAGAAAAAG AACTTTAAGT 120  
AAAAATTAAG GGAATATTAA TAAAGTATGC ATTTTGGTTA ATAATGTATC AATATTGGTT 180  
TATTAGTTGT GACAAATGTA CCAGAGGAAT GTAAAATGTC AACAATAAAG GAATTGGATG 240  
TGGGGTCCAT GAGATGCTGT ACTATTTTGT CACTTTTCTT AAATCTAAAC TCTTATAAAT 300  
TTAANCATAA AGN 313

SEQ ID NO:152  
SEQUENCE LENGTH:317  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS00166

## SEQUENCE DESCRIPTION:

GATCTGGCCA TCTACGAGCC AAAGACTTTN AAATCTTTGG CTGCCTTGGC CAGTAGGAGG 60  
 CGACACGAAG GATTTNCTGC TGCCTTGGGG GATGGGAAGN AACCTGAAGG CATTTTNNCC 120  
 AGAGTGGTGC AGTACCACTN AGGACTGTTG CTGTATTGAT TAGGAAAAGA GACAGAGTAA 180  
 TTTNCAGTTT GTTTGATTTA TACTTTTGGT TATCTACAAC CCAATAACAG ACATGAGGGA 240  
 TGGCCTGTC TCTCTGGGAC AGAGCCTCAA AGATGATGTC CATGTTTGT GTGAATGAAA 300  
 CTCAAACACT CTTCAA 317

SEQ ID NO:153

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00167

## SEQUENCE DESCRIPTION:

GATCCCCTGC CCCCTGTCCC CTGCCTCTTT TCCCAATTCC CTTCCATTATG CTGGACTTTT 60  
 AAAGCTTAAA AAAAATCCGA TTGAATATAA ATGCCTAATT TCATTCTTTG TGAAATGGTT 120  
 GCTTCCTCCT GATTCCTAA TTGTGCTGTG TTCGTGTCTT GCACTGGAAT TCAACATTCC 180  
 CTTCTCCTTT TGTACTGTGT TGTGCTTGCT GTCTCTCCCG GACANCCTTA AAGACTGTCT 240  
 TTTTAGCAAA AAATTCAGT AAAGTGTTTT CTGTAATCTT TTTTAAAAG GTGAGAACTA 300  
 ATTATTGTCN 310

SEQ ID NO:154

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00168

## SEQUENCE DESCRIPTION:

GATCACCACG GTTTTCAGCC ATGCTCAGAC AGTGGTTCTT TGTGTAGGTT GTTCAACAGT 60  
 GTTGTGCCAG CCTACAGGAG GAAAGGCCAG ACTCACAGAA GGGTGTTTAT TTAGAAGAAA 120  
 GCAACACTAA TGATTCAAAC AGCTTCCTGA ATTTTAATTT TGTGTGTCT CACAGAAAGC 180  
 CTTATCATAA ATTCCATAAT TCTAATTAAT TTACCAAGAT AATGTAATTA CATTTGGTTT 240  
 TGTAAGGTAT ACAGCAGTAA TCTCCTATTT TGGTGTGAGT TTTTCAATAA AGTTTTGATT 300  
 ATGGGCAAA 309

SEQ ID NO:155

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00169

## SEQUENCE DESCRIPTION:

GATCACATAC AGGGGAAAAG CCCTATGNAA TGTAACACAT GCAGGAAAAC CTTCTCTCAA 60  
 AAGTCAAATC TCATTGTACA TCAGAGAACA CACATAGGAG AAAANCCTTA TGANTGATTT 120  
 GGATATTAGA AATTNCCAGC CACAAGTCAG CCTCCATAAT GCNTCAGAGT CTTCACTG 180  
 TGGAGANGGG CCTGTTGACA TCCTGATTGT TCANTAATA TCCACAACCT CGCCTTATGT 240  
 TACTCCANNG TAACAGTAGG GGTTAANCCC ATAGNCTACA ACACCTNTNG GNTGGCTTTT 300



NTTAGGN

307

SEQ ID NO:156

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00170

SEQUENCE DESCRIPTION:

5 GATCCACCAA CTTTGGCCTC CCAAAGTGTT CAGATTACAG GTGTGAGCTG CTACCATGCC 60  
 TAGCCCCAGC TTCTACTGCT TGANGGCTCT CTTTGGCATC TCCACACATC ATCCTTAGCA 120  
 GCCCAGACTG CATTCTGTGA GCAGCCTCTT CCCTGGTCTC TTCTTTCAGT CTCTCTGCCT 180  
 CTAATCCAGT GGCTTTAAGA ATTTTTTGGC TGTGACTTCC AGTAAGAAAT ACAATTTACA 240  
 15 TTGTGACCTA GTAAATATGT GTGTAAGATT TATTAACTGA AATAAAAAATG TTATGATTTA 300  
 ATTTTNN 307

SEQ ID NO:157

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00171

SEQUENCE DESCRIPTION:

25 GATCTGTCCC TGTGGTGGTG TCTAAGAATC GGACACCTTG GTTTTTGTGT TAGATTGAGC 60  
 TGGGCAGCTG CAATCAGCTA CTTAATATGC AAATTAGGCA CGTCCCCTCT GTGGGTCTCT 120  
 GTTGGTGGCT AATGAAGTGA GGGGAGGGAG GGATGTCACC CCAAAGTAG GCCCTCCCAT 180  
 TGGCTTTGGC CAGGCCAGAC ACTTCACATC GTTTACATGG TTCTGTGTAA TTTTAAAGTT 240  
 TATGTGTATA AAGCGACGGT TTTCTGTGAA CTGTATATTT TGTAATAATAA TATATTGCTA 300  
 30 CTTTGN 306

SEQ ID NO:158

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00172

SEQUENCE DESCRIPTION:

40 GATCTTCAGA TAAATTCTGC CATTTTNATT TCACTTCCTG AAAGTNAGGG TCGGCTTGTN 60  
 AAAAGTTGTT AAACAACATG CTAAATGTGA AATGTCAACC CTCACTCTAA ACTTCCCTG 120  
 TTCAGAGCAT CAGATGAAGA CTTATTGGG TTTTATAGTG GCTTCTGAT TTNGGTTAGT 180  
 CCATTGAAGA AGGGAGTTTG AAAGTTGTTG TATACTGTGA ACGATTGTCT GCCCATGTCC 240  
 TGCCTGAAAT ACCATGATTG TNTATGGAAA GTATCTTTAA TAAAGCTGGA TACAGTTTGG 300  
 45 CTTGGAGAAA 310

SEQ ID NO:159

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00173

SEQUENCE DESCRIPTION:

5 GATCTACTTT GGAAAAACAA AGGATATCGT CAATGGGCTG AGGTCTGTNC AGACTTTTGC 60  
 AGACAAATCA AAACAAGAAG CTCTGAAGAA TGACCTGGTG GAGGCTTTGA AGAGAAAGCA 120  
 GCAATGCTAA ACCTCTGTTT CATGCTAACC AGACACGCCG TGCACTCGTT AGATTCCCTT 180  
 CTTAGAAAAC TCGTTTTCTG CTCCCTTCCC TCGTCCCTTC CCTCCCCGAC AGGTCACATA 240  
 10 ACAGCTGCAT CATTGACCGC ACAGCGCCAT CTCTCCCTGA GAATAAAGCC GATAGCCACC 300  
 NTCAAA 306

SEQ ID NO:160

SEQUENCE LENGTH:329

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00174

SEQUENCE DESCRIPTION:

20 GATCTATTGG ACTTTTTTTT GCAGGAAGTG CATTCTCTGG TCCTTCCCTA TTTTCTGTTC 60  
 TGGATGTCAG TGCAGTGCAC TGCTTACTGT TTTATCCACT TGGCCACAGA CTTTTTCTAA 120  
 CAGCTGCGTA TTATTTCTAT ATACTAATTG CATTGGCAGC ATTGTGTCTT TNACCTNGTA 180  
 TACTAGCTTG ANATAGTGCT GTCTCTGATT TCTAGGCTAG TTAATTGAGA TATGAATTTN 240  
 CCATAGAATA TGCAGTGATA CAACATTACC ATTCTTCTAT GGAAAGAGAA ACTTTTGCATG 300  
 25 ATGAAACAAT AAAGNTTTTA AATATCAAA 329

SEQ ID NO:161

SEQUENCE LENGTH:303

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00175

SEQUENCE DESCRIPTION:

35 GATCTGAATA AAGCAAATCT GCATAAATGG TAACCAGTAG CTCTACTTTN ATTTTNNATG 60  
 TTGCTTAACT GTTTTATTG AAGGAAACCT GTGTGATTGA AAAAGTTATA GCTTTTGCAA 120  
 CTTTATTACT GGTTATATAC ATTTGGCCAT TATNATGTGC AAGCAATTGG AAAAAAGTC 180  
 AAGTAAATGC TTGTTTTTGT AGTAGTTTGT TCTTGTTAAA AATGTTTATA TGATAATGTC 240  
 TGTAACAGC ATCACTTTGA TTACAATAGA TGTAGTGTG TAATAAACTG TTTAATGGGG 300  
 40 AAA 303

SEQ ID NO:162

SEQUENCE LENGTH:298

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00176

SEQUENCE DESCRIPTION:

50 GATCTCTCTA GCTTTGTCAT AGTTATGTGA TTTTCCTTTG TAGCTACTTT TGCAGGATAA 60  
 TAATTTTATA GAAAAGGAAC AGTTGCATTT AGCTTCTTTC CCTTAGTGAC TCTTGAAGTA 120  
 CTTAACATAC ACGTAACTG CAGAGTAAAT TGCTCTGTTC CCAGTAGTTA TAAAGTCCTT 180  
 GGACTGTTTT GAAAAGTTTC CTAGGATGTC ATGTCTGCTT GTCAAAAGAA ATAATCCCTG 240

55

# EP 0 679 716 A1

TAATATTTAG CTGTAAACTG AATATAAAGC TTAATAAAAN CAACCTTGCA TGATTAAA 298

5 SEQ ID NO:163  
SEQUENCE LENGTH:309  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00177

10 SEQUENCE DESCRIPTION:  
GATCTCCTTC ATCCCTCTCC AGAAGAGGAG AAGAGGAAAC ACAAGAAGAA ACGCCTGGTG 60  
CAGAGCCCCA ATTCCTACTT CATGGATGTN AAATGCCCAG GATGCTATAA AATCACCACG 120  
GTCTTTAGCC ATGCACAAAC GGTAGTTTGT TGTGTTGGCT GCTCCACTGT CCTCTGCCAG 180  
15 CCTACAGGAG GAAAAGCAAAG GCTTACAGAA GGATGTTTCT TCAGGAGGGA AGCAGCACCT 240  
AAAAGGCACT CTGAGGTCAA GGATGAGGTG GGAANCCAT CTCAATTAAC CACCATTTTT 300  
TGGGTAAA 309

20 SEQ ID NO:164  
SEQUENCE LENGTH:295  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00178

25 SEQUENCE DESCRIPTION:  
GATCTCGGTA AAAATCTACC ATTCCTACA TATTTTCCTG ATGGAGATGA AGAGGAACTG 60  
CCAGAAGATT TGTATGATGA AAACGTGTGT CAGCCCGGTG CGCCTTCTAT TACATTGCC 120  
TAACATCTTT GGACGTGGCA GAACCTTACA TATTCTGTGA GCTTCGATGA GCCAGAGTGA 180  
TATCATAACC ACCAGAAATC ATACTCTCCT TTCTTAGTCA CAACAAAATC ACACATGTCA 240  
30 TCTTTGTCAA GGGCATAAAT ATATCATTCA TACCCCATTA AAATTTTGTT AGAAA 295

35 SEQ ID NO:165  
SEQUENCE LENGTH:289  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00179

40 SEQUENCE DESCRIPTION:  
GATCCCCACC CCATGTGTTT TAAAAAGGCA GTAGCCTTTG CAGGGACCTG TCTGTCCCAA 60  
CTGTTTGAAC AGTGTGCTCC TCAGATTCTG TGTTCAGAAG NCCCCTGNTG CATTGAGACT 120  
TGAAACCTTT GGATAGGGGA AAAAATTATA TATATATATA TNNNTTGTG CTGTTTGCAT 180  
TTCTTAATTT GTGCTTGGA TGTGTTGATG TGCACAGCTA ATGATTCAAT GCGAGACAAG 240  
ATTGGCGTCT GTGTTGTGGA GGTTCAAAT AAAGAGCACT CTCATAAA 289

45 SEQ ID NO:166  
SEQUENCE LENGTH:300  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
50 CLONE:HUMGS00180  
SEQUENCE DESCRIPTION:

55

# EP 0 679 716 A1

GATCTGTAAA ATGTGATTTT TTACTTCCAC TTATAATACT TGTGATTGGG GAGGTTTGTG 60  
 GAAATTCAAT TATGATGAAA AACCTATCTT TTTTGTAATG TTGGCATACT TGGGGAATTT 120  
 AGTGGCAAAT ACATTCCCCA GCAGGCCTTT TGTGTTGTC ACTAACTGCA AGGTTGCTGG 180  
 GAAGTAGAGT CCATTTGGTT GATGAGCTTT GACTGCGGTT TTGGAACCTT ACCTCTCCTC 240  
 CTTAGCCCAA TATGCTGTCT TGGGTCCTAT TCAAATAAAG TTATTTCTCC TGGTCTCAAA 300

SEQ ID NO:167

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00181

SEQUENCE DESCRIPTION:

GATCAAAAAA CCATCTCCAC ATTTAAAAGA GATGTAAGGT GTATTCATAG GGATGGTGGC 60  
 TCAACAAATC AAGCAAATG GAATCAAGGG GAGGGGGAAG GGAATNAAAT GGAAAGGGAG 120  
 GCTGATTCCC TTCCCTGAC TTACCACTAA TTTACTAGGC TACCTACTTT NATGAGTAAC 180  
 CTCTCACAGC TACCCAGCAC ATGCCACAAT CCTATGCTCT TGCCTTCTTT NATCTGCACT 240  
 GTGTGAAGGG ACTCTTTTAA ATAAATNAGC AAGTGTCTTA AGCTATGTCA AA 292

SEQ ID NO:168

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00182

SEQUENCE DESCRIPTION:

GATCTTGGCT GTATTTAATG GCATAGGCTG ACTTTTGCAG ATGGAGGAAN TTCTTGATTA 60  
 ATGTTGAAAA AAAACCCCTTG ATTATACTCT GTTGACAAA CCGAGTGCAA TGAATGATGC 120  
 TTTTNTGAAA ATGAAATATA ACAAGTGGGT GAATGTGGTT ATGGCCGAAA AGGATATGCA 180  
 GTATGCTTAA TGGTAGCAAC TGAAAGAAGA CATCCTGAGC AGTGCCAGCT TTCTTCTGTT 240  
 GATGCCGTTT CCTGAACATA GGAAAATAGA AACTTGCTTA TCAAAACTTA AA 292

SEQ ID NO:169

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00183

SEQUENCE DESCRIPTION:

GATCCACATG AACGCACGCC TGAGATTGG CCACTCACCT ATGTTTTGGG TGGATTGCCT 60  
 AGGAAAGCAA GTCATATGGC CATTGATAGT TCTCATGTAA TTAGTTTTGC TCACCACTAG 120  
 TACAGATGAC CCGTTTACAC GTGGCTTCCC TCGGAAGCCT CCTCAACAGT AGCTGGTGTG 180  
 AAAGACTAAA TCAGTAGAGT TGGAAAAGCT TTATAACCGG TGTGTCATAT GCTTGCTATT 240  
 TAAAGCTGTG TGTGGTTTT GTTTTCTGC CACATTCCT AGTTTTTTAA TAAATATTTT 300  
 CCAAAANTGG AAAAAAANA NCCCCNCCN CCN 333

SEQ ID NO:170

SEQUENCE LENGTH:401

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00184

SEQUENCE DESCRIPTION:

GATCTGGANG GGACACGTCA TGCCTTGGGC CTAGAATACC CTGATGNGAA AAGAGAAGAN 60  
 AAAGGGAGGC CATATCTACA ACACAGCCTC TCGGCACTGC TGCTCCTTAT TTAACTTTG 120  
 TTTTGCATTG TCCTGTATTT ATCACAGTTT CTGTTGAACA GCTTTTCAAG TATTTGGGGA 180  
 GTTTATCTTG CCATCCTCCC CTCTGGTTC TCTGCACCCA CCTGTCCCAC TGCAGTTCCT 240  
 TCCGTGCTCT GTGACTTTAA GAGAAGAAGG GGGGAGGGGT CCCGGATTTT ATGTTTGT 300  
 GNTNTTCTC CTTAGCAGTA GGACTTGATA TTTTCAATTT TGGAAGAACT AAAAGATGAA 360  
 TAAACTGGGT TTTTTTGTGTT GTTTGNTTTT GNAAATTCAA A 401

SEQ ID NO:171

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00185

SEQUENCE DESCRIPTION:

GATCGAGCTC GCCTATNAGC AAGTGGCAAA CCCCTCAAA TAAGCCCCTC CTGGGACTCC 60  
 CTCACCCCC TCCATTTTCT CCACAAAGGC CCTGGTGGTT TCCACATTGC TACCCAATGG 120  
 ACACACTCCA AAATGGCCAG TGGGCAGGGA ATCCTGGAGC ACTTGTTCCG GGATGGTGTG 180  
 GTGGAAGAGG GGATGAGGGA AAGAAATGGG GGGCCTGGGT CAGATTTTTA TTGTGGGGTG 240  
 GGATGAGTAG GACAACATAT TTCAGTAATA AAATACAGAA TAAAAATCAA GTGTTTTTAC 300  
 GCAAA 305

SEQ ID NO:172

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00186

SEQUENCE DESCRIPTION:

GATCTGAGGC AAGCTGGACA GGAGAGGTGG ATATTTNTTG ATGGAAGAAT TCAAGTTTAT 60  
 AATCAATTCC CACTTAGCAC CTACTGTGTG CTAGGAACTT GAATGTGTAT GTTTGACAAG 120  
 TCCTGCTTGG CCTGATGGGT GGGAGANGGA ACCTGAGCCT GGCTGAGATG GCTAGGCGGA 180  
 GGGCTTTGAA GTCCAAGCAG CTGAACTGGC TGGGTGGGT TCTACCTTTG AAAGTGAAG 240  
 ACTTNTTTTG GAGCTCTTAA TTACAATATC TGATATTTT ACAGTCTGN 289

SEQ ID NO:173

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00187

SEQUENCE DESCRIPTION:

GATCCCTACC CTTNCCGTTG GTCTCTNTCG CTGACTCGAG GCACCTAACA TCCATTCACA 60  
 CCCAACACAG GCCAGCGACT TCTGGGGCTC AGCCACAGAC ATGGTTTGTN ACTNTTGAGC 120

# EP 0 679 716 A1

TTCTGTTCTT AGAGAATCCT AGAGGCTTGA TTGGCCCAGG CTGCTGTNTG TNCTGGAGGC 180  
AAAGAATCCC TACCTCCTAG GGGTGAAAGG AAATNAAAAT GGAAAGTTCT TGTAGCGCAA 240  
GGCCTGACAT GGGTAGCTGC TCAATAAATG CTAGTNTGTT ATTTCTN 286

SEQ ID NO:174  
SEQUENCE LENGTH:290  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00188  
SEQUENCE DESCRIPTION:

GATCGGGTTC TAAAGGAAAG GGTGGAGAGA TTCAACCAGT TAGCGTGAAA GTTGGAGATA 60  
AAGTTCTTCT CCCAGAATAT GGAGGCACCA AAGTAGTTCT AGATGACAAG NATTATTTCC 120  
TATTTAGAGA TGGTGACATT CTTGAAAAGT ACGTAGACTG AAATAAGTCA CTATTGAAAT 180  
GGCATCAACA TGATGCTGCC CATTCCACTG AAGTTCTGAA ATCTTTCGTC ATGTAAATAA 240  
TTTCCATATT TCNCTTTNAT AATAAACTAA TGATAACTAA TGNCATCAAA 290

SEQ ID NO:175  
SEQUENCE LENGTH:284  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00189

SEQUENCE DESCRIPTION:  
GATCAAGGCG CGGACGTATC TACGACCACA TCAACGAGGG GAAGCTGTGG AAACACATCA 60  
NGCACAANTA TGACAACAAG TAGTTCCTTG GNGGCCCTAT CCAGGCCAGA AGGCCANNGC 120  
CACCCAGCAG CTGTTTGCCA GAGCTGGAGC TCAGTTGAAG ATGATGCTCA AGGTACTCTT 180  
CATGCCACC ATTCGTGTTG GAAGAACGNT TTACTIONNA CAGCTCTTTA CCTTCTGTGT 240  
GTTTNAAGNTG TTAGNAGATN TCAGGAATAA TGTGATTGCC TTGN 284

SEQ ID NO:176  
SEQUENCE LENGTH:282  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00190

SEQUENCE DESCRIPTION:  
GATCAGAACA TGAAATGCCC TCCTAAATGT CAGCTGTTGT CACACAGTAG CTCCAACACT 60  
TTGAGCATTT TTAAGGGAGT GGCCTCATT CACTAGAGAC AAATCTTTAA GAATAGTTCT 120  
AAAATTGGGC TTGTGATTTC CATTTCTGAT GTCTCCAGAT TGGCACCCTT TTCTAGTTCA 180  
ATGCCTCACG AGATTTTGCC AGGGGCATCC AAGGCAAACA ATCCCAATCT TTCTATATAA 240  
ANTGTATTCA AGCAAACATC AAATAANTTT CTGGGATATT TN 282

SEQ ID NO:177  
SEQUENCE LENGTH:278  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00191

## SEQUENCE DESCRIPTION:

GATCAGAGTT TGAAATGAAA TGTTCGTCAG GGTGTTGGAA AAATTTTGGT GAGTTCTGCA 60  
 CATTTCCTT GGTTCAGGCT GGGCATGGAC CAGCCTTCAG ATGGCAGAAG TGGAAGATGA 120  
 GCCTACTTGT GAGCGATGTG ACTTTAAGGA AATGAAGACT GGGGAAGAAT AATTAGTGTT 180  
 TATAAGACAT TTAAGAGGCC CTTTTTCATA TACTGACTCA CTGATGAATC AGCATTNGCA 240  
 TTNTATGGAA NAATATAAAT CCAAAGAAAT AATTAAAA 278

SEQ ID NO:178

SEQUENCE LENGTH:281

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00192

## SEQUENCE DESCRIPTION:

GATCAAAATA ACCCTCGTAA AAATATATGT ANGGGGTACA CAAAGTAAGC CTCTTTATGA 60  
 AACAAATTGAG GATAATNATG TGAAAGGTTT TAATGATGAT GTTCTACTTC ANATAGTTCA 120  
 CTTTCTACTG AATAGACCAA AAGAAGAAAA ATCAGAGCTG TTGGAAAACT GAAAAAGCAT 180  
 ATTTNATTGA GAACTGTGGG AATATTTAAA TTTTACTGAA GGACCAATAA TGATGAGATT 240  
 TGTAACGTGC AACTATTTAA TACATTGATT TTTGAGACAA A 281

SEQ ID NO:179

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00193

## SEQUENCE DESCRIPTION:

GATCAGGCCC AGGAAGGGCA CAGGGGCTGA GCACTACAGA AGTCACATGG GTTCTCAGGG 60  
 TATGCCAGGG GCAGAAACAG TACCGGCTCT CTGTCACTCA CCTTGAGAGT AGAGCAGACC 120  
 CTGTTCTGCT CTGGGCTGTG AAGGGGTGGA GCAGGCAGTG GCCAGCTTTG CCCTTCCTGC 180  
 TGTCTCTGTT TCTAGCTCCA TGGTTGGCCT GGTGGGGGTG GAGTTCCTC CCAAACACCA 240  
 GACCACACAG TCCTCCAAA ATAACATTT TATATAGN 278

SEQ ID NO:180

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00194

## SEQUENCE DESCRIPTION:

GATCTACATT AATATCAAGT CTTGACTCCC TACTTCCCGT CATTCTCAC AGGACAGAAG 60  
 CAGAGTGGGT GGTGGTTATG TTTGACAGAA GGCATTAGGT TGACAACTTG TCATGATTTT 120  
 GACGGTAAGC CACCATGATT GTGTTCTCTG CCTCTGGTTG ACCTCNACAA AAACCATTGG 180  
 AACTGTGACT TTNAAGGTG CTCTTGCTAA GCTTATATGT GCCTGTAAAT GAAAGTGCCT 240  
 GAAAGACCTT CCTTAATAAA GAAGGTTCTA AGCTGAAA 278

SEQ ID NO:181

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00195

SEQUENCE DESCRIPTION:

GATCTCTCCC CCGTGAAGGA GTTGAGCACA TTAGCAACAA TGTACATTAA TTTTGGATTT 60  
 TCATTTTCAT GTTTTATTTT GTAAATATTA TCTGATGTTT GGAGCTTGAG TATACAGACT 120  
 GTAAATATAG TTCTTGATT TGTACTAATT CTGATTCTTT TGCTNNCNG CCTTAGATGT 180  
 GCAATGCAGA CACTATCTAA CTGTGTGTGG TAACCTTGCG TCACGGAGCT GTTAGTGAAC 240  
 GAGGTAAAAA TAATAAAGGT ACAGCCAGTG CATCAAA 277

SEQ ID NO:182

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00196

SEQUENCE DESCRIPTION:

GATCAAAACN GATTACGGT GGGGGAGGAA TNTGAGCTGG AGACAATNAC AGGGGAGAAA 60  
 GTCAAGACAG TGGTTCAGTT GGAAGGTGAC AATAAACTGG TGACAACTTT CAAAAACATC 120  
 AAGTCTGTGA CCGAACTCAA CGGCGACATA ATCACCAATA CCATGACATT NGGTGACATT 180  
 GTCTTCAAGA GAATCAGCAA GAGAATTTAA ACAAGTCTGC ATTTTCATATT ATTTTAGTGT 240  
 GTAAAAATTA AATGTAATTA AAAGTGANCT TTNGTTTTTA AA 282

SEQ ID NO:183

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00197

SEQUENCE DESCRIPTION:

GATCCAGATG ACCGTGGTNG TTGGGGTATA TCTCCTCGAG GAGCTGGTTA CACCTTTGGG 60  
 CAAGATATTT CTGAGACATT TAATCATGCC AATGGNCTCA CGTTGGTGTC TAGAGCTCAC 120  
 CAGCTAGTGA TGGAGGCATA TAACTGGTGN CNNGGCCCGG AATGTAGTAA CGATTTTCAG 180  
 TGCTCAAACT ATTGTTATCG TTGTGGTAAC CAAGCTGCAA TCATNGANCT TTTGCGATAC 240  
 TCTAAAATAC TCTNTCTTGC AGTTTCACCN AGNNNNN 277

SEQ ID NO:184

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00198

SEQUENCE DESCRIPTION:

GATCTGAGAT TTCCGTGTTT GGCTGAACCT GGGAGACCAG CTGGGCCTCC AAGTAGGATA 60  
 ACCCTCACT GAGCACCACA TTCTTAGCT TCTGTTGAG GCTGGAACCTG TTTCTTTAAA 120  
 ATCCCTTAAT TTTCCCATCT CAAAATTATA TCTGTACCTG GGTATCCAG CTCCTTCTTG 180  
 GGTGTGGGGA AATGAGTTTT CTTTGATAGT TTCTGCCTCA CTCATCCCTC CTGTACCCTG 240  
 GCCAGAACAT CTCACTGATA CTCGAATTCT TTTGGCN 277



SEQ ID NO:185

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00199

SEQUENCE DESCRIPTION:

GATCGGTTTT TGTTTCCTGC TTACCATATG ATTGTAAATT GTTTTATGTA TTAATCAGTT 60  
 AATGCTAATT AATTTTGGCT GATGTCATAT GTTAAAGAGC TATAAATTCC AACAACCAAC 120  
 TGGTGTGTAA AAATAATTTA AAATTTCCCTT TACTGAAAGG TATTCCCAT TTTGTGGGG 180  
 AAAAGAGCCA AATTATTAC TTTGTGTGG GGTTTTAAA ATATTAAGAA ATGTCTAAGT 240  
 TATTGTTTGC AACATAAAT ATGATTTTAA ATTCTCN 277

SEQ ID NO:186

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00200

SEQUENCE DESCRIPTION:

GATCCTGACA CTGACATGAA GGCAAGCCTT GATTTCGTAT GAACGTTGCT GAAGTGGTAA 60  
 TTGAGGAAAA CAGTTCCCA GATTGTTAAG AGTCACTGA AGATATTGAC ACAATTTNNA 120  
 AAAATCAGTA AAGGAATGTA TATAATATTG CNCTCGTGTT TTACAGTAAG ATTTGTTGCT 180  
 CTCAGACTGT GTAAACAAA ATTNATNGNT GTTTCTGCA TTTAAAAA TCTTATTGTA 240  
 CCANCTGGTA ANCTATTAAN TGCCTATAAN NCTAAA 276

SEQ ID NO:187

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00201

SEQUENCE DESCRIPTION:

GATCAAGGAN GAAAGANTGA CTTCAAATAT GCCTTGTTAG TGTAATGTG ACTTNTNGAA 60  
 CTGTATGAGT ATTTTAAGAT TATTNGAGTA AAGTAAGTTT TAAAAAGCAG TCCCTAATCA 120  
 TCAAAAGTAA AAAACTCTTG ATGTAGTCAT ATAACCACAC TAAGAACTCT TCCAGGTGAC 180  
 TTCAAAACAT AGGACAGTAC ATCTCTAGTA GANTNTGCCC TGAGAATGAA AAGAATGTAA 240  
 CAGTGTTAGT ATTTTGAATA AACATGTTAT TACTN 275

SEQ ID NO:188

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00202

SEQUENCE DESCRIPTION:

GATCACTTTT TTTAGAGTGA AGAAAGAACA ANCTTGTTTT TTGTGTTTTT TAAAGGAATA 60  
 TAAAATAATG AAGGATGTAT AATTGATGCC AAATAAGCTT GTNCTTTAGT CACACCGACG 120

TCTTATTTTT CCCTTTAGGC CAGTTCTGTT TTTAAGGTGT ACATGGNCAA TGTTACAGTG 180  
 TAAGAACTC CATATCCATA TGTNCCCATT CGCATTTTGT ATTGGTTCAT GTATACCATT 240  
 TTTNCAAAAN ANANGGAANA ANNGGNAGTN CTN 273

SEQ ID NO:189

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00203

SEQUENCE DESCRIPTION:

GATCTGAAAA GCTCACTTTA AACTCATACT ACATTGCTNA CGAGTATTTN ACGTTAACAT 60  
 AATTGAAAAG TACAAGGTCC AAGCTGGCTT TCAAATNATG TCTAAACAGA AATGGGACAA 120  
 ATAGACTTGA AAATAGAAGG GATTTATTCC ACCCCTGCAA GGGTAAGAGT CAGGTGAGAG 180  
 TCCCTTGGTG AGTCATTGT ACATCAGTGT CATTCTTCT TAACCTCTGA AGAAAGATGG 240  
 GCATCAGAAA TAAAGACAAA GCACTATCAA A 271

SEQ ID NO:190

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00204

SEQUENCE DESCRIPTION:

GATCTGCCAC GAGGGCAGCA GCCAAGAGGA CTTGCTCTCT CCATGTGAAT GTACAGGGAC 60  
 CTTGGGGACA ATTCATCGGA GCTGCCTGGA GCACTGGCTG TCATCCTCAA ACACCAGCTA 120  
 CTGTGAACTC TGCCACTTCA GGTTCGAGT CGAGCGAAAA CCCAGGCCGT TAGTGGAGTG 180  
 CCTGGGAAAC CTTGGCCCCC AGATTGGGAG GGGNCTTTT TTTGGNGANA TGGTNNNTT 240  
 TGGGTNTTAA ATCNCNGGG NNCCATNTNN 270

SEQ ID NO:191

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00205

SEQUENCE DESCRIPTION:

GATCTCTGAG CTGCCCAGCA TAGTCCAAGA CCTAGCCAAT GGCAACATCA CATGGGCTGA 60  
 TGTGGAGGCC AGGTATCCTC TGTGTAAGG GCAAGAGACT GGTAAAAAAG AGACAATCGA 120  
 GGAATGAGGA CAATTTTGAC AACTTTTGAC CACTTGCCT AATAAA 166

SEQ ID NO:192

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00206

SEQUENCE DESCRIPTION:

GATCTACATG AGAAGTATAG TGGCTCTACC CCCTGAAAGA GGGTGGATGC AGCTGCTTGT 60

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GTTCTTGGG GTGACTGTCA TTGGTAATAC GGACACAGTG ACCCATCCTC CATCCTATTT 120  
 ATAGTGGGAAG GGCCTTCAAT TGTATCAGTA CTTTNTTTTA AGCTCTGGCA CATTGACCTC 180  
 TATGTGTAC CAGTCATTAA TGAGCTGCTG CAGAGGTGAC TATTTGTTT ACTTTCTTGG 240  
 ATGTTAACAT TACACTACTC ACTACTCAAT CTCAAA 276

SEQ ID NO:193  
 SEQUENCE LENGTH:273  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00207

SEQUENCE DESCRIPTION:  
 GATCTGACAT TTGACATGAA CACAAAGTTG CTAGATGCTC TTGTTGACTT CCAGCAGATG 60  
 GGATGGGGGA AACACAGCAG TTCTTGGTAA AGTCCTTTGT AATAATAGTT TGATTTTTTT 120  
 ATTCGAGAG AATCTTTCAT TTCCTATGT ATGCTTTTTCN CCTTTTTTGC CCAGTTTCCT 180  
 TATCACTTGC TGTAGATGGC TTATNTNGCA TTCATGCAGA CTATGTTGCA AGTCTGTTTC 240  
 ATCTAGTAAA CTGAAAATNA TTGCTTAATC AAA 273

SEQ ID NO:194  
 SEQUENCE LENGTH:267  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00209

SEQUENCE DESCRIPTION:  
 GATCCCAGAG AGGGAAGAGA ACCAGGGGCC CTTTTCTCTT TNAGAATTTN CTTTTAATCA 60  
 GCCCACCTTT TGAATCCCCG CCCGCCCAA TCCATTATNT TTTCTGCCT TCCGGGTCCC 120  
 ATCCTTAGAG CTCGAGTCGT TCCTTCCCCT CCTGGATTCC GGGTAGCAGA GGCAGCGCCG 180  
 CAGGAGGCGG GTGCCCGTTT GTCCAGGNC TGGGCGTGGT GGAGNNAGGG GTGCTGGAAC 240  
 AATAAACGGC ACNNNNCAAA TGTCAA 267

SEQ ID NO:195  
 SEQUENCE LENGTH:384  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00210

SEQUENCE DESCRIPTION:  
 GATCCAAAAC ACTACTCAGC TCTCTTGCAC TGAGGAAATT TTTCCCCCTA CATTGACTCC 60  
 TGGCCTACAT CAGCCAACT TAACCTTGGT GGGGTTTGA TTTGATAGCC AATTAGTTCT 120  
 GTGCTGGTTG CAAAGAATTG ATATTTAGAT GGTTTTTAAT ACTCAGCAGA TTGTCTTCCT 180  
 TTATATTGTG TCTTTTTTAT GTNGCATGTN GCTTTTGTTA TCAGCCTGAT TTTTGTCTCA 240  
 GTATATGATA GTNCTGCTGA TGTTTGTGTT ATGGGCAGA CATATCTTCA TTAAGAGTTT 300  
 TTGGAAAAC CATCAAATTC GATGAATACA TTTCTTCAT AACCCATTG GAATTATTCC 360  
 TAATAAAATG ATAAATACG TAAA 384

SEQ ID NO:196  
 SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00211

SEQUENCE DESCRIPTION:

GATCTAAAAA AATTCAGAAG AAATATGATG AAAGGAAAAA GAATGCCAAA ATCAGCAGTC 60  
 TCCTGGAGGA GCAGTTCCAG CAGGGCAAGC TTCTTGCGTG CATCGCTTCA AGGCCGGGAC 120  
 AGTGTGGCCG AGCAGATGGC TATGTGCTAG AGGGCAAAGA GTTGGAGTTC TATCTTAGGA 180  
 AAATCAAGGC CCGCAAAGGC AAATAAATCC TTGTTTTGTC TTCACCCATG TAATAAAGGT 240  
 GTTTATTGTT TTGTTCCAC ATTTATGTTG CCTGAAA 277

SEQ ID NO:197

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00212

SEQUENCE DESCRIPTION:

GATCGGCGGC GCGCAGNAAC CGCTCCTACA GCAAGCTGCT GTGCGGCCTG CTGGCCGAGG 60  
 CGCCTGCGCA TCAGCCCGGA CAGGGTCTAC ATCAACTATT ACGACATGAA CGCGGCCAAT 120  
 GTGGGTGGA ACAACTCCAC CTTGCCTAA GAGCCGCAGG ACCCACGCTG TCTGCGCTGG 180  
 CTCCACCCGG GAACCCGCCG CACGCTGTGT TCTAGGCCCG NCCACCCCAA CCTTCTGGTG 240  
 GGGAGAAATA AACGGTTTAG AGACTAGGAA A 271

SEQ ID NO:198

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00213

SEQUENCE DESCRIPTION:

GATCCTGTAG TGTTCTGGA GAAGCTAGAG CCTGATTGTA GGCTACTACT CATCAATTAA 60  
 CTTCTACAGT GGAGACTACT TCTGGGACTG GAATATAAAA AAGAATCAAA GGTTCGTGATT 120  
 TTNAGTTGCA ATAAAGGGAA AGACCATGCT CATAGCAGTG CCAACATCTG AAGTGTGGAG 180  
 CCTTACCCAT TTCATCACCT ACAACGGAAG TAGTTAACTG GAAGAGATTA CCAAGAGAAT 240  
 AAAAAGAGAC TCATTCAGTG GAAA 264

SEQ ID NO:199

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00215

SEQUENCE DESCRIPTION:

GATCTGCCTT AAAGAAAAGA AAATTTTAGA AAGAAATATT GTTGCTCAGT GTTGTTAATA 60  
 TAGCTCAAGA ATTGAGTTTA TATTTGCAGT ATGCTATAAA TGATACCCCC CTACCACACC 120  
 CACACACACA GTTTTGTCT AATGAAAATG TTGCTGTGAT TATTTATAAT TGGTAGTATT 180  
 TCTTCCAGAA GAAGCTAAAA TAAGACTGGC ACTTACCCTG AAGTGCAATTA ATAAAACCAC 240  
 ACTTTAAAAAT TAANAAA 257

SEQ ID NO:200

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00216

SEQUENCE DESCRIPTION:

GATCAACCTG AGCNTGGAGA ATGCCTGGGG CATTTAACGC TGCCTCATTG ACATCTGCAT 60  
 GAAGCTGGAG GAGGGCAAAT ACCTCATCCT CAAGGACCCC AACAGCAGG TCATCCGTNT 120  
 CTACAGCCTC CCTGATGGCA CCTTCAGCTC TGATGAAGAT GAGGAGGAAG AGGAGGAGGA 180  
 AGAAGNGGAA GAAGATGNGG ANGAACTTA AACCAGTGAT GTGGAGCTGG AGTTTNTCCT 240  
 TCCACCGAGA CTACGNGGGC CTTTATGCT TAGTGGAATG TNTGTCTAAC TTTGCTCTCT 300  
 TGACATTTTA GCAGTTGAAA TTAAATTATA TANTCTGTTT TNNGTCTTTT NAAATAAANA 360  
 AAANNANATT NTGN 374

SEQ ID NO:201

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00217

SEQUENCE DESCRIPTION:

GATCTGAACT ATTTGCTTTC TCTTCAAGAT AAGTTGTATT TTACCATGGA AAAATACAGT 60  
 ATCTAACATT ACCATTCACG TTAAATGAAG TTTCTCATA ACATTTATCT TTAGTTTTAT 120  
 GAAGTCATCG TGACCAATGT TACAGTAATT TCTGTTAGCT GATTGTGGTA AACAATGTTT 180  
 AATGNGAAAA GAAATTAAAA CTTTCTTCAT CTGTTGTAGA ATATTTCTCT TCTTTAAAT 240  
 GGCTTCTATT CATAAA 256

SEQ ID NO:202

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00218

SEQUENCE DESCRIPTION:

GATCCCCACT GGAGCAGCCT CTGCAAAAGG GAGCCCATGT AGTGGCCAGG GGCTGTCCAA 60  
 ACTCCAGCTT CTTCCCTGG GAAAAACCC AAAGAACCAA AAACAAACCA CCCCAAGGAT 120  
 AATAATAGCT AACTGCTAG CTTCTCAAGT TCTTGTGAAA AACAATTTAC ATAATGACAC 180  
 AGTAGATGTG GAACACCTAG CCAGTGCCTG GGCAGGTCCC TATTATCATA AATGAACATA 240  
 AAGTGCTCTA AAAACN 256

SEQ ID NO:203

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00219

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCCAAATC AGGAAAAGAC GGCGCCACTA CAATGGAGAA GCATATNAGG ATGATGAACA 60  
 TCATCCCAGA GGTGGTGTTC AGTGTGAGAC CTCTTAATGG GCCAGTGAAT AACACTCACT 120  
 GCTGGCATTG AATGTGCAGT AGTGAATGAG TGAAGGACTG TAATCATAAT ATGCTCACTA 180  
 CTTGCTCTTG TTTTGTGTTT AATAAACTAT AGTAGTGTTA TAANNNGTTA AATGAAGAAT 240  
 AAACGCAAAT ATAANAGCTC TGAAA 265

SEQ ID NO:204

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00220

SEQUENCE DESCRIPTION:

GATCTAAAGA GACACTTAGA GACTCTTGGG GACCTCAGAT TTCCACCNCT CCACAGCATT 60  
 CTGCCTACAC AGTTCCCCTC ATTTTNCCTA GTTACTCGGA AGAGCGCTGG ACTTGAAATC 120  
 AAAATAATTG CGTTATGTCT TTGGTTATGT CGCTTCATCA TAGCACTTTC TAAAACTATT 180  
 TGACAAACAT GTATTGCATA CCTACNGCAT TCCAGTTCTN GTACANGTAA TTAAATGCTC 240  
 GACTAACGNN AAA 253

SEQ ID NO:205

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00221

SEQUENCE DESCRIPTION:

GATCTGGAAT TGGACATTTT TCTGTCAGAG CACAGAGGAG GCTCATATCA CCTCTTCCCT 60  
 CTCCTACTTG GCCCAGCTGC TTGGAGGACC GACCCCATGG CTGAGAATAT NACGGCAAGA 120  
 GGAACAGAGN TTGCTCCAAG TGGGAAAGGG TCCCAAGCAG TCCAGAGAAG ATGTCTGTGT 180  
 GGCTTTCCCT CCCTGCCTCC CCCAGCTCCC AACTGGCCT TTGTAAATAA ATGGCGTGGT 240  
 CTTTGTGTG AAA 253

SEQ ID NO:206

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00222

SEQUENCE DESCRIPTION:

GATCTGCCGT CTGTCACCTC TCTCCAAGTT GAGACAGGGG CCTGGATTTC AGCCCTTCCT 60  
 GCCGAGAAAT CTTNTAAATT TCAACCTACC TTAAAAATA AAGTCTCCCT ACTTAAATC 120  
 CAGTAGATAT CATGGCACTA ATGCTAACAC CCCTTTCCCC AAATTAATAA AACAAAAATA 180  
 AAAAAAGAA AAAANTGCAG GCATGCAAGC TTGGCGTANT CATGGNNTNA GCTGTTTCCC 240  
 NGTCACGGCG TGN 253

SEQ ID NO:207

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00223

SEQUENCE DESCRIPTION:

5 GATCGAGACA CGTGATGGGA AGCTGGTGTG TGAGTCCATN ACGTCCTNCC AAGTGAACAG 60  
 CTGCGGCAGC CCTCCCAGCC TACCCCTCCT GCGCTGACCC AGAGCCTGGG AAGGAGGCCG 120  
 CTATGAGGGT AGCACTGGGA ACAGGAGACC CACCTNAGNC TCAGCCTNGC CTCAGTNTAC 180  
 TGGGGAGTTT ACTACCTGGG GCCCANTTGA CATGCTCCAG CTACANACAN TTANTTGCTT 240  
 10 TTTTNTTGGN N 251

SEQ ID NO:208

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00224

SEQUENCE DESCRIPTION:

20 GATCGATTCT TGTATATTNA TTTTATCTCT TTCTGTATCT ATAGGTAAAT CTCAAGGGTA 60  
 AAATGTTAGG TGTTGACATT GAGAACCCTG AAACCCCATC CCCTGCTCAG AGGAACAGTG 120  
 TGAACAAAAA TCTCTTGAGA GATTTAGAAT ATCTTTTCTT TTGCTCATCT TAGACCACAG 180  
 ACTGACTTTG AAATTATGTT AAGTGAAATA TCAATGAAAA TAAAGTTTAC TATAAATAAT 240  
 AAA 243

25 SEQ ID NO:209

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS00225

SEQUENCE DESCRIPTION:

GATCACANTT AATGATTCAG TATAATGTTT GAGGCCAGAC AAGATATATA TTGTGCCTCT 60  
 TACAGCCTTT GGNNCNNTTG TTTCCATTTT TTAAATATCT TCTATATCCA TATAGTATTC 120  
 35 AAATNATTAA TGCTCATGTA CCAAGGTTT GCTATAAAAG TTTTGNCTGT ATGAATAATG 180  
 TGGCTTTAGT AAATAATCAT TTTTCAACTG TAAACTTATT CTGAAATAAA GTAAATTTCT 240  
 AATTGTTTN 249

SEQ ID NO:210

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00226

SEQUENCE DESCRIPTION:

45 GATCATAGAA ATATATGTAA AGTATTCAAT TTTCAATCAT TTTCAAATNA CTGTTATAAA 60  
 TTGTTTTTGC TGAGTTGTAA TACTTTTNAG ATACAATGTA TTCCTTGTA TGAAGAAGATG 120  
 AAAAAGGACT TTTTCAGCAT TTGAGGTAAG TNCTTTAACG TTTCATTAAA ANCATTTTTT 180  
 ACAAATATTT TGTACATGCA CTTGCAGTAT TGAGGTAAAT CATTTTAATA AATNCGGAAA 240  
 50 TTAACACN 248

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SEQ ID NO:211

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00227

SEQUENCE DESCRIPTION:

GATCTCAGCN TTGCAAACAC ANTTNCTACA TAGATAGTAC TAGGTATNNT TTAGATATGT 60  
 AAAGAAAGAA ATCACACCAT TAATAATGGT AAGATTGGTT TATGTGATTT TAGTGGTATT 120  
 TTTGGCACCC TTATATATGT TTTCCAAACT TTCAGCAGTG ATATTATTTT CATAACTTAA 180  
 AAAGTGAGTT TGAAAAAGAA AATCTCCAGC AAGCATCTCA TTTAAATAAA GGTTTGTCAT 240  
 CTTTAAA 247

SEQ ID NO:212

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00228

SEQUENCE DESCRIPTION:

GATCAAAACA AACAATCCAG ATGTATAAGT ACTAGGCAGA AGCCAATTTT AAAATTTTCTT 60  
 TGAATAATCC ATGAAAGGAA TAATTCAAAT ACAGATAAAC AGAGTTGGCA GTATATTATA 120  
 GTGATAATTT TGTATTTTCA CAAAAAAAAA NGTTAAACTC TTCTTTTCTT TTTATTATAA 180  
 TGNCCAGCTT TNGGTATTTC ATTGTTACCA NGTTCTATTT TTNGANTAAA ATGTTCTCTC 240  
 TTCTAAANGT TTAAA 256

SEQ ID NO:213

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00230

SEQUENCE DESCRIPTION:

GATCGGCAAG CCCACACTG TCCCTTGCAA GCCAAGGCCA CCTTTNATGC CATTTCTAAG 60  
 ACCTACAGCT ACCTGACCCC CGACCTCTGG AAGGAGACTG TATTCACCAA GTNTCCCTAT 120  
 CAGGAGTTCA CTGACCACCT NGTCAAGACC CACACCAGAG TCTCCGTGCA GCGGACTCAG 180  
 GCTCCAGCTG TGGCTACAAC ATAGGGTTTT TATACAAGAA AAATAAAGTG AATTAAGCGT 240  
 GAAA 244

SEQ ID NO:214

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00231

SEQUENCE DESCRIPTION:

GATCAGATTG GGTCTTGCTC CTCTCAACCT TGAAGTCCCC ACGTATGAGT TCACCAGTGA 60  
 CGATATGGTG ATGTTGGTT AAGAGACTTG GACTCAAGTC ATAGGCTTCT TTCAGTCTTT 120  
 ATGTCACCTC AGGAGACTTA TTTGAGAGGA AGCCTTCTGT ACTGAAGTT GATTTGAAAT 180



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ATGTAAGANT TGATGATGTA TTGGCAAACA TTAATGTGAA GTAAATNGAA TTNAATGTNG 240  
AAA 243

5 SEQ ID NO:215  
SEQUENCE LENGTH:243  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS00232  
SEQUENCE DESCRIPTION:  
GATCGCCAGT GGAAGAAGAT TAGTGCAATC ATTGAGAAGA GGAAGAAGAT GGAAGCTGAT 60  
GGGGTTGAAG TCAAAAGACC AAAATACTAA TCACTAGTTA CAACCAGAGA TGCTCCACAA 120  
GGATATGCTC CCCACGGTTT TCTTTCTACA ATTTCCAAAG GTTGCAAGAT GTTTTTTTGT 180  
15 GGATGAATAT AAAATTTTAT TGTGTAATTA CTTGGTTCCA TTAATAATTGG TTAAGTTGCT 240  
AAA 243

20 SEQ ID NO:216  
SEQUENCE LENGTH:243  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00233  
SEQUENCE DESCRIPTION:  
25 GATCGTAGAT GTTAACCAAA TCTACAAAAT CCACTACTCC CCCGTTATCA ACGGGATACG 60  
TTCCAAGACC CCCAGTGGAT GCCTGAAACT GGCTAATGCT GAACCCTACA TATACTATGT 120  
TTTTNCTGTA CATATATATG ATAAAGTTTA AATNATAAAT NAGGTACAGT AACAACAATA 180  
ACAGTAAAC AACAGTTATA ACAATATACT GTAATAAAAG TCATGTGAAT GTGGTGTTC 240  
30 TCN 243

35 SEQ ID NO:217  
SEQUENCE LENGTH:242  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00234  
SEQUENCE DESCRIPTION:  
GATCTTCTCC AGATTGGCAG AAAGTTGATA TAGGTGGACT TTTTACAGG TCAGTTGAGG 60  
40 CAAAAAATA TGGGTTTTTT CAGGTGAACC TCCCCATT AAATACTCAG AAGATAAGGT 120  
GTGAATGTAT GTATTATTAG AGTCCTAAAG TATTTTATAA GTACTGGTTT CACCACGCTT 180  
TGTGGGAGAG AAATCATTCA AATCATTTTT TTTGTCCGTA CAATAAAGTT TACTAAAAAC 240  
CN 242

45 SEQ ID NO:218  
SEQUENCE LENGTH:238  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00235  
50 SEQUENCE DESCRIPTION:

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# EP 0 679 716 A1

GATCTTCGTG ATACTGTACA TAGCTGTTTG AAATGCCAGA ATGACTTCTG ACATNCCAAG 60  
 TTTTTCACAA AATATATTN ATCTGTGATT AGCCATTGA CTAATAATAC TGGCTAACAG 120  
 ATGTTGAAAA AAATTGTCTG TTTTCTCATT AATTTTGGTC TAAAACATGT TTGCACTTGT 180  
 NTTTGAATTG TGTTTTATTA ACATTGATTG GCATATTAAA AGTCACTCNG AGCTTAAA 238

SEQ ID NO:219

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00236

SEQUENCE DESCRIPTION:

GATCCAAANN ATGACTTCAG AAAAACTTG AAAGTAACAG CAGTGCCTAC ACTACTTAAG 60  
 TATGGAACAC CTCAAAACT GGTAAGTCT GAGTGTCTT AGGCCAACCT GGTGGAAATN 120  
 TTGTTCTCTG AAGATTAAGA TNGGTAGGAT GGCAATCATG TCTTGATGTC CTGATTTGTT 180  
 CTAGTATCAA TAAACTGTAT ACTTGCTTTG AATTCATGTT AGCAATAAAT GATGTTAAA 239

SEQ ID NO:220

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00237

SEQUENCE DESCRIPTION:

GATCAGAGGT GAAGGGACAG AGAGAGGAGA GGAGGAAGAT TGAGCTGGGG GCAACAGCCA 60  
 AGCTCACCTG GGCAGGTCTC TGCCACCTCC TTGCTCTGTG AGCTGTCAGT CTAGGTTATT 120  
 CTCTTTTTTT GTGGCTATTT TTAATTGCTT TGGATTTGTT AAATGTTTTT TGTCTTCTGT 180  
 TAAGTGTGTT TTCTCTGGAG ATAGAATGTA AACCATATTA AAAGGAAAAA GTTTCAGACA 240  
 AGCAATTAAA 250

SEQ ID NO:221

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00238

SEQUENCE DESCRIPTION:

GATCAGCTTT GCTCCTGAAA TTGCATCCGA AGAAGAAAGA AAGGGGATGG TGGCTGCGTG 60  
 GTCCCAGAGG CTGCAGACCA TCTGGAAGGA AGAGCCCATC CCCTGCACAG CCCACTGGCA 120  
 CTTCTGGGCAA TAACTCTGTG GCACGTGGGC ATCACGTAAG CAGCACACTA CGAGGCCAG 180  
 GCGCAGGCAA AGAGAAGATG GTGCTGTCAT GAAATAAAAT TACAACATAG CTACAAA 237

SEQ ID NO:222

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00239

SEQUENCE DESCRIPTION:

GATCAGTGTA GAACTGGTCA TAGAGGAAGA GCTAGAAATC CAGTAGCATG ATTTTAAAT 60  
AACCTGTCCT TGTTTTGAT GTTAAACAGT AAATGCCAGT AGTGACCAAG AACACAGTGA 120  
TTATATACAC TATACTGGAG GGATTTCATT TTTAATTCAT CTTTATGANG ATTTAGAACT 180  
CATTCCCTGT GTTAAAGGG AATGTTTAAT TGAGAAATAA ACATTTGTGT ACAAATGCT 240  
AAA 243

SEQ ID NO:223

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00240

SEQUENCE DESCRIPTION:

GATCTAATAA CAGGTTGACA TAAGAAATAT TTGTCTCAAA AATCAATGTA TTTAATAGTT 60  
GACAGTTACA AATCTCATCA TTGAAAGATT TAATTTTAGT TACCTTTTGT TGATTTANNN 120  
NNNATTGCAT TTGTATATTG CTAAGTATA AGACAAATTG AGTTATTGAG CTATTAANTG 180  
CACATTTTAA TATAANTGCA GAAATCCCA ATAAATGCT AACATACTGA AA 232

SEQ ID NO:224

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00241

SEQUENCE DESCRIPTION:

GATCACCGTG ACATCCGAGG TGCCTTTCTC CAAAAGGTAT TTGAAATATC TCACCAAAAA 60  
ATATTTGAAG AAGAATAATC TACGTGACTG GTTGCGCGTA GTTGCTAACA GCAAAGAGAG 120  
TTACGAATTA CGTTACTTCC AGATTAACCA GGACGAAGAA GAGGAGGAAG ACGAGGATTA 180  
AATTTCAATT ATCTGGAAAA TTTTGTATGA GTTCTTGAAT AAAACTTGGG AACCAAA 237

SEQ ID NO:225

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00242

SEQUENCE DESCRIPTION:

GATCTTCACT TAANCTAAGT CTGTGAATTA CTTTTATATT ATTTTGAAAN ACTCCTTGCA 60  
GTATATTGGC ATGATACAGT AAAAGCANTT TCCACAGATT GTTATCACCT TCTTTAAAAG 120  
AAGTCAAAAT TTAATAAATA CAATAGCACG TTGTTGGTGT CATATTCAAT AACATTTCCA 180  
ATGCTACATA TAATTTTATA GACATAATAA AGAAGGTATT GAAAAAATA AATAAA 236

SEQ ID NO:226

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00243

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCGCCACC TACCGCCGCC TGCTGGAAGA TGGCGAGGAC TTTAATCTTG GTGATGCCTT 60  
 GGACAGCAGC AACTCCATGC AAACCATCCA AAAGACCACC ACCCGCCGGA TAGTGGATGG 120  
 CAAAGTGGTG TCTGAGACCA ATGACACCAA AGTTCTGAGG CATTAAAGCCA GCAGAAGCAG 180  
 GGTACCCTTT GGGGAGCAGG AGGCCAATAA AAAGTTCAGA GTTCAAA 227

SEQ ID NO:227

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00244

SEQUENCE DESCRIPTION:

GATCAGCAAG CAGGAGTATG ACGAGTCCGG CCCCTCCATC GTCCACCGCA AATNCTTCTA 60  
 GCGGACTAT GACTTAGTTG CGTTACACCC TTTCTTGACA AAACCTAACT TGCGCAGAAA 120  
 ACAAGATGAG ATTGGCATGG CTTTATTTGT TTTTITTTGT TTGTTTGGT TTTTTTTTTT 180  
 TTTTGGGT NNCCCCNGGT TAAA 205

SEQ ID NO:228

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00245

SEQUENCE DESCRIPTION:

GATCTGCCCC AAGAGGTGTT GGCTGAGCTT NAGGCCCTGG AGAGACGTGT GCACAAAATG 60  
 TNACCTGAGG CCCTAGTCTA GCAAGAGGAC ATAGCACCTT CATCTGGGAA TAGGGAAGGC 120  
 ACCTTGACAG AAATATGAGC AATTTGATAT TAACTAACAT CTTCAATGTG CCATAGACCT 180  
 TCCCACAAAG ACTGTCCAAT AATAAGAGAT GCTTATCTAT TTAAAA 226

SEQ ID NO:229

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00246

SEQUENCE DESCRIPTION:

GATCAGCCCC AGATTTGACG TGCAACTCAA AGACCTGGAA AAATGGCAGA ATAATCTGCT 60  
 TCCATCCCGC CAGTTTGGTT TCATTGTACT GACAACCTCA GCTGGCATCA TGGACCATGA 120  
 AGAAGCAAGA CGAAAACACA CAGGAGGGAA AATCCTGGGA TTCTTTTCT AGGGATGTAA 180  
 TACATATATT TNCAAATAAA ATGCCTCATG GACTCTGGTG CTTCCAAA 228

SEQ ID NO:230

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00247

SEQUENCE DESCRIPTION:

GATCTGCGAC CATTCTGTGA CAACACAAGC TGGCCTTGGC AGTTTCGGTG CATAGAAAAT 60

EP 0 679 716 A1

CAGGTGCTAC AGCTCGAGAG GGCAGAGCCA CAGTCCCTGG ACGGCGTGGA CTGAGGCCGG 120  
TTCCTTCCTG GAGGCCTCCT GTCCTCGGGG ACCCCAGCAC CTCATCATCA GCATTGCTGG 180  
AGCCAAGGGT AGGAGCCCTA CACTAGGAGC CCAGGATGGG ACGGNGNATN AGCCGAGAGG 240  
5 NAGGGAACCT TTNAGTNAAG TTCCTCAAAA AGAGGNTTAG AATAAANCCT TNGGCTTAAA 300  
AAGAGAAA 308

SEQ ID NO:231

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00248

SEQUENCE DESCRIPTION:

15 GATCCAAAGA CAGACCACAG ACTGGGAAAA GTTGAAGAT GAACACTTGA GGAATTCAGC 60  
TTCTCACCTA CTTAGTACAG TTGGGAACCA TACACTTCTG GCATGTTTGG AAATCAAAAT 120  
GTCACATTCT CGGGGAGGA AGCCAGAAA ATTGGGTATG TTCTAGAGAT TTACCACCAT 180  
TGCTTATTGC TTTTNTCTTT TAATAAAGTT TAGGAAAGTA GAATTTTAAA 230

SEQ ID NO:232

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00249

SEQUENCE DESCRIPTION:

25 GATCTAAAGA TTTCTCTATC CAATGAATCT AACAAAGTCA ATGGAAATTG AACTCTAGAA 60  
TTGTCTCTAG AAAACATAGC TTCTTACTGA ACTTGAACAT TTTTACAACA TTCCTGGTT 120  
30 TTTGTTTTGT TAGCTAATAA TCTATAATAG TTGAGTATCT CTGGGAATGG GGAGGGAAT 180  
TATATGTAAT AGAGCTTAAA AATAAAGTGT CAATTTCCAA GGNCTAAA 228

SEQ ID NO:233

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00250

SEQUENCE DESCRIPTION:

40 GATCAATAAG CATGTCAGAC TGATTAATGT CTAATGTGAA AATTTGGTAG TAAATTTNCA 60  
TTTGATATTA GATATAAATA TCTGAATATA AATAATTTNA ATATACTAGT CATGATGTGT 120  
GTTGTATTTN AAAAATTATC TGCAACCTTA ATTCAGCTGA AGTNCTTTAT ATTTCAAAAG 180  
AATGAATAAC ATTGATAATA AAATCGCTAC TTAAAGGGAA A 221

SEQ ID NO:234

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00251

SEQUENCE DESCRIPTION:

5 GATCTCTATG AATGTCAGAG CCCTAACTTT CAGGCTTTGC ATTTTGTATA TGGGAAGAAA 60  
TATGACAATC CTAGGTAATT AAACCATAGA CCCAAAGCCC TTACGTTTGA TGCAATTTAT 120  
TTTTAAAATA GGCCTTGTTT TTCAGCTTCA TCTGCAGTTC TATGTGAAGA TTGATAAATC 180  
AGTTTTTACT TGTTTTATTA ATAAAACGTA ATTNNGGAAA 219

SEQ ID NO:235

SEQUENCE LENGTH:287

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00252

SEQUENCE DESCRIPTION:

15 GATCTCCGTT CCGCTCCCAG CGGCTCCAGT GTAAATTCCC CTTCCCCCTG GGGAAATGCA 60  
CTACCTTGTT TTGGGGGGTT TAGGGGTGTT TTTGTTTTTC AGTTGTTTG TTTTTTTGTT 120  
TTTTTTTTTN CCTTGCCTT TTNCCCTTT NATTTGGNGG GAATGGGAGG AAGTGGGANC 180  
AGGGAGGTGG GAGGTGGATT TTGTTNATTT TTTAAGCTCA TTTCCAGGGG TGGGANTTTT 240  
TTTNAANAT GNGNCATGAA NAAAGTTTGT TTTGAAANT AACCAAA 287

SEQ ID NO:236

SEQUENCE LENGTH:222

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00253

SEQUENCE DESCRIPTION:

30 GATCAGAATT GGCAGCACAA AGAAAACGCC CTCTCCTGAC TTGTATTGTG GCAGTCTGAA 60  
CGNCCCAGA AAATTGTGCC AAAGAGTTTA GAAAAATAAA TATACAATAA AAGTAAACAC 120  
ATACACACAA AACAGCAAAC TTCAGGTAAC TATTTTGGAT TGCAACAGG ATAAATTAAA 180  
TGTTCAAACA ATCTGATAAA ATAACCATTT GGGNCTTGNA AA 222

SEQ ID NO:237

35 SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00254

SEQUENCE DESCRIPTION:

40 GATCATCTTT CCTNTTCCAG AGAAGTGGGC TGGATGTCTC CATCTCTGTC TCAACTTTAC 60  
GTGTACTGAG CTGCAACNTC TTA CTTCCT ACTGAAAATA AGAATCTGAA TATAAATTTG 120  
TTTTCTCAA TATTTGCTAT GAGAGGTGA TGGATTAATT AAATAAGTCA ATTCCTGGAA 180  
GTTGAGAGAG CAAATAANGT CCTGAGAACC TTCCAGACAA A 221

45 SEQ ID NO:238

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS00255

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCAGACGT TTTACAAATN CATGAAGCGA ATTGCTGCTT GTAAGGAGCA GATTTTAAGG 60  
TATTCCTGGA GTGGAGAGCC ACTCTTTTTA ACCTGCCCTA CATCAGANGT CACCGAGCTC 120  
CCAGCCTGCA GCCAGTNTGG AGGCCAAAGG ATATTNNATT TTCANCTTAT GCCAGCNCTG 180  
GTCAGCATGC TCAANAGTGC TANTTTAGGT CTTNCTN 217

SEQ ID NO:239

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00256

SEQUENCE DESCRIPTION:

GATCTCTCTG AGTCCTGGCA ACATCCAGCA AACTACTGC TTATTCTCCA AAGAATATTG 60  
GGAGCTCTCA ATCCTCGGTG ATATGGGAAA GAGAACTGAG TATTTGCCCT ATGACTGAGC 120  
TTTCTATAGG AATTTTATTA AAGAATGTTT AATTNGTTG TCCTNCTNAA TGTTCCTCAGT 180  
CAAATAAATG AGTGAGCTGG TTTCGGCTGC TCTTGGN 217

SEQ ID NO:240

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00257

SEQUENCE DESCRIPTION:

GATCCCATGG ACATTTGGGG AAAGGGCTCC TTGGGCTGCT GGTGAAGTTC TGTGGCCACC 60  
ACCTCCTGCT CTTGACCTCC CTGGGAGGTG CTATCAGTCT GTCCTGGCCT TTCAGTTTTA 120  
TAAGTNGNTT CCAGCCCCAG TGTCTGACT TCTNCTGCAN AATAGGAGGG AGGCCTCCTT 180  
TTNGGANGGN NGTACTTTGG GNGATAGTGN GGCCTN 216

SEQ ID NO:241

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00258

SEQUENCE DESCRIPTION:

GATCTTTTAA GTTTCCTTCC CTACCCAGTC CCCATTTTCT GGTAAGGTTT CTAGGAGGTC 60  
TGTTAGGTGT ACATCCTGCA GCTTATTGGC TTAAAATGTA CTCTCCTTTT ATNTGGTCTC 120  
TTTGGGGCCG ATTNNGNGAA AGCGAAATCA NTAGTGCAAC TGTTTTGATA CTGAATATTG 180  
ACAAGTGTCT NTTNAAATA AAGACCCANT CCCTTCCAAA 220

SEQ ID NO:242

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00259

SEQUENCE DESCRIPTION:

GATCACTAAT CAATAATCTG ATATTTAACA AAATATGGAC AGGCCACTTA TGCTCAGTTT 60

TACCTTAGTT ATTCCTTGGT ATCCACAGGC CCAAGTCCCT TTAAATAAAA TACCCTCATA 120  
 TTTCCATATA ATCTACATAC ATTCTCCCAT ATACTTTAAA TCATCTCTAG ATTACTNATA 180  
 ATGTCTAATN CAAAATAAAT GCTATGTAAA TGTAATTATT AAA 223

SEQ ID NO:243

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00260

SEQUENCE DESCRIPTION:

GATCAACTTA ATTCCTTTTC TTTATCTTCC NTCCCTCACT TCCCTTTTCT CCCACCCTCT 60  
 TTTCCAAGCT GTTTCGCTTT GCAATATATT ACTGNNTAAT NAGTTGCAGG ATAATGCAGT 120  
 CATAACTTGT TTTCTCCNAA GTATTTGAGT TCAAAACGCC NGTATCTAAA GAAATACGGT 180  
 TGGGGTCATT AATAAAGAAA ATCTTTCTAT CTTAAA 216

SEQ ID NO:244

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00261

SEQUENCE DESCRIPTION:

GATCTCAGAA CAATCAGATG CAAAGCTGAA AGAGATTGTA ACAAATTTCT NTGGCTGGAT 60  
 TTGAAGCTTA AACTCCTGTG GATTCACATC ANATACCAGT TCAGTTTGTG CATTGTTCTA 120  
 GTAAATTAGT TCCATTTGTA AAAGGGTTAC TCTCATACTC CTTATGTACA GAAATCACAT 180  
 GAAAAATAAA GGTTCATAA TGCATAGTTA AA 212

SEQ ID NO:245

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00262

SEQUENCE DESCRIPTION:

GATCCATCTG CCTTTGTGGC TGCTGCCCCCT GTGGCTGCTG CCACCAACAG CTGCTCCTGC 60  
 TGCTGCTGCA GCCCAGCTAA GGTTGAAGCC AAGAAAGAGT CGGAGGAGTC GGACGAGGAT 120  
 ATGGGATTTG GTCTCTTTGA CTAATCACCA AAAAGCAACC AACTTAGCCA GTTTTATTTG 180  
 CAAAACAAGG AAATAAAGGC TTACTTCTTT AAAAAGTCAA A 221

SEQ ID NO:246

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00263

SEQUENCE DESCRIPTION:

GATCCCATTG GAAGGAATGC TCTACCTCAC AGAACTCTGA ACCCTACAGA AATATGGGCC 60  
 TGCTGCCATT TCCTGAAGAC CGGGGCATCG GGGTGGGGTG ATAAAGGATA CAACCTGCAC 120



AGGGGGAAGT TATTAAAGAG GCTGCAAAGT CCAGCCACCC TGAAGATACT CCCCAGTGCT 180  
CCCCTCCTGC TAAAGAACCA GTTACCCAG GAAA 214

5

SEQ ID NO:247  
SEQUENCE LENGTH:208  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS00264

SEQUENCE DESCRIPTION:

15

GATCCTCAAC TATTGGAAAT NATGGACTGG TGGCCCTGGT ACAGAACCAT GACTGGCTGC 60  
TGAATTCTGA AAACCAGGAC TTGGTTCAAC ATTTAAATTT GATAGTTGCC CTGATTCCCA 120  
TTTTGGGTTT GTGAAAAGTG TATGTATTTA AATTTGCTGT AAAACATAAT CACTAATAAT 180  
ATGCAATAAA TATTCCTTG AAGGGAAA 208

SEQ ID NO:248  
SEQUENCE LENGTH:208  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS00265

SEQUENCE DESCRIPTION:

25

GATCTGTGGG AGGAATGGCA AGAGAAGCAA CCGGACCCTG AGAGAAGAGT GTTAAGGAAC 60  
CTGCGCATGT GGTTAGCTTG ACCTTTCTGT TGGGCATGAC ATGGGGTTTT GCATTCTTTG 120  
CCTGGGGACC NTTAAATATC CCCTTCATGT ACCTCTTCTC CATCTTCAN TTCATTACAA 180  
GGTAAGATAA ATTGTACATG AATAGTCN 208

30

SEQ ID NO:249  
SEQUENCE LENGTH:201  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

35

CLONE:HUMGS00266

SEQUENCE DESCRIPTION:

40

GATCAAATAT CACTAAATAC TTAAATTTGT TTTACTTAAG AGTCTAATCT GGGAAGTTTT 60  
CAAATCATAC TATTAATGTG TAATCTAAGC TCTTCAGATG TATCCATGAA TAATCCTGGA 120  
ACAATATTGC TTGTATTCCT GTCATAGAAC AGGTTTTGTA ATCTTTAAAA GAAATGAAAA 180  
TTTATATAAT AAAGTTTCAA A 201

SEQ ID NO:250  
SEQUENCE LENGTH:211  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

45

CLONE:HUMGS00267

SEQUENCE DESCRIPTION:

50

GATCACCTTG GTGTTCTTG TTTGGAAGAT TATTCCTCT GAATTTCTGG GCTTGGTCTT 60  
CCAGTTGGCA TTGCTTGAA GTTGATTGA AACAATTTAN TGAAAATATT AAATATTTGG 120  
TTTCAAAAGG CAGATTTATC TTCTCCCAAC ATTCTGTTAT TTCTGATACT TTTGAAAAAC 180

55

TAATAAAAAAT TAATAAAAGA CATGAACTAA A

211

SEQ ID NO:251

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00268

SEQUENCE DESCRIPTION:

GATCCAAGAA AACGCCTCAC TGCCTTAACC TTAAGTGTTC TTCCTGGCGC TAAAAAGAGC 60  
 TGTATTTTTT AAAGTGTCTGG GGCAAACAAA GNANCCCCAA AAGAGTTGAT GTGTGTTTTA 120  
 AAAGNAAAAA CCCAATGAGG AACAATTGGA GATTTTTATG CAGAACTAA ATAATCCTTA 180  
 ATAAATAAAT CTCTATTTTG GAATCAAA 208

SEQ ID NO:252

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00269

SEQUENCE DESCRIPTION:

GATCTTCTAA AAAAGGAACA GAAAATGGTG TGAATGGAAC ATTAAGTCA AATGTAGCAG 60  
 ACTCTCCCG GAATAAAAAA GAGAAATCTT CATAATGAAT TATAANCTAA TTGATTAATG 120  
 TCCCCAAAGA AATCTGCTTT CTACTATATC TTTCAGCATT AGAGATTTTC CTGTTCTNGA 180  
 AAATNCAGTC TGTGCTCTTT GATTN 205

SEQ ID NO:253

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00270

SEQUENCE DESCRIPTION:

GATCTAGGCA AAGAAGAATA CAAATNAAAC CCCNTTCTTT CTCGTTTCN GTCCAACAAC 60  
 TCTGTAGAGC TCTCTGCACC CGTTACCCCT TTCCACCTTT TGTATTTAAT TTAAAGTCA 120  
 NGTGTACNTG CAAGGAATGC TGGATGCAAG ATAGATACTA TATTAACTG TACTGTTATT 180  
 TAAGATGTAA TAAAGCAGTT TGACATGAGA AA 212

SEQ ID NO:254

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00271

SEQUENCE DESCRIPTION:

GATCTAAGAT GATTATTTTG TAAAAGACTT TCTAGTGTAC AAGACACCAT TGTGTCCAAC 60  
 TGTATATAGC TGCCAATTAG TTTTCTTTGT TTTTACTTTG TCCTTTGCTA TCTGTGTTAT 120  
 GACTCAATGT GGATTGTTT ATACACATTT TATTTGTATC ATTTTCATGTT AAACCTCAA 180  
 TAAATGCTTC CTTATGTGAA AAAAACAAA 209

EP 0 679 716 A1

SEQ ID NO:255

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00272

SEQUENCE DESCRIPTION:

GATCTGCCAG CAGTGTTCCTT GCAATATGAG GAAGACAGTT ACAGCCACAT TATGGCTCTC 60  
ATTGAACAGT ACGCAGCACC CCTGCCCCCA GCCGTCTTTC TGGGGCTTGC GCGCAAAATC 120  
TACAAGCGGA GAAAGTGACC TAGAGATTGC AAGGGCGGGG AGAGGAGGCT CTCAATAAAT 180  
AATCGTGTA CTTAAA 197

SEQ ID NO:256

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00273

SEQUENCE DESCRIPTION:

GATCTATCAC CTGTAATCAT AACTGGCTTC TGCTTGTAAT CCACACAACA CCAGGACTTA 60  
AGACAAATGG GACTNATGTC ATCTTGAGCT CTTCAATTTAT NTTAACTGTA ATTTATTTGG 120  
AGTGGAGGCA TTGTTTNA AAAAAACATG TCATGTAGGT TGTCTAAAAA TAAAATGCAT 180  
TTAACTCAT TTGAAA 196

SEQ ID NO:257

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00274

SEQUENCE DESCRIPTION:

GATCTCACCA GGAGAAATGA ATATGTGAGG TGATGGATGT AACTAGCTTG ATTGTGGTAA 60  
TCAATTTTCGC AATGTGTACA TATATCAAAA CATCACATTG TACAAAATAC ATACAGTTTT 120  
TGTCATTTA AAGATATCAG AATTCTAGAA TATGATAAAG TTGTGTTTTT AAGCAAGTAA 180  
AGATAGNTTA CTTAAA 196

SEQ ID NO:258

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00275

SEQUENCE DESCRIPTION:

GATCAGATTT TNCATTTTNN AATGTTCCGT GTTTTCTTAA GTAGCATGTA TGACATTTAT 60  
AATNTTAAAA AATNTTTTAA AATATGTGTA TGATACATAT TTTCNATTGT CTTAGGGCAG 120  
GCTTTTGAAA ATNTCAGCCT GTAGCCAAAT GCAAGATTTT CTCCATCCTT TAATAAAAAG 180  
CACACTGAGA AATCCTN 197

SEQ ID NO:259

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00276

SEQUENCE DESCRIPTION:

GATCTCTGTC TTGAGTTTCT CCTTCCCAT CAGCTGAAGC ACTCTTCAGA GACTACGTCC 60  
ACAGACACTG ATGCTGAGGC CTCCCTGGAG GAAGGAGGGT TAGGGGTGCC TATCCTCAAG 120  
TATTGGAAGA GCAGAATTGA GGGAGAGACC TTTCTTCCTT GTTGAGGGTG AAAAATAAAT 180  
ANGAATTACA TGTCTAAA 199

SEQ ID NO:260

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00277

SEQUENCE DESCRIPTION:

GATCAAGAAG GCTGGAACGG AACTGGTTAA CTTCTTGAGC TATTTCTGGG AACTTGGAAC 60  
ACAGCCTGCC ACCCAGTGAA GTGTCCAGAC CATTGTCTTC CAACCCAGC TGGCCTCTAG 120  
AACACCCACT GGCCAGTCCT AGAGCTCCTG TCCCTACCCA CTCTTTGCTA CAATAAATGC 180  
TGAATGAATC CNNNAAA 197

SEQ ID NO:261

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00278

SEQUENCE DESCRIPTION:

GATCTGAGTC AGTCGGAATT TGTGAAACAG GGTAGCAAAC AAGATATTTT ACTTCCATGT 60  
ATACAATAAT TTTTAAAN NNTGCAATTT GCGTTGCAGC AATCAGTGTT AAATCATTTG 120  
CATAAGATTT AACAGCATTT TTTATAATGA ATGTAAACAT TTAACTTAA TGGTACTTAA 180  
AATAATTTAA AAGGN 195

SEQ ID NO:262

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00279

SEQUENCE DESCRIPTION:

GATCTAGTGT AATGGAAGAC CTTTGAGAAC CTGGGTGTAT TAACTTTGTG TATATAGTGT 60  
AAATATCCCC ACTGTACTGT TAGAGGCCAA CAATTCTAGT ATGGCTTGTT GGCAAAGAGT 120  
GCTACACCGT TTCAATGAAA CAATGTATGT TTGTTTAAAC TGAATAAAA TAAATACATG 180  
CTTAATCCTG AAA 193

SEQ ID NO:263

EP 0 679 716 A1

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00280

SEQUENCE DESCRIPTION:

GATCCCTGGG ACCAACCGCA TCCTCAGCTT CTTCCCCGAG AAATGCTGGA GCAGGCTGTT 60  
CAGACCGACG TTGCCATCAA AACACATACA CCCAGAAAGA AACAACAGAA ACCAAAACTC 120  
ACAAGGCGCA TGATTACTTG TTTTATATTT CATGTTGGGT TTTCCCTCCC ACTATTAAAC 180  
AGTCTGTTTC CGTAAA 196

SEQ ID NO:264

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00281

SEQUENCE DESCRIPTION:

GATCTGTTAA AAAAGAAATC TGTTCACAA GATGACCGTG TACAATACCG TGTGGTGAAA 60  
ATGAATTCAG ACTTATTAAA TGATGAACCT GTTAAATCTN CTCAGTGTCT ATTTATCAGC 120  
ACAATACACA CAGGAGANCT GTTGATGGCA TATTGAATAG ATTTNCCTGA ATAANTTGCT 180  
CTGGAACCA AA 192

SEQ ID NO:265

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00282

SEQUENCE DESCRIPTION:

GATCCTCGTC TTACAGCGAA TGGTTTCAAG ATAAAATTGA TACCAGGAGT TTCAATTACT 60  
GAAAATTACT TGGAAATAGA AGGAATGGCT AATTGTNTCC CATTCTATGG AGTAGCAGAT 120  
TTAAAAGAAA TNCTTAATGC TATATTAANC AGAAATGCAA AGGNNGTTA TGANTGTNGA 180  
CCTCGCANN 189

SEQ ID NO:266

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00283

SEQUENCE DESCRIPTION:

GATCTTTTGT ACTTTAGGAC ATTAAATTGT ACAACTTTTG TATATATAAA AGCTTAGGAA 60  
CTTTCTGTTT AGCAGGAAGG CAACACATTC CTACACTTTT AATGTATATG TTTGTTATAA 120  
TGTCCATGTA AACATGCCCT ATGTTTGTC CTTTAAATTA GTTGTCTCA ATAAACAAAA 180  
TG TAGAGN 188

SEQ ID NO:267

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00284

SEQUENCE DESCRIPTION:

GATCCTGAGA ACTTGAATT CCTTGTAAGT GGAGCTCGGA GCTGCACCGA GGGCAACCAG 60  
 GACAGCTGTG TGTGCAGACC TCATGTGTTG GGTTCCTCTCC CCTCCTTCCT GTTCCTCTTA 120  
 TATACCAGTT TATCCCCATT CTTTTTTTTT TCTTACTCCA AAATAAATCA NGGCTGCAAT 180  
 GCAGCTGGTG CTGTTTCAGAT TCTAAA 206

SEQ ID NO:268

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00285

SEQUENCE DESCRIPTION:

GATCAGAAAA AGAAAGAAGC CAAAGAGAAA GGTACCTGGG TTCAACTAAA GCGCCANCCT 60  
 GCTCCACCCA GAGAAGCACA CTTTGTGAGA ACCAATGGGA AGGAGCCTGA GCTGCTGGAA 120  
 CCTATTCCCT ATGAATTCAT GGCATAATAG GTGTTAAAAA AAAAANTAAA GGGCCCTCTG 180  
 GGGCTACAAA 190

SEQ ID NO:269

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00286

SEQUENCE DESCRIPTION:

GATCAAGATA TTAAAATNTC GGATTTATCT TTCCCATAT CCAAGTACCA ATNCTGTTGT 60  
 AAACAACGTG TATAGTGCCT AAAATTGTAT GAAAATCCTT TTAACCATT TAACCTAGAT 120  
 GTTTAACAAA TCTAATCTCT TATTCTAATA AATATACTAT GAAATAAAAA AAANNGNTTG 180  
 AAAGCTAAA 189

SEQ ID NO:270

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00287

SEQUENCE DESCRIPTION:

GATCTTGTGT ATTGAGCTTA TTGTTGAAAG GGATTTTGA AGGACAGAAC AATTACTGCA 60  
 TGATGAATCT TCCTNTCTCT GCCTTCTGAG CACCGNCTTT AATTTCCATA TCTTCAAGTC 120  
 TTGAAGAAGT TGATGTAAAT TGAAGAATTC ACTTGTCTGG TTGAAATAAA GCCTGTTTCT 180  
 GTTGTGAAA 189

SEQ ID NO:271

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00288

SEQUENCE DESCRIPTION:

GATCTGATTT GCTAGTTCTT CCTTGTGAGA GTTATAAACT GAGAGTGACG TCACTTCAGC 60  
CAGAACATAT TCTCCATACT CTGCATATAA TTTGTGGCTG CAGAATATTG TAATTTGTTG 120  
CACACTATGT AACAAAACAA CTGAAGATAT GTTAAATAAA TATTGTACTT ATTGGAAGTA 180  
ATATCN 186

SEQ ID NO:272

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00289

SEQUENCE DESCRIPTION:

GATCTAAAAT GTCAGCATCA TGCAAAGTGC ACGATATATA GTGAATTTNG CTCTAAAAGA 60  
GCATGAACAA GTCTTTCTAA TGTTTTGTAC AGTGCCTGGC ACTCTGTGGG TGCTCAATAA 120  
ATGGATAGGA GTTTTCATTT GAAGGATATT TGAATTTTAA AAATAAAGTG TTTTATTCCC 180  
NTAAA 185

SEQ ID NO:273

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00290

SEQUENCE DESCRIPTION:

GATCTGGTCA CTGTGGTTCC TGCATGAAGA CAGTGGCTGG CGGTGCCTGG ACGTACAATA 60  
CCACTTCCGC TGTCACGGTA AAGTCCGCCA TCAGAAGACT GAAGGAGTTG AAAGACCAGT 120  
AGACGCTCCT CTACTCTTTG AGACATCACT GGCCTATAAT AAATGGGTAA ATTTATGTAA 180  
CAAA 184

SEQ ID NO:274

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00291

SEQUENCE DESCRIPTION:

GATCTGATTT GCTAGTTCTT CCTTGTAGAG TTATAAATGG AAANATTACA CTATCTGATT 60  
AATAGTTTCT TNATACTCTG CATATAATTT NTGGCTGCAG AATATTGTAA TTTGTTGCAC 120  
ACTATGTAAC AAAACAACCTG AAGATATGTT TAATNNATAT TGTACTTATT GGAAGTAATA 180  
TCAAA 185

SEQ ID NO:275

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS00292

SEQUENCE DESCRIPTION:

GATCAAAGAC ATCCTCATCC AGTATGACCG GACCCTGCTG GTAGCTGACC CTCGTCGCTG 60  
 CGAGTCCAAA AAGTTTGGAG GCCCTGGTGC CCGCGCTCGC TACCAGAAAT CCTACCGATA 120  
 AGCCCATCGT GACTCAAAAC TCACCTGTAT AATAAACAGT TTTTGAGGGA TTTTAAAGTT 180  
 TCAAGAAA 188

SEQ ID NO:276

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00293

SEQUENCE DESCRIPTION:

GATCGGGNTA CTACAAAGTT CTGGGAAAGG GAAAGCTCCC AAAGCAGCCT NGTCATCGTG 60  
 AAGGCCAAAT NCTTCAGCAG AAGAGCTGAG GAGAAGATTA AGAGTGTTGG GGGGGCCTGT 120  
 NTCCTGGTGG CTTGAAGCCA CATGGAGGGN GTTTCATTAA ATGCTAACTA CTTTNCCTA 180  
 AA 182

SEQ ID NO:277

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00294

SEQUENCE DESCRIPTION:

GATCCAGCCA GAGGATGCCA CGCCAGCCCA GCGCTACCAG GCTGCCCAAG GGGGGCGGGC 60  
 CTGGGAAGAG CCCTACACGG GGCAGCACCT AGGATGGGGC AGAGACTTGT TGCATCTTTG 120  
 TCCCCAGCAA AGGCTACATG TTACCTCCTT CAATTGATAA TAAACCTTTC TGAGATGCAG 180  
 AGGGTCCAGG TCAA 195

SEQ ID NO:278

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00295

SEQUENCE DESCRIPTION:

GATCCCATTA ACTCGATGCT GAGTATCTAC ATGGATACAT TAAATATATT TATGCGAGTT 60  
 GCAACTATGC TGGCAACTGG AGGCAACAGA AAGAAATNAA GTGACTCAGC TTCTGGCTTC 120  
 TCTGCTACAT CAAATATCTT GTTTAATGGG GCAGATATGC ATTAAATAGT TTGTACAAGC 180  
 AGCTTTCGTT GAAGTTTAGA AGATAAGAAA CATGTCATCA TATTTAAATG TTCCGGTAAT 240  
 GTGATGCCTC AGNTCTGCCT TTTTTTCTGG AGAATAAATG CAGTAATCCT CTCCCCAAAA 300  
 AAAAAAAAAAN NNNNNNTNN NNNNNN 327

SEQ ID NO:279

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid



TOPOLOGY:linear

CLONE:HUMGS00296

SEQUENCE DESCRIPTION:

GATCCAAATC CTCATCTTAC TTTCCCGACC TTAAGGATGT AGCTGCTGCT TGTCTGTTC 60  
AAGTTGCTGG AGCAGGGGTC ATGTGAGGCC AGGCCTGTAG CTCCTACCTG GGGCCTATTT 120  
CTACTTTTCAT TTTGTATTTT TGGTCTGTGA AAATGATTTA ATAAAGGGAA CTGACTTTGG 180  
AAA 183

SEQ ID NO:280

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00297

SEQUENCE DESCRIPTION:

GATCAAAGTG GCTGCAGCAG AGTTAGCTGT CTAGCGCCTA GCAAGGTGCC TTTGTACCTC 60  
AGGTGTTTTA GGTGTGAGAT GTTTCAGTGA ACCAAAGTTC TGATACCTTG TTTACATGTT 120  
TGTTTTTATG GCATTTCTAT CTATTGTGGC TTTACCAAAA AATAAAATGT CCCTACCAGN 180

SEQ ID NO:281

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00298

SEQUENCE DESCRIPTION:

GATCACATGA TTTTGTCTCT CAGTTCTATT AATGTTCTTG GATTCTGTTC AATGTTCTGT 60  
TCACATTGCA GAAAAAGCAT TTGACAAAAT AATTTAGTA GCTGCTGAAA AAGCATTTGA 120  
TAAATTCAG CATACCTTTA TGATACAAAA AACCTTCAAT AACTGGGTA TATATGNACN 180

SEQ ID NO:282

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00299

SEQUENCE DESCRIPTION:

GATCTTGAAT TATTTATAAA CTGGAAAGTG GTTTGATTAT TGTGAGTCAA AACTCTAAGT 60  
GGTTAAAAAT TAGTATGAAT TTTTGTGCTT CTTAATGAAT ATGGATTAA AACTCTCCAG 120  
TTCTTATTTT ATGAAATGAC TTGCCTTTCT GGTAATACAA TGCTGATTTT TTAGTAAA 178

SEQ ID NO:283

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00300

SEQUENCE DESCRIPTION:

GATCCCAAAT ATGAAGTCAT CGAAAAACCC CAGGCCTGAA GAAATAAAGT AAAAATNAAT 60

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CTGGTAATTT GTCACGGATT AGTTGTACAA CTAGTTAGAA GTTTCAGAAT AAACATGCAT 120  
TTCATAACTG TCAAATGTTT TTTTAATTCT GAGTCCAAAT AAATTATTTG GTGATGTTGA 180  
AA 182

SEQ ID NO:284

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00301

SEQUENCE DESCRIPTION:

GATCTCTGAG TGAGAGGGAA ANAGGTCAGA TTTATACAAC TGAGCGCCAG AGGGGAAAAAT 60  
GCACCTTGTT GGAGTGAGAA ATGTTCTGAA ACTGAATTAC TTCTTGTA GCTGAGATAG 120  
CTTCTTCTGA ACTATTATTA AATAAGTGAA TACAAAGGCC CTATGATGGG AAATCCAGN 179

SEQ ID NO:285

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00302

SEQUENCE DESCRIPTION:

GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG CTGTGGACCG GGATGCAGTN 60  
TCAGGCATGG GAGTCATTGT CCACATCATC GAGAAGGACA AAATCACCAC CAGGACACTG 120  
AAGGCCCGAA TGGACTAACC CTGTTCCCAG AGNCCACTTT TTTTCTNTT TTTGANATAA 180  
AATAGCCTGT CTTCAANAA A 201

SEQ ID NO:286

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00303

SEQUENCE DESCRIPTION:

GATCGGAGAT GCTTTGTAAT CTA CTGTCCA GCTGGAACA GCTCATGTTA CGCGGAAAAA 60  
ACTACAAGTA ATGTTCAAAT CTATTTTGGG TCATTTTAT GTACCTTTGG GTTCAGGCAT 120  
TATTTGGGGG GTTTTGTTC CAAAGGAAC AAATAAAGTC ATATTGCTTA TAGAAA 176

SEQ ID NO:287

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00304

SEQUENCE DESCRIPTION:

GATCTTTGCT GGGAAACAGC TGTGAAGATG GACGCACCCT GTCTGACTAC AACATCCAGA 60  
AAGAGTCCAC TCTGCACTTG GTCCTGCGCT TGAGGGGGGG TGTCTAAGTT TCCCCTTTTA 120  
AGGTTTCAAC AAATTTTATT GCACTTTCCT TTCAATAAAG TTGTTGCATT CCCAAA 176

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SEQ ID NO:288

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00305

SEQUENCE DESCRIPTION:

GATCCGCAAG ACCAAGTACC GCCCCGACCT GCGCATGGCA GCCATCCGCA GGCCAGCNTC 60  
ATCCTGCGCA NCAGAAGCCT GTAATNGTGA AGAGGAAGCG GACCCGACCC ACCAAGAGCT 120  
CCTGAGCCCC CTGCCCCCAG AGCAATAAAG TCAGCTGGCT TTCTNACCTG AAGAAA 176

SEQ ID NO:289

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00306

SEQUENCE DESCRIPTION:

GATCTCAAAA CACAGTGAGA GGTCTGAAGG CTGGCTTCTG AAGAATCCCT GATGTCTTAT 60  
TGGAACAACC ACTGAGCTAC GGAGAGCTCT GCTGTGATGG GCTAGGCACT TTATATCTGT 120  
GTGAATACAG ATTTATAAAA CAGGTTAATA AACTTATCCA AGGTCACATT TCAAA 175

SEQ ID NO:290

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00307

SEQUENCE DESCRIPTION:

GATCTGAATT CTTTATGTAT ATTTGTAGCT ATATTTTATA CAAAGTGCTT TAAGTGTGGA 60  
GAGTCAATTA AACACCTTTA CTCTTAGAAA TACGGATTCT GCAGCCTTCA GTGAATATTG 120  
GTTTCTCTTT GGTATGTCAA TAAAAGTTTA TCCGTATGTC AGAAA 165

SEQ ID NO:291

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00308

SEQUENCE DESCRIPTION:

GATCATTCCT TCTGTAGCTC AGGAGAGCAC CCCTCCACCC CATTTGCTCG CAGTATCCTA 60  
GAATCTTTGT GCTCTCGCTG CAGTTCCTT TGGGTTCCAT GTTTTCCTTG TTCCCTNCCA 120  
TGCCTAGCTG GNTTGCAGAG TTAAGTTTAT GATTATGAAA TAAAAAATA ACTGACAATT 180  
NTCAAA 186

SEQ ID NO:292

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00309

SEQUENCE DESCRIPTION:

5 GATCTGTAG AAAATTTTGA TGAGGCATCA AAGAATGAAG CTAACATAAA GTTTGGTTTT 60  
 TGGAAGCTGG CATGGACTAG ATTTAACAAA TCAGCTATGT GGTTCCAAAG TTTTACAGAC 120  
 ATGGAGAACA TCACCTGTGA CTAGTTCAGT AATATAAATA TTTTGTATAT TAATN 175

SEQ ID NO:293

SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00310

SEQUENCE DESCRIPTION:

15 GATCAGATTA CCAGGAACAT CAGGAGTGGA TTCCTGCCCC AACCAAACCG CATTTCGTGTG 60  
 GATTTTTTTA TTCAACTTAA TTGGCTATTC CAAAGATTTT TTTTTCCTA TTTTGTACGA 120  
 TTGGNGCCCT TAAGATGCAC GATGGAATTG TGTTTTNCGT TTTTNGGTAA AAGGAGCAAA 180  
 20 GCGNGGNCCT GGAGATAAAC GCTGGAGCAA TCTCCTTGGA AGGATTCAGC ACGAGTAGAT 240  
 GGTAAACATT TAAAGGGGAA AGGGGGGTTT GTTTAAAATA GTAAATCAGT AAGTCACTTC 300  
 TAAATTTAAA GAAACCAAAA TTGGGAGTTG AAGAATAAGT AGGGTTTCCA ATTGGGCTAT 360  
 TGCCGNTTIN CTTTGNAAAA ATTAACCAT TNTTTAAAAA CCTAAA 406

SEQ ID NO:294

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00311

SEQUENCE DESCRIPTION:

30 GATCCCATAG ACCAGAGCCC ACCTTTTNA TAAACTTAGT AAAGTCTTNG AGACTAGAAG 60  
 CAAGATAGTT TGTGACACAT AAGCTTCCCA AAAACTNGAA TAGATTTTNA CTGAATAGTG 120  
 GTCTATCTGA TGGTATATGT TTCTTAAAGG TCCAANTGTA ATAAAAAAA TTGAAAAANA 180  
 35 GGTCTCAGTG TTTNAATGC ACTNCATATT TGTNTGCN 218

SEQ ID NO:295

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00312

SEQUENCE DESCRIPTION:

45 GATCCACCAA GCACGCCTAT NAATACAAAG TAACTATNA TTTTNATTGT GAAATTTTCA 60  
 TAGATGGAAA ATTGAATATN CTGTCCATTT CATTTTACAA TNATCTTACC ACTTATTTT 120  
 GTACCATGTA TTTCAATTGC CTGTTTAGTG AAAAAATAAA ATTAAAAAAA CCTAAA 176

SEQ ID NO:296

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00313

SEQUENCE DESCRIPTION:

5 GATCCCAGCA AGATAATGTC CTGTCTTCTA AGATGTGCAT CAAGCCTGGT ACATACTGAA 60  
 AACCCCTATAA GGCCTGGAT AATTTTGTGTT TGATTATTCA TTGAAGAAAC ATTTATTTTC 120  
 CAATTGTGTG AAGTTTTTGA CTGTTAATAA AAGAATCTGT CAACCATCTA AA 172

SEQ ID NO:297

10 SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00314

15 SEQUENCE DESCRIPTION:

GATCGGTGAC ATCGTCAAGA TGGGCGAGTG CCGGCCTCTG AGCAAGACAG TCGGCTTCAA 60  
 CGTGCTCAAG GTCACCAAGG CTGCCGGCAC CAAGAAGCAG TTCCAGAAGT TCTGAGGCTG 120  
 GACATCGGCC CGCTCCCCAC AATGAAATAA AGTTATTTTC TCATTCCAG AAA 173

20 SEQ ID NO:298

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00315

25 SEQUENCE DESCRIPTION:

GATCGTTTCC AGATGAGAAT TCACAAGCGA CTCATTGACT TGCACAGTCC TTCTGAGATN 60  
 TGTTAAGCAG ATTACTTCCA TCAGTATTGA GCCAGGAGTT GAGGTGGAAG TCACCATTGC 120  
 AGATGCTTAA GTCAACTATT TTAATAAATT GATGACCAGT TGTAAA 167

30 SEQ ID NO:299

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00316

35 SEQUENCE DESCRIPTION:

40 GATCTGGTGG TGGAAGTGGT GGATATGGTA GCAGAAGGTT CTAAAAACAG CAGAAAAGGG 60  
 TTGAATGAGA ACCCTACTTG CCTAAATNAG GAATGTCTTT CCTACCATCT AAAATACGAA 120  
 GGTTCCTGGC TGGGTAAGGT TTGTAGTTGA CAGTAAAACC TGATGACACC N 171

SEQ ID NO:300

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00317

SEQUENCE DESCRIPTION:

50 GATCCGAGTG TGATTTGAAT TCTGTGATAT TTTCACACTG GTAAATGTTA CCTCTATTTT 60  
 ACTTACTGCT ATAAATAGGT TTATATTATT GATTCACCTA CTGACTTTGC ATTTTCGTTT 120  
 TTAAAGGAT GTATAAATTT TTACCTGTTT AAATAAAATT TAATTTCAAA TGTAAG 176

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SEQ ID NO:301

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00320

SEQUENCE DESCRIPTION:

GATCTTTGTT TTGTGTTTAA CCATAATGGT TGTGTACTGA ACCACTTCAT ATTTGTAATA 60  
TATAATATAT ATATATNNGN TNCCCTNAAG ACTCAGCCTC CTGGTTTACC CCCCCGGCCT 120  
GGGCATCTNA CCTCCCCAC CCCAGTGTGA TTAAACATCC NGGNACTGN 169

SEQ ID NO:302

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00322

SEQUENCE DESCRIPTION:

GATCTAGCTC TGAATGTATG TTTCTGACG TTTTACATTT CCACTTTCCT ATTCCATTCA 60  
TTAAGCTAGC CAACAATCCA CCATCCTTTA AAGATTGTTC TCATAACTGA AAAAAACCA 120  
CATAATCTAA ATAGAGCAA GCTACAAGAA ATAAATTTAT TTAAACGCAA GAAA 174

SEQ ID NO:303

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00323

SEQUENCE DESCRIPTION:

GATCCTAGCA TATGTTAAAA TTCAAATTAA TGTA AACAG ATTAACAACA ACAAAGAAAC 60  
TGTCTATTG AGTGAAGTCA TGCTTTCTAT TATAATACT TGGCTTCGGT TATCCATCAA 120  
ATGCACACNN ATACTGTTAT CTGATTGTTT ATAATAAAGA ATACTGTACC TNNTAAA 177

SEQ ID NO:304

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00325

SEQUENCE DESCRIPTION:

GATCAGATGG TTTTAGTATT GTGGCAGAAG CGAGAAAAC TGTGTTATTG AAAAAAAAAAG 60  
AAAAAGAAAG CAAGAAAAAA AGATACTATG GGGTCAAGTG TAACTCCATG GAAATGCCAC 120  
GTCTGCTCTT CAGTGAAGAA GCTGGTTTAG AGTCTCACAG AAAACTN 167

SEQ ID NO:305

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00327

SEQUENCE DESCRIPTION:

GATCGCTCAC AATNTTTCCT CCAAGAACCG CAAAGCCATC GTGGAAAGAG CTGCCCAACT 60  
 GGCCATCANA GTCACCAACC CCAATNCCAG GCTGCGCAGT GAAGAAAATA AGTAGGCAGC 120  
 TCATGTGCAC ATTTTCTGTT TAAATAAATG TAAAAACTGC CATCTGGAAG 170

SEQ ID NO:306

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00328

SEQUENCE DESCRIPTION:

GATCGGGAAT GGTCTGTGTG TTATCAGCTG CGACTGGTTC ACTGCGNCTT AGACAAGCCT 60  
 CATGGGGACT GGGGATTCTG GCCAGTGTA TTTCTGTCAA CCACGGACGT TTGCCTTCAT 120  
 GTGTAGAATT TACTGTTGTT ATGCAAATTA TATTTTCAAT TATAAATGAA A 171

SEQ ID NO:307

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00329

SEQUENCE DESCRIPTION:

GATCAGACAG AATAATATTT NCTAGTTATT ATGTGTAAGA TGAGTTGCTA TTTTCCTAAT 60  
 GCTCATTCTG ATACAACTAT TTTCCGTGTC AAATATCTAC TGTGCCCAA TGTACTCAAT 120  
 TTAATCATT ACTCTGTAAA ATAAATAAGC AGATGATTCT TAAA 164

SEQ ID NO:308

SEQUENCE LENGTH:261

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00330

SEQUENCE DESCRIPTION:

GATCCCCGCC CTGGGGTCTG GTCCTCGCCC ATCCTGCAGG GATTGCCAC CGTCTTCCAG 60  
 ACACCCACC TGAGGGGGGC ACCAGGTTTA GTGCTGCTGC TTTCCTGNT GCACCCGCGC 120  
 CCTCGGCCGG CCCCCGAGC AGCCTTTGTA CTCTGCTTGC GGAGGGCTGG GAGACCCTCC 180  
 AGGACATTCC CACNNTCNCC CATGCTGCCA AGTTNNNNCT ATAGCTACAA ATAAAAAAAAA 240  
 ACCTTGTTTT CAAGAAATAA A 261

SEQ ID NO:309

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00331

SEQUENCE DESCRIPTION:

GATCGAGTCA AGATGAGTTA GTGGAGCTGG GCTTGCCAG GGAGTCTGGG GACAAGGAAG 60

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CAGATTTTCC TGATTCTGGC TCTAGCTTCC CTGCCAAGAT TTTGGTTTTN ATTTTTTTAT 120  
TTGAACTTTA GTCGTGTAAT AAACCTACCA GTGGCAAACC AAA 163

5 SEQ ID NO:310  
SEQUENCE LENGTH:165  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00332

10 SEQUENCE DESCRIPTION:  
GATCATGCTG CTGTGATACT GAGTTTTCTA AACAGCATAA GGAAGACTTG CTCCCCTGTC 60  
CTATGAAAGA GTATAGTTTT GGAGGGGAGA AGTGGGACAA AAAAGATGCA GTTTTCCTTT 120  
GTATTGGGAA ATGTGAAAAT AAAATTNTCA ACTCTTTCAG TAAA 165

15 SEQ ID NO:311  
SEQUENCE LENGTH:164  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00333

20 SEQUENCE DESCRIPTION:  
GATCTCAGTT TCCTGGCTTT TCCTCCCTCA GCCCCTTCTC ACCCCTTTGC TGTCTGTGT 60  
AGTGATTTGG TGAGAAATCG TTGCTGCACC CTTCCCCAG CACCATTAT GAGTCTCAAG 120  
25 TTTTATTATT GCAATAAAAG TGCTTTATGC CGGCTTTTCT CAAA 164

SEQ ID NO:312  
SEQUENCE LENGTH:337  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00334

30 SEQUENCE DESCRIPTION:  
GATCATTGAA TGTGAGACCC TTCTAACATG ATTTGAGAAG CTGTACAAGT ATAGGCAGAG 60  
35 TTATTTTCCT GTTTACATTT TTTTTTTGTT TTGGGGAAAA AATTGGTAGG TGTCTAATNA 120  
CTGTTTACTT CATTGTTATA TTGCAGTAAA AGTTTTAAAN CANCCATTGC ATGTTNGCTT 180  
TTGATGTATC CCTTTGNGAA ATTAGCACTT TTGGGGCCAN TGGNGAAATG CAGCATTAC 240  
TCTCCCTGTC TTTTCCCCTT CCCTCAGCAG AAACGTGTTT ATCAGCANGT CGTGAGTCAA 300  
40 ACTGCTGCCT TTTAAAAANC CCACAAANTT GNTNNGN 337

SEQ ID NO:313  
SEQUENCE LENGTH:176  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00335

45 SEQUENCE DESCRIPTION:  
GATCCGCCGT CACTGGGGTG GCAATGTCCT GGGTCCTAAG TCTGTGGCTC GTATCGCCAA 60  
50 GCTCGAAAAG GCAAAGGCTA AAGAACTG CACTAACTG GGTAAATGT AACTGTTGA 120  
GTTTCTGTA CATAAAATA ATTGAAATAA TACAAATTTT CCTTCAGCCA GTGAAA 176

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SEQ ID NO:314

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00336

SEQUENCE DESCRIPTION:

GATCACCTCT GAGACCCACC TTGCTCATAA ACAAATGCC CATGTTGGTC CTCTGCCCTG 60  
GACCTGTGAC ATTCTGGACT ATTNNTGTGT TTATTGTGG CCGAGTGTA CAACCATATA 120  
ATAAATCACC TCTCCGCTG TTTTAGCTGA AGNATTANGN CATCTTGTCT ATTAAA 176

SEQ ID NO:315

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00337

SEQUENCE DESCRIPTION:

GATCATATTT AATGAATTAT AGTATAATGC TTGCAGGCC AGTACAAGCA TATATATNGT 60  
GCCTCTTACA GCCTTTGGAA TACATTGTTT CCATTTTATA AATATCTTCT ATATCCNNNT 120  
AGTATTCAAA TTATTAATGC TCATGTACCA AGGTNTTGCT ATAAAAGTTT TGTCTGTATG 180  
AATAATGTGG CTTTAGTAAA TAATCATTTN TCAACTGTAA ACTNATTCTG AAATAAAGTA 240  
AAATNCTAAT TGTTTAAA 258

SEQ ID NO:316

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00338

SEQUENCE DESCRIPTION:

GATCTTGGAC ACTTACAGAT TGAGCTGTAT GAATTCAGCG GGTCTCACTC CAGAGGGTCA 60  
GAACGTTTGC TTTAGTTTT TCATCTGTTT TGTCCTTGA GTCAGTGCTG TTGATGATGA 120  
GTTGTCTTGA ATAAATNATG TGTTCTTTGC AAA 153

SEQ ID NO:317

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00339

SEQUENCE DESCRIPTION:

GATCAAAGCT AGAAAATGNA GATTCCTTAG CCTGGATTTC CTTCTAACAT GTTATCAAAT 60  
CTGGGTATCT TTCCAGGCTT CCCTGACTTG CTTTAGTTTT TAAGATTTGT GTTTNCTNT 120  
NTCCACAAGG AATAAATGAG AGGGAATCGA CTGTAAA 157

SEQ ID NO:318

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00340

SEQUENCE DESCRIPTION:

GATCTCCTTA TATAGCAGCC AAAATCAATG AAGCTAAAGA TTTACTAGAA GGTCAAGCTA 60  
 AAAAAATGAAG TAAATGTATG ATGAATTTTA AGTTCGTATT AGTTTATGTA TATGAGTACT 120  
 AAGNNTTTTA TAATAAAATG CCTCAGAGCT ACAATTTTAA A 161

SEQ ID NO:319

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00341

SEQUENCE DESCRIPTION:

GATCTGAAAA CATGTAGAGA AGATGAGTTG AGGACAGCTT TTCTAAGGCA ATGTNATGTC 60  
 TTTCTTTTCT NATTTCTNTT TCTCTGCGTT GTTAGTTTTN AAGAGTGGAG GAGCTAGGGG 120  
 CTCCAGAAAG AATCTTACAC ATGTTTTGAA GACATTGATG TCATAGGGAG CGGGGAGCTG 180  
 CATTCCCTTC TGGGCTGTGA CTGCTAAATC TCAGTATGAA CAGACCAGGC GGAAAGCTTG 240  
 GTGGCCAAGC AGTCTGTGTG CTCCCCGCT GATGGAGAAC GTTGCCTTGT TCACAATAGG 300  
 GCCTCATGGG TGN 313

SEQ ID NO:320

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00342

SEQUENCE DESCRIPTION:

GATCTTGTTT ACAAGTAATC TGTTGACAGT GCCAATAAAT NATAAAAAAA AAATTAACAT 60  
 GTCACAATGT AACGGATGAC CATATGCACA ATTCCATGAA TTAAATCTGT TTCCTGTGTT 120  
 AGTCAGTATT CTTAAATAAA ATTTATAATT GAAACATGAA A 161

SEQ ID NO:321

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00343

SEQUENCE DESCRIPTION:

GATCTATTGA NAGCCCTCTC TCNCATTCTG TAATGAGTAC AGCAGAGACC TTCCTGCTTT 60  
 TAACTGGGGA CTCCAGATTT TCCCCAAACT TGCTTCTGTT GAGATTTTTC CCTCACCTTG 120  
 CCTCTCAGGC ACAATAAATA TAGTTATACC ACTGCCCATC AAA 163

SEQ ID NO:322

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00344

SEQUENCE DESCRIPTION:

5 GATCATCCTA ACAATGTGGG GCTGTAGGT TTTACCTTG ANCTTTCATA GCACTGCAGA 60  
 AACCTTTAAA AAAAAAATGN TNNATGAATT TTTCTTTCC TACAGTTGGG TAGGGTAGGG 120  
 GAAGGNGGNT AAGCTTTTTT TTTNAAATG ACTGAN 156

SEQ ID NO:323

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00346

SEQUENCE DESCRIPTION:

15 GATCATGCTG CCCTGGGACC CAACTGGTAA GATTGGCCCT AAGAAGCCCC TGCCTGACCA 60  
 CGTGAGCATT GTGGAACCCA AAGATGAGAT ACTGCCCACC ACCCCCATCT CAGAACAGAA 120  
 GGGTGGGAAG CCAGAGCCGN CTGCCATGCC CCAGCCAGTC CCCACAGCAT AACAGGGTCT 180  
 20 CCTTGGCAGC TGTATTCTGG AGTCTGGATG TTGCTCTCTA AAGACCTTTA ATAAATTTT 240  
 GTACAAAGGC ACAA 255

SEQ ID NO:324

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00347

SEQUENCE DESCRIPTION:

25 GATCTCTAGT ATAACACTCA GGCTACTGAG GTATTTTAGA GCAACAAGCT GGGTTACTTT 60  
 30 CAGAGCAACC AGCTTGACTG GAACTGAGAG TAAATTGGGA ATGTATGACC AATCTTAGAC 120  
 CCTGAAAAAT GGCAGAAAAT ACATGGAAAT TTGN 154

SEQ ID NO:325

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00348

SEQUENCE DESCRIPTION:

40 GATCTAGGGA AGACAACGTA GTCACCCTCG GTGCTTCCTC TGTCTCCTCT TTCTCCCTGG 60  
 CCTGTGGTTG TCCCCAGCC TCTGCCACCC TCCACCTCCT CGGTCAGCCC CAGCCCCAGG 120  
 TTGATAAATC TATTGATTGA TTGTGATAGT AAA 153

SEQ ID NO:326

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00349

SEQUENCE DESCRIPTION:

50 GATCTCTAAT ATTTTAAAGC CCAAGCCCCT TGGACACTGC AGCTCTTTTC AGTTTTTGCT 60

TATACACAAT TCATTCTTTG CAGCTAATTA AGCCGAAGAA GCCTGGGAAT CAAGTTTGAA 120  
 ACAAAGATTA ATAAAGTTCT TTGCCTAGTA TAAA 154

SEQ ID NO:327

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00350

SEQUENCE DESCRIPTION:

GATCAAATTC TAATGGAATT GAGCCGGTTT CTTATCCTAA ATGTTTCCTC CCTTTTACA 60  
 ATCTCTGTCC AGCACCTCTT GGTAAATAA TGTATGCTGT GAGACATGNA ATTAAACAG 120  
 GCCTATGGAA TAAATTATTT TAAAACCAGN AGGTTAAA 158

SEQ ID NO:328

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00351

SEQUENCE DESCRIPTION:

GATCTTAAAG CAGAATGCCN TTTNCTTTTT TTGCTTCAGT TGTAAGAAG AGGGAATACA 60  
 TGATAAAGTA ACTGGTTTGA TTTCTCGTTC ATTGTACACT GCCTCTGAAC ANCTAATTGT 120  
 TTTTAGTTGT CTAAATAAAA TGCCTCTAAA ACAA 155

SEQ ID NO:329

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00352

SEQUENCE DESCRIPTION:

GATCCAAGAG GAAGAATCCA GCTGCCTATG AAAATAACAA ATNAGCAACG CATCCGGATG 60  
 ACGGTTCCCT GTCTCTGAAA GACCTTCTC TGGAAGAGGA GTCTGCATTG TAGTGTCTCA 120  
 AAGACACAAT AAACCTCCTA TGGTCTGCAC TGTGTGATA TTAAA 165

SEQ ID NO:330

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00353

SEQUENCE DESCRIPTION:

GATCTACTTT GTTTGAGCAA AACAGCATT TTTGTTATGT TAATNATGGT TAATTTCCAT 60  
 TTTATTGGTT TTATGTTTAT TTTAATTTGT AAATGTTTTA GCATTATNA TTGTATGTNA 120  
 NCTATATTN CCTATTTNAT GTTGATAAA 149

SEQ ID NO:331

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00354

SEQUENCE DESCRIPTION:

GATCAAAATG CTAAACATG ATGATTAAGT GCACACCGTG TGCCATAGAA TGGCACATGT 60  
 CATTGCCCAC TTCTGTGTAG ACATGGTTCT GGTTTAACTA ATATTTGTCT GTGTGCTACT 120  
 AACAGATTAT AATAAATTGT CATCAGTGAA A 151

SEQ ID NO:332

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00355

SEQUENCE DESCRIPTION:

GATCTTTGTT CTAGGCAGCT GGAATAGAC ATGGTACTTA CCTTAGAGTT TTCCAATTTA 60  
 TCTCAATTTT ATATGGCTTG TGATTCATTT NCTTAATCCA AATATATATA ANCGTGTGTG 120  
 GTCTNATTCT NCCCCCGCA ANANNAN 147

SEQ ID NO:333

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00356

SEQUENCE DESCRIPTION:

GATCCTTACG GAAAAGGAAC AGATTGTNCC TAAACCAGAN GAGGAGGTTG CCCAGANGAA 60  
 AAAGATATCC CAGANGAAAC TGAAGAAACA AAAACTTATG GCACGGGAGT AAATTCAGCA 120  
 TTAAAATAAA TGTAATTAAA AGGAAAAGAA A 151

SEQ ID NO:334

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00357

SEQUENCE DESCRIPTION:

GATCTTTGCA GTAATTTCTA GGAGCTGTTT ATGTTTGGAG GTAATTGGTC CTTTGTCCAT 60  
 ATATATGAGA TGTAAGTNTT ATTTTCCAGT TTATCTTTT GCTTATTTT TTTGACTTTT 120  
 TATTGTAAAA TAAACATCA AACTGCACAG AACAGTTGAA TAGCTTAATG AATAACTACA 180  
 GTAAAAGCTA TGGTAACCAC TAAA 204

SEQ ID NO:335

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00358

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCCAATTA ACATGTGGGG TTCTTGGTNT GGGTCTGGGG AGCTGAAGGA TTTNATGGAG 60  
CTGGTGCTTT GGAGGAATCT TAAGGGAAAG NAGTAGAAGC TCAGGCCTTT AAAGGATTC 120  
ANCTCCTCCT CTCTGTAATT NNTNCN 146

SEQ ID NO:336

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00359

SEQUENCE DESCRIPTION:

GATCGCATCT NTTAAACAGG TACAAGTTGA CATGAGGTTA GTTTAATTGT ACACCATGAT 60  
ATTGGTGGTA TTTATGCTGT TAAGTCCAAA CCTTTATCTG TCTGTNATTC TTAATGTTGA 120  
ATAANCTTTG ANTTTTTTCC TTAAAA 146

SEQ ID NO:337

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00360

SEQUENCE DESCRIPTION:

GATCAGTGTT GAAGAAAGTG CAAAAGGAAC TTTTATATAT TTAACAGTGT AGGAAATTGT 60  
CTATTCTGA TATAATTACT GTAGTACTCT TGCTTAAGGC AAGNGTTTCA NATTTACNGT 120  
TGAAATAAAC CCAACTCTTC NTGNAAC 147

SEQ ID NO:338

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00361

SEQUENCE DESCRIPTION:

GATCTNGAAA ATNATCATTG AACATATTAA TGGTTATTC TTTTCTTGG ATTTCCAGAA 60  
AAGCCTCTTA ATTTATGCT TTCTCATCGA AGTAATGTAC CCTTTTTTTC TGAAACTGAA 120  
TTAAATACTC ATTNATCNN NTGNAAC 147

SEQ ID NO:339

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00362

SEQUENCE DESCRIPTION:

GATCAGTTTT TTCACCTGGA AGCATTTGTT TCTACTTTGA TATGACTGTT TTTCGGACAG 60  
TTTATTTGTT GAGAGTGTGA CAAAAGTTA CATGTTTGCA CCTTCTAGT TGAAAATAAA 120  
GTGTATATTT TTCCTATAAA 140

SEQ ID NO:340

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00363

SEQUENCE DESCRIPTION:

GATCTGAACT TTTCATCTGC AGAGGCAAGA AAAATATTTA ACATTGTGAC TTGACTGTGG 60  
AAGATGATGG TTGCATGTTT CTAGTTTGTA TATGTTTCCA TCTTTGTAAT AAGATGATTT 120  
AATAAATCTC TTAAATACT TAAA 144

SEQ ID NO:341

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00364

SEQUENCE DESCRIPTION:

GATCAAAAGC TTATTCATCT GTTTTNCCTT TTCGTTGGTG TAAAGCCAAC ACCCTGTCTA 60  
AAAAACATAA ATTTCTTTAA TCATTTTGCC TCTTTTCTCT GTGCTTCAAT TAATAAAAAA 120  
TGGAAGAAT CTAATAGAGT GGTACAGCAC TGTTATTTT CAAAGATGTG TTGCTATCCT 180  
GAAAATTCTG TAGGTTCTGT GGAAGTTCCA GTGTTCTCTC TTATTCCACT TCGGTAGAGG 240  
ATTTCTAGTT TCTTGTGGGC TAATTAAATA AATCATTAACT ACTCTTCTAA A 291

SEQ ID NO:342

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00365

SEQUENCE DESCRIPTION:

GATCTTAAAC CTATGATTCA GTAACCTCTT ACCATATAAA AACGATAATT GCTTTATTTG 60  
GAAAAGAATT TAGGAATACT AAGGACAATT ATTTTATAG ACAAAGTAAA AAGACAGATA 120  
TTTAAGAGGC ATAACCAAA 139

SEQ ID NO:343

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00366

SEQUENCE DESCRIPTION:

GATCCGTGGC AGGGCTGCTG AGGCCTGTGG GTGGGACACC ANNTGCGAAA CCCTCATCCA 60  
GTTTTCTCTC CATCTCTTTT CTTTGTACAA TCCCATTTCC TATTACCATT CTNTGCAATA 120  
AACTCAAATC ACATGTCTGC AAA 143

SEQ ID NO:344

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00367

SEQUENCE DESCRIPTION:

5 GATCCAGTGA CATTGTGAGT GAAGACGCAA ACAGGTTTGG ACTCCTGCAT GGCCGATGAC 60  
 CTTTCTGTGA GGCTTACCAG AAAAGTACAT NCAACAGTTC TTTGAGGTTT AACTAGAGCA 120  
 GCAAATAAAG CAAAAGTTN 139

SEQ ID NO:345

10 SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00368

15 SEQUENCE DESCRIPTION:

GATCAAGAAT CTTTGTGAA ATTATAGAAA TTTACTATGT AAATGCTTGA TGGAATTTTT 60  
 TCCTGCTAGT GTAGCTTCTG AAAGGTGCTT TCTCCATTTA TTTAAACTA CCCATGCAAT 120  
 TAAAAGGTAC AATGCAGAAA 140

20 SEQ ID NO:346

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS00369

SEQUENCE DESCRIPTION:

GATCCAGCTT GCCAGGGACT TAGGTTTATC CTGTTTGTGTT TGCTACTGGT TACAAATTCT 60  
 ATTTCTGTGA CAATTAGTCA GACTAAAGTT TTCCTGTGT TTGTTTGGCA AAACAAATTA 120  
 AACAAAAAGT AAGGTTTTTA AA 142

30

SEQ ID NO:347

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35

CLONE:HUMGS00370

SEQUENCE DESCRIPTION:

40 GATCTCCGTN AACACATTT TTNTCTTAG TCTATCTCTT GTACAAACGA TGTGCTTTGA 60  
 AGATGTTAGT GTATAACAAT TGATGTTTGT TTTCTNTTTG ATTTTAAACA GAGAAAAAAT 120  
 AAAAGGGGGT AATAGCTCCT TTTTCTTCT TTCAA 156

SEQ ID NO:348

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45

CLONE:HUMGS00372

SEQUENCE DESCRIPTION:

50 GATCTACAAT NGGAGTTGTG AGTNGCAATC TTACATGGCT ACGNCTTTCG TTTGATAGCC 60  
 AGTCATGGTN ACCACATGAG AACCATATGC TGAGATGCAA TAAAGTAAGA GAATGTTTTC 120  
 TGACAAAAAA ATCTN 135

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# EP 0 679 716 A1

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133

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SEQ ID NO:349
SEQUENCE LENGTH:133
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00373
SEQUENCE DESCRIPTION:
GATCTTAAGC GTGTCTTGAG TTCCATGCAA ATTCAATTCT GTTGATAATG TGTCCATAAT  60
CAAATCATCA TCTTGCAATG CAAGGGCTAC CCCATAATTA TCAGACATTA AAATAGTTTA 120
TTTCTTTTTC AAA
    
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15  
20  
137

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SEQ ID NO:350
SEQUENCE LENGTH:137
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00374
SEQUENCE DESCRIPTION:
GATCTCGTTC CGCCGGTTCC CCTTGGCCGC CAGTTCCGTT CTCCTCACGG GCCGAACGGA  60
ACAAGGGGTC CAGCTTGCGG GGGACCCTCC CCAGCCCATT CCTGCTGTCA AACAAACAAA 120
ACCTTGCAA GCGCAA
    
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30  
132

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SEQ ID NO:351
SEQUENCE LENGTH:132
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00375
SEQUENCE DESCRIPTION:
GATCAAGCGT GCTTTCCTTA TCCGAGGAGC AGAAAATCGT TGTGAAAGTG TTGAAGGCAC  60
AAGCACAGAG TCAGAAAGCT AAATAAAAAA ATGAAACTTT TTTGAGTAAT AAAAATGAAA 120
AGACGCTGTA AA
    
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45  
142

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SEQ ID NO:352
SEQUENCE LENGTH:142
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00376
SEQUENCE DESCRIPTION:
GATCAAGTTC CCGCTGCCCC ACCGGGTNCT GCGCCGTCAG CACAAGCCAC GNTTCACCAC  60
CAAGAGGCCC AACACCTTCT TCTAGGTGCA GGGCCCTCTT CCGNGTTTTG CCCCAAATAA 120
ACTCANGAAC GNCCCGGTTA AA
    
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SEQ ID NO:353
SEQUENCE LENGTH:142
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
    
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EP 0 679 716 A1

CLONE:HUMGS00377

SEQUENCE DESCRIPTION:

5 GATCAAGGAT ATTTGAAATC ACTACTGTGT TTNCTGCGT ATCTGGGGCG GGGGCAGGTT 60  
GGGGGGCACA AAGTTAACAT ATTCTTGGTT AACCATGGTT AAATATGCTA TTTAATAAA 120  
AATATTGAAA CTCACCAGTA AA 142

SEQ ID NO:354

10 SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00378

SEQUENCE DESCRIPTION:

15 GATCTCTAAT GAAAAAGGGA TGTCTTTTGT TTTATAGTCA TGTGGCAAGA TGAGAGTAAA 60  
ACCAGAGAGC AAACCTCTAT AAGTNTTGAG TATATGTATA CATTTGAAAT AAACCAGAAA 120  
TTTGTTACCT TAAA 134

20 SEQ ID NO:355

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00379

25 SEQUENCE DESCRIPTION:

GATCAGCTCT GAGGTGCACT TCTTCACATA CTGTACATAC CTGTGACCAC TCTTGGGAGT 60  
GCTGCAGTCT TTAATCATGC TGTTTAACT GTTGTGGCAC AAGTTCTCTT GTCCAAATAA 120  
AATTATTAA TN 132

30 SEQ ID NO:356

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00380

SEQUENCE DESCRIPTION:

35 GATCNGGGCT GGATTGACGG ATGTCACCCC CNATCCCCTC GTGACATGCA CGTCNGCAGG 60  
AATGGGGGGT CTGCNGTGGT CGCCNGTCGT GTGAACAAGA TTCCGTCAAA ATATTTTCTG 120  
40 TTAATAAATT GCCTTCATGT AAA 143

SEQ ID NO:357

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00381

SEQUENCE DESCRIPTION:

45 GATCTAGAAG ATGATGTTCA AACTATGAAA CTGCTTGTGA ATTGTGAAAT GACTTTGTTC 60  
50 TTGCTTGT TTTTNAATT TCCTATAATG NACATACTAA CTTTAAAAA ATAAAGGTTA 120  
TTTTAAAAGC CTGAAA 136

55

SEQ ID NO:358

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00382

SEQUENCE DESCRIPTION:

GATCTTCTAT GTAACAGTTG AAATNTGGAA GTGACGTCAC TTACCTGTCT AACGTGGTGT 60  
GGGNGAGAAT TTACAAGTCC TTTATTGNAA GAATAATTGT TGCAAAATAT ATTGCTTCTA 120  
CTTTGCCTGG AAA 133

SEQ ID NO:359

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00383

SEQUENCE DESCRIPTION:

GATCAAGAAT TTGGGTGGGA GAAAAGAAAG TGGGTTATCA AGGGTGATNN GAAATTTTCT 60  
GCAGCATTAAGCTGGCGCT TAATAAGAAT AAGTAATAAT AAAGAAATTT CTAACATTCC 120  
ATGTCAGAAA 130

SEQ ID NO:360

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00384

SEQUENCE DESCRIPTION:

GATCTGAAAC TAATAGTAGG AGTTTCCCA GAAGTCATTT TCAGCCTTAA TTCTCATCAT 60  
GTATAAATTA CCATAAATNA TGCATGTNTG TTTACTTTAG TGACGTTCCA CAGAATAAAA 120  
GGAAACAAGT TTGCCATCTT GGTGTTGCAA TATGAAA 157

SEQ ID NO:361

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00385

SEQUENCE DESCRIPTION:

GATCTGAAAA GCGTCTNCA CTGCTTTATC TCATGATGCT TGCTTGTAAG ACTTGATTTN 60  
AGTTTTTCAT NNCTCAAATA GGAATACTAC CTTTGAATTC AATAAAATTC ACTGCAGGAT 120  
AGACCAGTTA AA 132

SEQ ID NO:362

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00386

SEQUENCE DESCRIPTION:

GATCTGCCAG GNTGGGTGGT TCTACTGCTT TCTCAATTTC TAAGAACCTT TTTTTTTTCT 60  
 NAAAGAGTTC TGCTGAATTA TTTGACAATA TTTGNAAGTA CCATGTTTCC TNGNGGGGTA 120  
 TGCTCTGTNC TGGTTTCTGT TTTNAAATCA AATGCCTGTT TGGGAGGAGA TGAACGNATT 180  
 NAGTCTATTA GATTTGN 197

SEQ ID NO:363

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00387

SEQUENCE DESCRIPTION:

GATCACAGTG TCAGAGACGC GTCCTCTTTC TTGGGGAAGT TGAGGAGTGC CCTTCAGAGC 60  
 CAGTAGCAGG CAGGGGTGGG TAGGCACCCT CCTTCCTGTT TTTATCTAAT AAAATGCTAA 120  
 CCTGCAAA 128

SEQ ID NO:364

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00388

SEQUENCE DESCRIPTION:

GATCCCAGGA GACACCAGGG CCAGAGTGAC CACAGCAGGG CAGGCATCAT CGTGTGTGTG 60  
 TGTGTGTGGA TGTGTGTGTG TGGGTTTTNT AAAGAATTCT TGACCAATAA AAGCAAAAAC 120  
 TGTCAAA 127

SEQ ID NO:365

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00389

SEQUENCE DESCRIPTION:

GATCTACAAA TGGGAAGCTT GTGAGTGGCC CATCTTTGTT GGCCTACGAA CTTTGGTTTG 60  
 ATGCCAGTCA GGTGCCACAT GAGAACCTTT GCTGAGATGC AAATAAAGTA AGAGAATGTT 120  
 TTCCTGAAA 129

SEQ ID NO:366

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00390

SEQUENCE DESCRIPTION:

GATCAGCTAT TAAATTTATA TAAACATAG GCATGTTTGT ACTAATGAAA CGTACTGTCA 60  
 ACCTCTATCA CATTGTTAAA TTAACACTTT TGGTGGAAC TCAATAAAAT TGAGAAAATT 120

GGAAA

125

5

SEQ ID NO:367

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00391

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SEQUENCE DESCRIPTION:

GATCTTTTTA ATTATAATTT TGTGTATTT GTTTCCTAGG AGCAAGTGTT CTGCTGCCA 60

GTTCTTTCCT CTTTAGGCGT GGTTGAGAAA AAGCAGAAAC TTTACATAAA GCTGTATTTC 120

TTAATCATCT TTAATTTGAA ACTTAAGNAA ATGAATTTAT TCTGTNATAT TTATGTAAC 180

15

NATTCCTGG NAGTNATATC TACTAGTNTT GNTTGATAAT AATAAAATTN GGCTATACCT 240

TGNAAA 246

SEQ ID NO:368

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00392

20

SEQUENCE DESCRIPTION:

GATCTAAAT TTATTGTTG GATGTTTGCA TAACAGTGCA AATATACTGA AAACCACTGA 60

ATTTTACACT TTAAATCAGT GGCTTCTGTG GTATGTTATC AATATTTCTC AATAAACTT 120

CAAAAAATA AA 132

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SEQ ID NO:369

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00393

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SEQUENCE DESCRIPTION:

GATCTGGTAT TAGGAAATTA CTTTCACAGT AAATATCAAA GAAAAAAGAT TAAGGGTCTC 60

TTTGCCATGC TTTTCATCAT ATGCACCAAA TGTAATTTT GTACAATAAA ATTTTATTTC 120

CTAAGTAGAA A 131

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SEQ ID NO:370

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00394

45

SEQUENCE DESCRIPTION:

GATCTGAAAA AGAACACTGT GCGAGATTGT ATTCCTGCTT ATCCTTTCCA AGTTAGTAGG 60

CAGATTGGAA CTATAGAATT TATCCGTGAT AATAATAAAG TCCGCATAAC TTTTGTCTGT 120

AAA 123

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SEQ ID NO:371

55

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00395

SEQUENCE DESCRIPTION:

GATCTAAAGA GAAACTGTAG ATTGTTTTCC TGACAGCAAA AGACTAATGT GACAAAATGA 60  
 AGTCATTGTA AAGAAGCGAT GCAACTTGTC AAATATTAA TAAAGAATTA TGGAAGCTGG 120  
 AAA 123

SEQ ID NO:372

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00396

SEQUENCE DESCRIPTION:

GATCACAAC GNAAGATAAC AAGAGATTAA AGTTTAAAGG GCATTTAATC AGGAGGAAAG 60  
 GTTTGGAAAA CTAATCAGG TGTATTNTT GTTAAAGCAG AAATAAAGTT TAATTTTNC 120  
 TTGN 124

SEQ ID NO:373

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00397

SEQUENCE DESCRIPTION:

GATCTGTGTT AGAATGAGTG CTTCCCTTC CTAATGATGT GATTGTGGAT TAGGAATTCG 60  
 TGACCGAGTG ATTTTGGCC AGTGGTTGGG TTAAATTC TATTAATTTGTTAGTTTGG 120  
 GN 122

SEQ ID NO:374

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00398

SEQUENCE DESCRIPTION:

GATCGCCGCC CTGCTGGCCA CCTGCGNTGG NGCTGGCNCCT CGTGGTCGTC GCGCTGAGAA 60  
 AGTTTTCTCC CTCCTGAAGC GAATAAAGGG GCCGCNGCCG GCCGCGGCGC GACTCGGCAA 120  
 A 121

SEQ ID NO:375

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00399

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCAGGCCC GGTGCCTGCA GACCTGGTGC TCCCTCGGGC AGGGCTGGGT GCCGCACCGC 60  
CTGCTGGCTT TTCTGGCAGC TCCTCTGTAT CAGAACCAAT AAAGTGCACT TGTTCCTCGGN 120

5 SEQ ID NO:376  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00400  
10 SEQUENCE DESCRIPTION:  
GATCAGGCAG TCCTTNAGGA TAGACAGATA TACACACCAC ACACACACAC CACATACACC 60  
ACACACACAC GTCCCCATCC ACTNACCCAC AACTACACA GNCTGNTNCC TTATAGCTN 119

15 SEQ ID NO:377  
SEQUENCE LENGTH:225  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00401  
20 SEQUENCE DESCRIPTION:  
GATCTNATTT GTAACCCACT GAGAGGACAG AGAGAAATAA GTGCCCTCTC CCACCCTCTN 60  
CCTACTGGTC TCTCTATGCC TCTCTACAGT CTCGTCTCTT NTACCCTGGC CCCTCTCCCT 120  
TGGGCTGTGA TGAAAAATTG CTGACTGTAG CTTTGGGAG TTTAGCTCTG AGAACCGTAG 180  
25 ATGGATTNCA GTTCTGGGAA AATAAAACCC GTTGATTACT NNAAA 225

SEQ ID NO:378  
SEQUENCE LENGTH:125  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS00402  
SEQUENCE DESCRIPTION:  
GATCTTAATA TATTGAAAA AAACCTCATT CTCGTGAGTC ATTTAAATGT GTACAATGTA 60  
35 CACACTGGTA CTTAGAGTTT CNGTTTGATT CTTTTTAAAT AAACACTCTT TTGATTAAAA 120  
GCAAA 125

SEQ ID NO:379  
SEQUENCE LENGTH:147  
SEQUENCE TYPE:nucleic acid  
40 TOPOLOGY:linear  
CLONE:HUMGS00403  
SEQUENCE DESCRIPTION:  
GATCTCAGTT CTGCGTTTAT TGTAAGTTGA TAAAAACATC TGGAAGAAAA TAACTAAAC 60  
45 TGTTTGCATC TTTGTATGTA TTTATTACTT GATGTAATAA AGCTTATTTT CATTAACAAT 120  
TTGTATTAAA ATNTGGGTTC CTTGAAA 147

50 SEQ ID NO:380  
SEQUENCE LENGTH:116

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00404

SEQUENCE DESCRIPTION:

GATCACCTTT TCAGAAATTT AGATGTGAAC ACCAAAAGAA GCATTTTCTC AACAAAAATT 60  
AATAGCTGGT TCTATTTTTT TTAAACCTAG AAAAAATAAA GTTGATTTTT TTCAAA 116

SEQ ID NO:381

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00405

SEQUENCE DESCRIPTION:

GATCAATAGG GAGAGAAAAT CCACATTCTT GGGCTGAACG CGGGCCTCTG AACTGCTTA 60  
CACTGCACTC TGACCTGTA GTACAGCAAT AACCGTCTAA TAAAGAGCCT ACCCCCCAA 119

SEQ ID NO:382

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00406

SEQUENCE DESCRIPTION:

GATCTTTATT ATGGAAANCA TTTCAAGTTT ACTCCTTCTG TTTTAAGTTT TGTAGCAGTG 60  
TACCCACGCT GGGTATTACN NCCNAAATAA TCTGTNAGTG AAAGTTGCCA TTATN 115

SEQ ID NO:383

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00407

SEQUENCE DESCRIPTION:

GATCGANCTG CGCAANTGNG NAAGCTGCAG AGGACATCGC GTACCANCTC TCACGCTCTC 60  
GGAACATCAC CTACCTGCCA GCGGGGCAGT CCGTGCTCCT CCAGCTGCCC CAGTN 115

SEQ ID NO:384

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00408

SEQUENCE DESCRIPTION:

GATCTCTCAA AAAACAAAGA ATTACATGAG TTAGTACATG AAAAAATTAT GGGAAACTAC 60  
ATGAAATATA CTGTTACGTT CAATAAACAT TAGCTTCTGT ATATAATANT AAA 113

SEQ ID NO:385

SEQUENCE LENGTH:116



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00409

SEQUENCE DESCRIPTION:

GATCTCTTCC CCCAACTTCC TAACACTTAT TAATTTATGA AACTGTTTTT CTCAGCGCAG 60  
TTTTGTTTTG TGTGTCCATT GGATTACAAA CTTTATTAAA AAATATAAAA CACAAA 116

SEQ ID NO:386

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00410

SEQUENCE DESCRIPTION:

GATCTCTCTC TTCTCGCGCG CGCACTCTCT CTTCAACACT CCCCTGCGTA CCCCGGTTCT 60  
AGCAAACACC AATTGATTGA CTGAGAATCT GATAAAGCAA CAAAAGATTG GTCCCAAA 118

SEQ ID NO:387

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00411

SEQUENCE DESCRIPTION:

GATCTATAAA AAGTCAGCAA CTGATGTGTT TGAAAAGCAT CCTTGTCTNT ATATCCTAAT 60  
GTTTGGATGT GTCTTTNCTA AAGTCTCACA AAAATTAGTG GTAGCTCACA TGACCAAAAG 120  
TGAACATAT CTNCAAGACA CTGTCTNNGG GGGGCCAGGT CTTTTGTTTT TAGGNCCAGT 180  
ACTTNNATAA TTTNTAGAC GGATATGGTT GTCCTATGGA TGGCAATGGG TGNTTNTCTC 240  
ATTGNN 247

SEQ ID NO:388

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00412

SEQUENCE DESCRIPTION:

GATCCTAGGA AGAGAGAACA GAGTGGCTCA CAAGCCCCAA CACAGTNAGC AGCAGATGAC 60  
AGGCACNCTN AGACCACACT NTAGGCCACC CATGGGNCCA AAAGGGAACA GN 112

SEQ ID NO:389

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00413

SEQUENCE DESCRIPTION:

GATCACCACN TAAGTCAGAA AAATGTATTT TTAAATGTTT CTTGAAGTGC CTTTGAACA 60  
TTTTTAAACA GCGGATTAA ATAATGCATA AANTAAATTG CCATGNTCAA A 111

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SEQ ID NO:390  
SEQUENCE LENGTH:109  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00414  
SEQUENCE DESCRIPTION:  
GATCACCTTA GTTTGATTCT ATTTTTCAGC TTGCAAAAAG TGACTTATAT TCCAAAGAAA 60  
TTAAAATGTT GAAATCCAAA TCCTAGAAAT AAAATGAGTT AACTTCAA 109

SEQ ID NO:391  
SEQUENCE LENGTH:111  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00415  
SEQUENCE DESCRIPTION:  
GATCGTNACG CTCGCATCTA TAGATAACGG CTCTCCAGAC CTGAGCTTTC CGCGTCANAA 60  
TGTAGGAATN GTTTTTCCTG CAGAGAATAA AAGGACCACG TGNAATACTT N 111

SEQ ID NO:392  
SEQUENCE LENGTH:109  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00416  
SEQUENCE DESCRIPTION:  
GATCTTATTG AAGGACATCT TACAGCTTCC CAATGAGAGG CCAGGAAGTG TGAACATACT 60  
GATAGAAAAA GACTATATTT TATCCCTCAT AAAATGTTTT AAATGTAAA 109

SEQ ID NO:393  
SEQUENCE LENGTH:116  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00417  
SEQUENCE DESCRIPTION:  
GATCACTGAG TGTACAGAAG AGAGAAATTC AAACAAAATA TTGCTGTTCT TCAGTTTTGT 60  
TTGTGGAATT TAAAATNACT CAAATTTAAA ATAAATNACT GGACTGTGGA AATAAA 116

SEQ ID NO:394  
SEQUENCE LENGTH:115  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00418  
SEQUENCE DESCRIPTION:  
GATCTCAAGA GTTCACCTGG CTNACAGAAA GAAGATGCCA GATGACACTT AAGACCTACT 60  
TGTGATATTT AAATGATGCA ATAAAAGACC TATTGATTG GACCTTCTTC TTAAA 115

# EP 0 679 716 A1

5  
10

SEQ ID NO:395  
SEQUENCE LENGTH:114  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00419  
SEQUENCE DESCRIPTION:  
GATCATTCTG AACTGTACAT ATTTATGTNG CGAGAGGCAA AGGGCAAGTT TTGGATTTTC 60  
CTTCTTCCAA GTTTGTTTTT AAACGACAAA TAAAAAAGA ACATTTTAAA TAAA 114

15  
20

SEQ ID NO:396  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00420  
SEQUENCE DESCRIPTION:  
GATCTGAATC TNTGACTTAT TGATTATGGA ACCTGTCAAG TAGTTTTNAA CTCTCCCAGT 60  
GAGGATAATT AAACATGCTC AGCCTGAGCC ACCTCTAAGT NTCAAA 106

25  
30

SEQ ID NO:397  
SEQUENCE LENGTH:107  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00421  
SEQUENCE DESCRIPTION:  
GATCGTTTCTT CATGGGGGTA AGAAAAGCTG GTCTGGAGTT GCTGAATGTT GCATTAATTG 60  
TGCTGTTTGC TTGTAGTTGA ATAAAAATAG AAACCTGAAT GAAGAAA 107

35  
40

SEQ ID NO:398  
SEQUENCE LENGTH:112  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00422  
SEQUENCE DESCRIPTION:  
GATCCCTTCA AAAGGCAGGA NTGCTGCCCT CTNCCATGGT GCCCGTNCCT CTTTGCTGTN 60  
TATGTNAACC ACCCATGTAA GGGAATAAAC CTGGCACTAG GTCTTAAATA AA 112

45  
50

SEQ ID NO:399  
SEQUENCE LENGTH:105  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00423  
SEQUENCE DESCRIPTION:  
GATCANCTCT AAGGTGCAAC TNCCTCCACA TACTGTACAT ACCTGTNACC ACTCTTGGA 60  
GTCCTGCAGT CTTTAATCAT NCTGTTTAAAN CTGTTGTGGC ACAAN 105

55

SEQ ID NO:400

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00424

SEQUENCE DESCRIPTION:

GATCTGGAAC TTGAAGATGC CATTATACA GCCACTTAAC CTAAAGGGAA AGCTTTGAAG 60  
GGCAAATGAC AGAGGGTAAC ATAGGAGGTN GGATNCTNAA TNNN 104

SEQ ID NO:401

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00425

SEQUENCE DESCRIPTION:

GATCTTTGAT ATATCATAGT CATTAAAAGA CNNTTTCGTA TTTGTATTGA TAATGTATTA 60  
AAAGTNGTTT GTNCTTAATA AAAGACTTCT TTAANCATCT NAAA 104

SEQ ID NO:402

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00426

SEQUENCE DESCRIPTION:

GATCCCCGGC CTCAGTCCCT ACTCTGCTTT GGGATAGTGT GAGCTTCATT TTGTACACGT 60  
GTGACTTCGT CCAGTTACAA ACCCAATAAA CTCTGTAGAG TGGAACAAA 109

SEQ ID NO:403

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00427

SEQUENCE DESCRIPTION:

GATCACCTGC AGCTGGCCAC ACCACAGGCC CCCGNTGCCT GCAGCACTAC TCNGTNCCTN 60  
AAACACCTGG CCTGCTAGGA GGCTCCAATA AAGCTAACCC GGACCAGAAA 110

SEQ ID NO:404

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00428

SEQUENCE DESCRIPTION:

GATCCTCAGA ACTTCTCTGG GACAATTTCA GTTCTAATAA TGTCCTTAAA TTTTATTTCC 60  
AGTCCTGTT CCTTGGAAAA TNTCCATTGT ATGTGCATTT TTTAAATGAT GTCTGTACAT 120

AAAGGCAGTT CTGAAATAAA GAAAATTTTA AAATAAA

157

SEQ ID NO:405

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00429

SEQUENCE DESCRIPTION:

GATCAGCAAC ATTTGCTGAG CCTGTTTTN AAGCTAATGT GTATTCTNAC TAATNTNCCT 60  
 ATCAAGAATG GATTGTGAAT ATATNCTGTC TATTTCTAAT GTN 103

SEQ ID NO:406

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00430

SEQUENCE DESCRIPTION:

GATCTGTAAG CACAGTCTTA TTTNCTTTTG TTGTCCAGAA TACTTATAAT TCTTGAGCCT 60  
 CCCAGAAATT GGAAGCTAAA TAAAGCAACT CAAGTTTCCT TTAAA 105

SEQ ID NO:407

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00431

SEQUENCE DESCRIPTION:

GATCAGCATC ATTGGAACAT GGGGACGAGT GACGGCAGGA GGACCACGAG GAAATACCCT 60  
 CAAACTAAC TTGTTTACAA CAAAATAAAG TATTCCTAC CAAA 104

SEQ ID NO:408

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00433

SEQUENCE DESCRIPTION:

GATCTATCAC TCTCGTNCTT GTAGCTCCCA GCCGAGGACG TCGGATGTAA TCGTCCTTNC 60  
 TGCTTTGCCA CCCCATTCCC GTCAATAAAG TGGTTTGAAC CAAA 105

SEQ ID NO:409

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00434

SEQUENCE DESCRIPTION:

GATCAAACCT TTCTGGCCTG TTATGATTCT NAACATTGA CTTGAACCAC AAGTGAATCT 60

TTCTCCTGGT GACTCAAATA AAAGTATAAT TTNACCTGC GGAAA 105

SEQ ID NO:410

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00435

SEQUENCE DESCRIPTION:

GATCAACACA AAGCACAATG NATTACNCGN AATTCAGTAT TTTCAAATTT ACATATTTAA 60  
AGTCATGCAA GCTGTAACTT CCCNGTCAAA ATTACTNGCT N 101

SEQ ID NO:411

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00436

SEQUENCE DESCRIPTION:

GATCATAAAG NNCTATCAAG GAGTTCTATC AAGGCATCCA TGTCAGTGGT GCTATGCTGG 60  
TTACAACTTG AGATTTTGA AATAAAAAAT TTGCATAAA 103

SEQ ID NO:412

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00437

SEQUENCE DESCRIPTION:

GATCAACAGG CTTATTAGAA GAATGAACTA AGGTGTCTAC CATGATTATN TTTCTAAGCT 60  
GGTTGGTTAA TAAACAGTAC CTGCTCTCAA ATTGAAAAAG AAA 103

SEQ ID NO:413

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00438

SEQUENCE DESCRIPTION:

GATCTTGTGC TGTGTCAAAG TAACAGACTA GAACCTTCTT TCAAGTACCT GAATTGAAAT 60  
NAAACTCATT TTGAATAATA AAAACTCTAG AAACCTCAA 99

SEQ ID NO:414

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00439

SEQUENCE DESCRIPTION:

GATCTGTAAT AGCATATTGT AGATGCACTT TGCAGCAGTT GGAAAAGAAA GTGTTGTGTG 60

ATTTGATTGA AATAAACTA AATGTGTTGT CCTCCTAAA

99

SEQ ID NO:415

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00440

SEQUENCE DESCRIPTION:

GATCCCTGTG CCAGGAGCCA ACCTGGTCTT CCCGAGGGTC AGTGCCCCAG TGAAGACAGA 60  
AGCGAGAGAA TAAAGTTCCC TGTAGGTCCT CTGTCN 96

SEQ ID NO:416

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00441

SEQUENCE DESCRIPTION:

GATCCTCCCA TCCGTGTTGT GAGCACAGGC ATTTGTGTNT GGNCTGTCCT CCCTGTTGAT 60  
TGGTCTGGCA TTTCCGGTAT TAAAATGATA ANATAAA 97

SEQ ID NO:417

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00442

SEQUENCE DESCRIPTION:

GATCCTGCAT ATCTCAAGGA CCCTAAAGTT TGTAACATCA GATATCGGGA ATAAATTCTA 60  
TCACGTTACC ACTAATAAAC TTATTTTACA GTN 93

SEQ ID NO:418

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00443

SEQUENCE DESCRIPTION:

GATCTGTATT TTGCAAATAT TTTCTTCAAT ATGTGGCTTG TCTTTTGGTT CTCTTAACAA 60  
GGTCTCTTCC AGAGTATAAN CTGTAAATAT TAAGAAA 97

SEQ ID NO:419

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00444

SEQUENCE DESCRIPTION:

GATCTGGACA GAATCGCCGG ACAGGTGGCA GCTGCAACAA GAAGCATTAG AACAAACCAT 60

GCTGGGTAA TAAATTGCCT CATTCGTAAT CCTGAAA

98

SEQ ID NO:420

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00445

SEQUENCE DESCRIPTION:

GATCTATTCT GAGTATTTTT TAGAGAGTTA ATATTTATAT TTTAGTAAT TTTCTGGTAG 60  
AAGGAAATTG CACAATAAAA TNATTGGTT TGGTTTGAAA 100

SEQ ID NO:421

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00446

SEQUENCE DESCRIPTION:

GATCGTTGGC ACCATAGCCT TATGGCCAAC AGGTGGTNTG TGGTGAAAGG GCGTGGAGT 60  
TTCAATATCA ATAAACCACC TGATATCAAT AAA 93

SEQ ID NO:422

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00447

SEQUENCE DESCRIPTION:

GATCTGTGTT TNCCCTGACG AATGGAATTT ATCCTCACAA ATTGGTGTTT TAAATGTNTT 60  
AAGAACCTAA TTAAATAGCT GACTACAAA CAAA 94

SEQ ID NO:423

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00448

SEQUENCE DESCRIPTION:

GATCCCAAAC CTTACGGCCA AGTTTCTTCT AGTATGATGG AAAGTTTCTT TTTCTTTGC 60  
TCTGAATAAA ACTGAACTGT GGGTTCTCTA TAAGTGGCAT TTTGGGCTT CCCTCTTTT 120  
TGTAAGCAA TGTCTGCCTA GTTATTGTC CAGTTAACTT TAGTGACCTT TAAAAGTTG 180  
GCATTGTAAA TAAAACAACT TGCAAA 206

SEQ ID NO:424

SEQUENCE LENGTH:481

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00450



## SEQUENCE DESCRIPTION:

GATCTCACCA CTGCACTCCA GCCTGGGCAA CAGAGCGAGA CTCTGTCTCA ACAACAACAA 60  
 CAAAAAGTCC TGAACATGAT TGTGGAAGTG TGTGCTCTT TCAAGTTCTA TCACTTTTTG 120  
 TTTGCAAAGT TCAAAGCTGT ATTGTTGGT ACATATACAT GTAGGTTTGC CAAGTCTTTG 180  
 TGGTGAATTG ACTCTTCTGT CATTATGTGA TGTCATTTT TTGCCTTTTA ATAGTCTTGT 240  
 CAATACTTTA CCTGATGTTT TCATAGTGAC TCCTGCATAT TTTGATTAAT GTTTGCATGG 300  
 TTAATATTTC TTCATTTTAT TTTAAAGCTT ACCTGTATCA TTACTTATGA AGTCAGTTTC 360  
 TTTGAACAGC ATATACTCAG GCCATGCTTT TTTTNATTCA TTCCTGCATA TGGCTCTCCT 420  
 TAAATTGGGA ATGGTGAAA ATGGNTTAC CATTANAAT AAATTAATTG GTATTTTAA 480  
 A 481

SEQ ID NO:425

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00451

SEQUENCE DESCRIPTION:

GATCTGGTCC ATGAGGCTGC CCAGAGAAAG CACTGCTTCT NTATGTCTCT TGTGGTATTG 60  
 GAACAATAAA CCCGTACAAC CTGCAA 87

SEQ ID NO:426

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00453

SEQUENCE DESCRIPTION:

GATCATACTT GAAAGTGAAC TTAAACATTG AAAAATCGTA CAGTCATTTT AAGAATAAGA 60  
 AAATAAAATT TTCTCTTGT CTGAACCTGC AAA 93

SEQ ID NO:427

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00454

SEQUENCE DESCRIPTION:

GATCCCATGT GCTCTCACAC CATGTTTTTG TACAGAACTG ATGGTTGAAT CTTTGTCTC 60  
 TTGAAATAAA CAGAAGAAAA TGAAA 85

SEQ ID NO:428

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00455

SEQUENCE DESCRIPTION:

GATCTATTAA AGAAGTAATT GGCCTTTCTG AGCTGATTTT TCCATCTTTT GTAATTATCT 60

TTATTAAAAA ATTGTACTTG GATTAAA

87

SEQ ID NO:429

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00456

SEQUENCE DESCRIPTION:

GATCTCATTG CATGGGAAAA AAAAAAATCC TGTCTTNTTC ANAAATTGAC AATGTAAATA 60  
 AATTNAAATA TGGTTCCTG TTA CTCTTAA A 91

SEQ ID NO:430

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00457

SEQUENCE DESCRIPTION:

GATCTGAGAA ACAGGTGTGA CAAGAGCATG AACCANAGGT GCACCTGGGG CAGTTCCTTA 60  
 ATAAACTGG TTTGTACAGT CAAA 84

SEQ ID NO:431

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00458

SEQUENCE DESCRIPTION:

GATCATGAGA GTGCTGTCC CTTGTGAGCA CTATGAAAGT GTTAGCTGTT CTTTACCAGA 60  
 ATAAATGCAT TTCTATATCT TCN 83

SEQ ID NO:432

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00459

SEQUENCE DESCRIPTION:

GATCACCAGC TGAATATATT GTTTTACAAT AGTTCTGTGG GGCTGTTTTT TTGTTATNAA 60  
 ACAAATAATT TAGATGGTGG TAAA 84

SEQ ID NO:433

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00460

SEQUENCE DESCRIPTION:

GATCTTGATG GATTTNCATA CGATTGTAAA TGNAGCTATA TTAAAGTCTA TTAAAGGAAG 60

CCCTTCTTGT TTGAGGGAGN

80

5

SEQ ID NO:434

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00461

10

SEQUENCE DESCRIPTION:

GATCTATGCT TGTTTGTTTT TGTAATCCAT ATCATAGTTG CTTTCTTTAA TTGTTCTTC 60

TGAATAAACA GTTTATTTAA GATAAA 86

15

SEQ ID NO:435

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00462

20

SEQUENCE DESCRIPTION:

GATCCAGTCA CTGACTCTGT CTGGTGTGA CAGAGGATTT ATTTAAGCTA TTATTTTAAT 60

AAAGNACTTT GTACATTTTT AAA 83

25

SEQ ID NO:436

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00463

30

SEQUENCE DESCRIPTION:

GATCTACATA CAAACAAATG CAACCAACTA TCCAAGTCGT TATACCAACG TAAAACCCCC 60

AATAAACCGT TGAACATGTG ACAAA 85

35

SEQ ID NO:437

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00464

40

SEQUENCE DESCRIPTION:

GATCTGCTTT TACTTTGTAA TTTGTAGTTC TCAAAAGACT TTTTTTTAA AAAATAAAGN 60

CCATACTTAC ACTTAGGCTT TATAAA 86

45

SEQ ID NO:438

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00465

50

SEQUENCE DESCRIPTION:

GATCATTCTG AGTGTGCGAG TGTGTGTGCA CATGTTACAA AGGCANCTGC CATGTTAATA 60

55

AAATATTCAA TTTGAAATCC AAA

83

5

SEQ ID NO:439

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00466

10

SEQUENCE DESCRIPTION:

GATCCAAACT GTCTTTTTTT TGTATCTGTT ATTTAAAGCC CAGTGGATAT TTCAATNAAA 60

AAAAAAATCT AAAGATGN 78

15

SEQ ID NO:440

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00467

20

SEQUENCE DESCRIPTION:

GATCTGACCA CCTCTGCCCT GTCCACCAGG ATAAGTGACA CCTAGGACCC AGGAAATAAA 60

TGCCGATGAT TTGTGTGAAA 80

25

SEQ ID NO:441

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00468

30

SEQUENCE DESCRIPTION:

GATCTTACAG GGAGAGAGAT TGGGTGCAAT TTGCCTCTTT CTTGAATAA AAAGCTCTTT 60

GCTCACCTC AAA 73

35

SEQ ID NO:442

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00469

40

SEQUENCE DESCRIPTION:

GATCAAAAGT CTACATAACT AATACTCACA GCTGAGCTAT GTAGTATGCT ATGATTAAAT 60

TTACTTATGT AACTTTTATT GTCITTGGCA TTAACAGTGT TTCAAAAAAT TTCCTGTGTA 120

TACCCATCAG TGATTCATTC CCAAATCTNC TAGAAGCATA AGTGTCTCAA TATATTAAAA 180

45

CATATTGAAT AATCAAA 197

50

SEQ ID NO:443

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00470

55

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCCAGGCG CCACGCTGGC GGTTCGTGAG TGTCGAGGCA CCACTAAATA TAGCTGTCTG 60  
CCGTCCACTC ATAAA 75

SEQ ID NO:444

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00471

SEQUENCE DESCRIPTION:

GATCANATTG TAAGCTTTTC TGTTNATTT CTTTAAAGAA CCTTTGAATA AAAAACATCT 60  
GAAATTTTAA NAAA 74

SEQ ID NO:445

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00473

SEQUENCE DESCRIPTION:

GATCTCTTTG TAGCCATCCT GTTAAATTG TAAACAATCT AATTAAATGG CATCAGCACT 60  
TTAACCAATG AAA 73

SEQ ID NO:446

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00474

SEQUENCE DESCRIPTION:

GATCATGTCT GAATTATGTA TGAAAATTAT TCTATGTTTT TATAATAAAA ATAATATATC 60  
AGACATCGAA A 71

SEQ ID NO:447

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00475

SEQUENCE DESCRIPTION:

GATCTCTACC CACCCCATGC CTCTCCNAG TCTTGGATAC TAATAAAATG ATAAGCATTC 60  
TGGTTCTCN 69

SEQ ID NO:448

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00477

## SEQUENCE DESCRIPTION:

GATCGTAATG TAAAATTCTT TTACCATGTA CAAGAATTAT TAAAATACAG GTACTTGACC 60  
ACATTCTN 68

SEQ ID NO:449

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00478

## SEQUENCE DESCRIPTION:

GATCGGGCCC CGGGGGCCTG AGCCTGGGAC CCCACCCNGT GTTAATGAAA AATGAGTTT 60  
GGCAGCGCCA AA 72

SEQ ID NO:450

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00479

## SEQUENCE DESCRIPTION:

GATCCTTTTG TAATGACTTA CACTGGAAAT GCGAACATTT GCAGTAAAAA AATATATATA 60  
TAAA 64

SEQ ID NO:451

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00480

## SEQUENCE DESCRIPTION:

GATCATGCAT TTAGATTAT ATTTTNNCCA NAAAATACAA GGTATAATA AACTAAGAN 60  
CTACCN 66

SEQ ID NO:452

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00481

## SEQUENCE DESCRIPTION:

GATCTCTATT GTAATCTCTA TTGGAGATTA CAATGATTAA ATCAATAAAT AACTGAAACT 60  
TGAANATAAA 70

SEQ ID NO:453

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00482

## SEQUENCE DESCRIPTION:

GATCACTAAT TTTGCATCAG TAAAATGAAT TTTTAAAA CCAATAAATC ATCAATTATT 60  
AGAAA 65

SEQ ID NO:454

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00483

## SEQUENCE DESCRIPTION:

GATCACAGTT GCGTCATTGT GTATTAAATA CTTGGAATAA ATCAAGCAGG TCTCAACGCC 60  
AAA 63

SEQ ID NO:455

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00484

## SEQUENCE DESCRIPTION:

GATCATTAAAT TGTAAGCGC TTTGTAAAAT TCACATTTAC AAAATAATAA AGTCAGTTCA 60  
AACCTAAA 68

SEQ ID NO:456

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00485

## SEQUENCE DESCRIPTION:

GATCTGTGTC TGAGTCATCT TTGTATCTTG CCTAGCACCT ATCAATAAAT ACTTCTTGAA 60  
TGN 63

SEQ ID NO:457

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00486

## SEQUENCE DESCRIPTION:

GATCATGGGA ATATGCAGAA TTTCCAATGT ATTTTAAAT ACAAATAAAA TTGTAATTTA 60  
GN 62

SEQ ID NO:458

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00487

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## SEQUENCE DESCRIPTION:

GATCTAACAC TAACTGTATT GTTTTGTTC CATCAAATAA ACATCTTCTG TGGACCAGGA 60  
AA 62

SEQ ID NO:459

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00488

## SEQUENCE DESCRIPTION:

GATCTCGGCT CACTGCAATC TCTGCCTCCC GGGTTTCAAG CTTGTCCAGG NNNATCTCAA 60  
A 61

SEQ ID NO:460

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00489

## SEQUENCE DESCRIPTION:

GATCAACCTG AGTTTAAAA TACCTTTAAT AAATATNAGT NGAAAAAATG TCTACTTNAA 60  
A 61

SEQ ID NO:461

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00491

## SEQUENCE DESCRIPTION:

GATCAAACAC CCCACCCTCA CAAAAATGGC CACGTTGCAA TAAAAATTGT GGCATATTAC 60  
N 61

SEQ ID NO:462

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00493

## SEQUENCE DESCRIPTION:

GATCTTTATT TTCCCTTTGT ATTCATTTTA AGCATCTAAA TAAATTGCTG TATTGTGCTT 60  
AATGTAAATA TTTGCTTTAT TACAAA 86

SEQ ID NO:463

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00494



## SEQUENCE DESCRIPTION:

GATCTCTACT ACTGTTGATT TTGCCCTCGG AGCAAAGTGA ATAAAGCAAC AAGATGAAAA 60  
CTGAAA 66

SEQ ID NO:464

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00495

## SEQUENCE DESCRIPTION:

GATCAAACTA GAACTCATAT GCCATACTAG ATATGGTTGT CAATAAACTT ATGACGTGAA 60  
AAAAAAGAAA 70

SEQ ID NO:465

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00496

## SEQUENCE DESCRIPTION:

GATCCAAAAA GTGCGCGATG CGAGTAGTCA AGTCGTACTC CGCCATCTTG CCAAAGN 57

SEQ ID NO:466

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00497

## SEQUENCE DESCRIPTION:

GATCTAAAGC TCTTTCGATT TTATACTGAT TAAATCAGTA CTGCAGTATT TGATTAACCA 60  
AGAAA 65

SEQ ID NO:467

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00498

## SEQUENCE DESCRIPTION:

GATCTAAGGC AAGAGTTTCA GATTTACTGT TGGAAATAGA CCCAACTCTT CATGN 55

SEQ ID NO:468

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00500

## SEQUENCE DESCRIPTION:

GATCATAAAT ATTAATGGNG AAAACACTGT AGTAATAAAT TTCNATATGC CAGAAA 56

5 SEQ ID NO:469  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00503  
 SEQUENCE DESCRIPTION:  
 GATCTGTTCA GTGTCACCTCT GTACCCTCAA CATATATCCC TTGTGCGATA AA 52

10 SEQ ID NO:470  
 SEQUENCE LENGTH:54  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 15 CLONE:HUMGS00504  
 SEQUENCE DESCRIPTION:  
 GATCCCCGGT NGGTTTTGTG CTCAAAATAA AAAGCCTCAG TGACCCATGA GAAA 54

20 SEQ ID NO:471  
 SEQUENCE LENGTH:57  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00505  
 25 SEQUENCE DESCRIPTION:  
 GATCATCCGG TTATAGAGCA TAATTGCCA ATAAAGCTTT TGGAAGCGGG AAAGAAA 57

30 SEQ ID NO:472  
 SEQUENCE LENGTH:60  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00506  
 SEQUENCE DESCRIPTION:  
 35 GATCCAGTGT TGGNATTCTT TGGTGTAAT AAACGTTTGG TTTTATTAT NCAGGTTAAA 60

40 SEQ ID NO:473  
 SEQUENCE LENGTH:51  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00507  
 SEQUENCE DESCRIPTION:  
 45 GATCTCATTT ATTGCCACAG ATGCACAAAA TAAATAACCC AAAATCACAA A 51

50 SEQ ID NO:474  
 SEQUENCE LENGTH:80  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS00510

SEQUENCE DESCRIPTION:

5 GATCATATAT TTTGACAAAA TATATTTATA ACTACGTATT AAAAGAAAAA AATAAAATGA 60  
GTCATTATTT TAAAGGTAAA 80

SEQ ID NO:475

SEQUENCE LENGTH:77

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00511

SEQUENCE DESCRIPTION:

15 GATCCAAAAC TTAAATGTTG CACNTGTATT CCAAATAAAG GGTAAAAACA GAACCAAAGT 60  
TATAACTCCA ACACAAA 77

SEQ ID NO:476

SEQUENCE LENGTH:669

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00532

SEQUENCE DESCRIPTION:

25 GATCAAAAAG AAGGCTTAGA ATTCTGCAGT TAAGCTGAGG TTAAACTAA AAANTGTTTC 60  
CTTGGGTCAG TGGTTTTNAG GTCCAGTAGC TAGGCTTTTT TCTTTTGTCC TTCCTGTTGG 120  
AATGAAAACA TTTCGATTTT CCTTCATCTG TGAAGGTGTC CATAGACACA GGTTCATAGT 180  
TTTAACCTAC AGTATTGTTT GAAATTTACC TGTTTTNTT GTCAAACCTG AGCACTCCTC 240  
CTGCTGAAGT TTCTTATTTA ATTCCAGAGT ACTGTCCTCT ACTCTAAGGC ATTACTTTTA 300  
30 AGTGTATTAT GAAGGCAGTT TTCAAAGGAT ATGACCAGTT GGGGGTAATT CAAATTAAAA 360  
AGGAAAAGAT TTGTTTGGGA AGTAACTGGG TGTCTCTAAG AGGGAATTTT TAGGATGTCC 420  
AGTTTGGGAG GCTCTTTCCC CCCTCAAATT GAGANGCTCC TTGGTTAATT CAGAGCTCCC 480  
ANGACTAGGC CCTGGGCTAA CCAANCATTN GGGNGGCCAA AGGTTAGGGA ACCATTNGNT 540  
ACCAAGCTTT TGNANCAGGG GGNTTTNTNC CATTTGGGTA ATAGGGCCCT TTTCANGCCT 600  
35 TTANGGGTAN GCTTTTTTAN CCCNGAAACC NTTNNTNNNT TTGNAATTAA ACCGGAACCT 660  
TTTGNCAAA 669

SEQ ID NO:477

SEQUENCE LENGTH:651

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00533

SEQUENCE DESCRIPTION:

45 GATCAACCTG GAGCTCTACG CCTCCTACGT TTACCTGTCC ATGTCTTACT ACTTTNACCG 60  
CGATGATGTG GCTTTNAAGA ACTTTGCCAA ATACTTTCTT CACCAATCTC ATGAGGAGAG 120  
GGAACATGCT GAGAACTGA TGAAGCTGCA GAACCAACGA GGTGGCCGAA TCTTCCTTCA 180  
GGATATCAAG AAACCAGACT GTGATGACTG GGAGAGCGGG CTGAATGCAA TGGAGTGTGC 240  
50 ATTACATTTG GAAAAAATG TGAATCAGTC ACTACTGGAA CTGCACAAAC TGGCCACTGA 300  
CAAAAATGAC CNCCATTTGT GTGACTTCAT TGAGACACAT TACCTGAATG AGCAGGTGAA 360

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# EP 0 679 716 A1

AGCCATCAAA GAATTGGGTG ACCACGTGAC CAACTTGCGC AAGATGGGAG CGCCCGANTC 420  
 TGGCTTNGGC GGAATATCTC TTTGACAAGC ACACNTGGG AGACAGTGNT AATGGAAGCT 480  
 TAAGCCTTGG GGNTAATTTN CCCCATANGC NGTTGGGTTG ACTTCNCTGG TCANCAGGGC 540  
 AGTTCANTGA ATGTTNGGGG TTNCCTTTAC CTTTNCNTTA GGTNGTCCNA AACAAATCCNT 600  
 NAAAGTCTTT GNTTTGNACC NTTCCGNNA TAANGGATTN GGGCCCNAA A 651

SEQ ID NO:478

SEQUENCE LENGTH:617

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00534

SEQUENCE DESCRIPTION:

GATCAAGAAA GTGGGGGGAA AAAAAACAAA CGTTAAAACC TCAATCCTCA GTAGGAAGGT 60  
 AGATTACATT AGGTGAAATT ATAGGTAATC TATGTATGTN CTAATGGGGT TGGAAAGAAC 120  
 CTTACAGAGC ATATTACCTG ATAAACTGGA GTGGGTTTGG GAGAACAAAC TAATAGGATT 180  
 ATNGTNTCTC CTAGTTGGTA CCTGGGAGCA ATTGACATGC CCCCTTCAGA ACCTTAACTG 240  
 TTAGTAGCAG TGGCTGTAAC AACACAAACC AGTGACCAGA GATAACAGCT TTTNGGCCAA 300  
 GCTGGCCTGA CGGTATGGCT GCAGGANGTG ACTGAGCAGT AGCGGTACTC AGCCAGACCA 360  
 AGACGGAGAG GGGAGAGTCC ACAGCTTTCT GGAGCTAAGG CATTCTGGTG GTAGAAAAGT 420  
 GTGCCNAAG CCTTCATNGG CGGGTTATAN GGTCTNAAGA TAAGTCTCCT CTTGTNTGGG 480  
 ATNCCATACT NTGCTAAATA ACCNNGGTAT TANCCGGGTT TTCCNTGTAA CNGCCTCTNG 540  
 GGAGGAANTG ACTNNGNAAG NTGGCACAGG TTTTAAGCN TNAATGGAAA GGGNNAATC 600  
 CTNCTCAAAN TAGAACN 617

SEQ ID NO:479

SEQUENCE LENGTH:569

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00535

SEQUENCE DESCRIPTION:

GATCTGTCAG CTGCTTAATT AATTGAACT TCTCTGTCAT TGATGTTGCA TTTCCAAGGA 60  
 GATAATCTCC TTCTTGGTGC CTAATTTTCT AGATGATAAT AGGCTAGTTT TGATTCTTG 120  
 CTCATTTTCA GAATAACTTT CCAGGAAGAG ATGGCATTTA GAACTTCAGC TTTGGTGCTC 180  
 AGGTATAAAG CCAATTAAGG TACAATTGTA CCATAAAGGG AACAATCTGT TTCTGATTGC 240  
 ACAGTTTCTA ATTTTAAAA CTGNNGTGGT TTGCATTCA TAAAAGGCAA AGTTTACAGA 300  
 NCCATAACA TTCTCAATT TCTTTATGCT AGACATATAA ATTTATTTT CCAAACGTGA 360  
 ATAGGATTG GGGTAAAAAG NTTGTCTCAG GTNCCTCTNC CCANTTTGCC AATGGGGNAA 420  
 AAAAAAGGCT TAATTTTTC CATNNTACT TNAATTTTC TAAAACCCNT GGTAACCCCC 480  
 CATTGGNACC CCNATTTTTC CANCTTTAAG GGTCTNGCAT NGGCNGGCTT TTTNAATTNN 540  
 CCCTGGGGGG GTTTTNCCTG GGAGGGCCN 569

SEQ ID NO:480

SEQUENCE LENGTH:556

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00536

SEQUENCE DESCRIPTION:

5 GATCCTGAGC NTGGTGCTGT GCTGTGGCAT CCGGAACAGC TCCGTGTACT GAGGCCCCGC 60  
 AGCTCTGGCC ACAGGGACCT CTGCAGTGCC CCCTAAGTGA CCCGGACACT TCCGAGGGGG 120  
 CCATCACC GC CTGTNTATAT AACGTTTCCG GTATTACTCT GCTACACGTA GCCTTTTAC 180  
 TTTTGGGGTT TTGTTTTTGT TCTGAACTTT CCTGTTACCT TTTCAGGGCT GACGTCACAT 240  
 GTAGGTGGCG TGTATGAGTG GAGACGGGCC TGGGTCTTGG GGA CTNGAGG GCAAGGGGTC 300  
 10 CTTCTGCCCT GGGGTCCCAG GGTGCTCTGC CTGCTCAGCC AGGCCTNTCC TGGGAGCCAA 360  
 TNGNCCAAGA GACTCAGCTT GGNCAAANTT GGGGGGGNTN TGTNCAACCA NGCCCGCNNN 420  
 TCCTNTTNGG GTTGAAAAGT TTAACCTTGT TTCCCTTTCT NGCCCCGGTT TTGGAGAACC 480  
 CGANTTTTTT GGGGNAATTT TTTGCTTNA ATNAACTTNT NCCTTTTTTA AAAANGTGGG 540  
 15 TTTAAAACTN TNAATN 556

SEQ ID NO:481

SEQUENCE LENGTH:551

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS00537

SEQUENCE DESCRIPTION:

25 GATCTACTGT CTTTGTTC AA AGGTCAAATA AAAACCTAGT CTCCTTTTAT TCTACTTTCT 60  
 ATTCTTAGCT AGAATGAAAC TCAGCATATA TACACTTCTG GACATAATAA TATTGAATAG 120  
 TAATTACCTT TACTAGATGA AAGAAATTTT CATTACAAAC TTAAATCATG TAAAACTCAA 180  
 CAACTCAGAT TCCTGGACCT GGTGTCCTGG NTGGGTCCAA GGTGATTTTA CAGAAGNAAA 240  
 AANCAACTNA AGCATTCTGG TGGCAACATA GAGATTGTAG GCTGCTTCTA AGGAAGTNAT 300  
 TAACAATTNG GAAATTCCNA AGTAGGATGA GAGTTAGTAA CTGGATACGA GTGAAGTTTA 360  
 30 TATCCAAGTT CAGNCTCAA GGCATNATTA TGATTNGCTT CTCCCATGT CTNCCATGGN 420  
 CCTGCTTCTC AAAGTTTTTC TNATCNATCA CACTGCTGCC TAACTGCTCT GAGNATGCAT 480  
 GNGGTNTTCA ATTCAGCGTN NTNTNAATCN GGNNTANCTN TGGATTGGGA TGGGGATACG 540  
 GACNTTAAGG N 551

35 SEQ ID NO:482

SEQUENCE LENGTH:520

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00538

SEQUENCE DESCRIPTION:

45 GATCTTAATT TTGAAATTGA CATGAAAGTG TCATATCAGT AATCTGTGAA CCACCAGTCC 60  
 TTGGTACCTA TCAGAGGGTC AAAAATCACG ATTAAATATA ACCAAAAAAC TTTATAGTGA 120  
 CTGATTCAAA TTTGAATACT GGTTTTAGCT AATGTAGTAG TAATGAACTG GTTTGGGGGT 180  
 AAGATTTTCC TGGTATCTTA TTGCTGTAGA AATTTTCCTT TAACAGTTAC AGTGTTTTCT 240  
 TCCAAATCCT TCACTTCTCT GTCCTGGCTT GTAAAGAAAA CATCTGAGGA CTGAGGGGTC 300  
 ATATTTGAAT TGCTCTNTAT AATACCATAG ACTACTCATT GCTTAGACTN TACTAAGCTA 360  
 GAAATCACAA GAGCATAAGC NACTCTNAAA ATTNATATNA TGNGAATGTA AAAGGTACCT 420  
 50 GNCTGCAAAT ATCTNGANCN TCACTTTGGC TCAAGTNTCN NGTTAACCTG TNNNNTAATA 480  
 CNGNNATGTG AATTNGGCCA CCAGGTCCAT GNTTGGCAAA 520

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SEQ ID NO:483

SEQUENCE LENGTH:517

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00539

SEQUENCE DESCRIPTION:

GATCATGCTT TTNGTGCCTG TCACCAGGTC TCCCAAGTGC ACTCATCCAG GTCAGTGCTC 60  
 AGATGTGTTT AAGGAGACCC TATATTCAGG GAAGTTGCGT GAACACTGCA GTGGGGAGAA 120  
 TTGAGAATAG TCAGGCCTAT CAGTCTCACA GAATCACCCC TCTACCTTTG ATATTCCACT 180  
 TAGCTGTAGA GTCCATCTGT TTGTCCATCT GCTGAAATGA GAAAAGAAAA ATTTATGCAC 240  
 TGATTTAAAA CAAACCAAAA AAAAAGAAAA AAACAAAAAA AAAAATCCNT CCTTTCTNGC 300  
 TGACCAAAAN TGTGCAGTTA ATNCTGGGNG CTTGAAANTG CAGTGGTGAA TNTGGACCAA 360  
 GCCTGTCTGT ATATCTGGTA GCTCTTTTCT GGCTTNGTTT TTNCTTACCA GTATTCTNGC 420  
 CTAACGTTTT GCTTCGGGNN TGGTAATATN NCCTNGNAAG NACANCNGTG GGTGTGGAA 480  
 ATGGGTTNGG CAAAANGGAA NTTCCNGGGG TNTTGGN 517

SEQ ID NO:484

SEQUENCE LENGTH:515

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00540

SEQUENCE DESCRIPTION:

GATCTTCTGG CTCTACCACC ACAAGATATT ATCCTTGCAT CTNATGTGTT CTTTGAACCA 60  
 GAAGATTTTA AAGACATTTT GGCTACAATA TATTTNTTAA TGCACAAGAA TCCCAAGGTC 120  
 CAATTGTGGT CACTTATCA AGTTAGGAGT GCTGACTGGT CACTTGAAGC TTTACTCTAC 180  
 AAATGGGATA TGAAATGTGT CCACANNGNT CTTGAGTCTT TTGATGCAGA CAAAGAAGAT 240  
 ATAGCAGAAT CTACNNTTCC AGGAAGACAT ACAGTTGAAA TGCTGGTCAT TTCCTTTGCA 300  
 AAGNACAGTC TCTGAATNAT ACCNACAACC NGTNCTGGGA CAGTATCAAT ACTGATGAGC 360  
 AACCNGGCAC ACAAATATG AGCAGACCAC TTCAGCTTGA GGAATGCAGT GGGTCTGAGG 420  
 ATGGTCAAGT CTGTTTGCCT TAGATTTTGN TGTCACCTGG CCACACTTGA AANCTNNTTT 480  
 GGAACAAAAN TTAAATTCG GGTTCCTAAG GTAAA 515

SEQ ID NO:485

SEQUENCE LENGTH:510

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00541

SEQUENCE DESCRIPTION:

GATCTGCAGC TCTCAGAGGA CGACTGAGGC AGCCCATCTG GGGGGCCTGT AGGGGCTGCC 60  
 GGGCTGGTGG CCAGTNTTTC CACCTCCCTG GCAGTCAGGC CTAGAGGCTG GCGTCTGTGC 120  
 AGTTGGGGGA GGCAGTAGAC ACGGGACAGG CTTTATNATT TATTTTNTAG CATGAAAGAC 180  
 CAAACGTATC GAGAGCTGGG CTGGGCTGGG CTGGTGTGGC TGCTGAAGCC CCACAGCTGT 240  
 GGGCTGCTGA AGTCAGCTCC GCGGGGAGC TGCCCTGACG TCAGCAGACC GAGACCAGTC 300  
 CCAGTTCCAG GGGGAGGCCT GCAGGCNCTG GCCCTTCCAC CACCTNTGCC CTNCGTCTGC 360

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AGANCTTGGT NCATCTGCAC CAGGCTCTGC TTNACTCNNN NANAGTNTTT GGAAATTTGT 420  
TCTNNTCCTN TGAAAGTCAC ATTTGNTTNT AAAAAATTTG TGGNTTGAAT CGGAAACGGG 480  
AAGNAATAAA GCGGTGGGNG GNAGGGCAAA 510

SEQ ID NO:486

SEQUENCE LENGTH:507

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00542

SEQUENCE DESCRIPTION:

GATCCTTACA TCTGCCCAT CTGTGGTTAG TCAATGGCTT GCAATAAATG TGCAAACTGC 60  
ATCTATAGGA AACATTTTGT TGATTACGGA ATACTTTAGT TGATTGCTGA AAATATTGAA 120  
AGGTCTTCAT TTTACAGTGA TGAGTACATA TGCATGTTTC GGGGACTTGG CCCTTCTGAT 180  
GAGGGGCCCT CGGTACTCTG GATAACGAAG CTTGTGCAGA GTGGTAACCA TGCTTACACA 240  
CTAAACTATA ATATAAGGA AATGAAGCCA TGTTAATCTG AGAGCAGTGT CGCCATAGTT 300  
GTGTTGTTTA CAATACTCTA TAAATGGGGT TCCTGTTGCC CTGTAATTAA CCTGCTGCCC 360  
GTAGAGGCCT TTCCAGTTCC TTTTCTGTCC TTNCCCCTTT CTTAACACAA GCTCAAATTT 420  
TCCTAACTNG GTTTTNNATT TGGAGGNCCT TTAAAANGGN CCATTTTCAA TACCATNAAA 480  
ANTAACCAGG GCTTTATAAT ANTAAAA 507

SEQ ID NO:487

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00543

SEQUENCE DESCRIPTION:

GATCCACTAC CGGAAGAAGA AACAGCTCAT NAGGCTACGG AAACAGGCCG AGAAGAACGT 60  
NGAGAAGAAA ATTGACAAAT ACACAGAGGT CCTCAAGACC CACGGACTCC TGGTCTTAGC 120  
CCAATAAAGA CTGTTAATTC CTCAAAAAAA NGAAA 155

SEQ ID NO:488

SEQUENCE LENGTH:499

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00544

SEQUENCE DESCRIPTION:

GATCTTAAAA ACTAACTTCT AAGATGATTT CATCTTCTCA TAGTATAGAG TTTACTTTGT 60  
ACACGTTTGA AACCAACTAC TGTAGAAGAT GAGGAATCTA TTGTAATTTT TTGCTTTATT 120  
TTCATCTGCC AGTGGACTTA TTTGAAATTT TCACTTTAGT CAAATNATTT TTNGTATTAG 180  
TTTTTGATGC AGACATAAAA ATAGCAATCA TTTTAAATNG TCAAAATTTT CAGATTACTG 240  
GTAAAAATTA TTTGAAAACA AACTTATGGG TAATAAAGGC TAGTCAGAAC CNTATACCAT 300  
AAAGTGTAGT TACCATACAG ATTAATATGT AGCAAAANTG TATGCTTGAT ATTNCTCACC 360  
NGTGNTAATG TTNCTGCNGT ATTCCAGCNG ACCAAACCAA TATTAAGNAT GCATCTGTAT 420  
AAAATGGGNG CCTATNGGNT AATGGGAATN ATTNGGGTAA TNGGCCTNTA CCNGGNTGGT 480  
NATAATGGNG CCCTNTGGN 499

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SEQ ID NO:489

SEQUENCE LENGTH:516

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00545

SEQUENCE DESCRIPTION:

GATCTACCCC GGACACGGGA GGCCTACGC CAGGNCCGAC GGGAAGGTTT TCCAGTTTCT 60  
 TAATGCGAAA TCGAGTCGG CTTTCCTTTC CAAGAGGAAT CCTCGGCAGA TAAACTGGAC 120  
 TGTCTCTAC AGAAGGAAGC AAAAAAGGG ACAGTCGGAA GAAATCAAA AGAAAAGAAC 180  
 CCGCCGAGCA GTCAAATTCC AGAGGGCCAT TACTGGTGCA TCTTTGCTG ATATAATGGC 240  
 CAAGAGGAAT CAGAAACCTG AAGTTAGAAA GGCTCAACGA GAACAAGCTA TCAGGGCTGC 300  
 TAAGGNAGCA AAANAGGGCT AAGCAAGCAT CTAAGAGGNC TTGCAATGG CTGCTTGCTA 360  
 AGGCACCTTC AAAGGGCAGC ACCTTAGGCN AAAAGGATTT GTNTAAGCCN TGTTGAAAAG 420  
 TTTCCAGCTT CCCCGTNTTT TGGTTGGGAA NNGGNTAAAC CTTGGCAGGG TTTTGNNTTT 480  
 TTTAATTAAN AGGTTTGGGG TTTTAANCTN TTAAAA 516

SEQ ID NO:490

SEQUENCE LENGTH:497

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00546

SEQUENCE DESCRIPTION:

GATCAAGCTG ACAGACCCNN CTCTGCTCTG ACCTGGAGGT CTCCACTCTG GTCAGCAAGT 60  
 ATCCAGACAT CAGGGATGAC CACATCGGTG CGCTNCTGGC TGTGCGTGGG GACGCCAGCC 120  
 GTGACATGAA GCAGACCATC ATGGAGACCC TGGAGCAGGG CCCAGCACAG GCCAGCCCCA 180  
 GCTACGTGCC CCTCTTCAAG GACATTGTGG TGCCCAGCTG AACGTGGCCA AGCTGCTCAA 240  
 GTAGCCTCCG CGGCTGCCT GCTCGCCCTC CACAGCTNGG TCCTGCTTTA GAACGCGGGC 300  
 AGTNATTGTC TCTTGGCACA CGTGTCTTTT TAGTGACGGC TGTNTTTAGG TGCANTGTNA 360  
 TGACNNGGTG TGCGTCGAGT GANGTCNGAG GGCACGTGCG GAGGCNGTAN TTTGCTGTAA 420  
 AGGCTGTGGG TTCAGNGTTT NCNGACAGCG TTNNTTGGGT GTTGTNTTTC AGNGGTGAAG 480  
 TGTTNGGGAA AGNGNCN 497

SEQ ID NO:491

SEQUENCE LENGTH:494

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00547

SEQUENCE DESCRIPTION:

GATCCAAGAA ACAATTTCTG ATAATTGTGT GGTGATTTTN TCAAAAACAT CCTGTTCTTA 60  
 CTGTACAATG GCAAAAAAGC TTTTCCATGA CATGAATGTT AACTATAAAG TGGTGGAAGT 120  
 GGACCTGCTT GAATATGGAA ACCAGTTCCA AGATGCTCTT TACAAAATGA CTGGTGAAAG 180  
 ANCTGTTCCA AGANTATTTG TCAATGGTAC TTTTATTGGA GGTGCAACTG AACTCATAG 240  
 GCTTCACAAA GAAGGAAAAT TGCTCCCACT AGTTCATCAG TGTTATTAA NNNNAAGTAA 300  
 GAGGAAAGAA TTTCAGTGAT GTTTATACTA ATAAGTTTGC TAGTACAGTG TCAGTTATTT 360



AAAGTGGTAA TGCCCGNTAA TGTCTTTTAA ATGTTTTGAG GGATGTTTTA AAATACATGC 420  
 NATTGTCTTC ACGGAGGAGG GNTGTAAAAA TTANTGGGCC AATAAATTGC GGGTGGGAAN 480  
 CCNTNTTCTT NAAA 494

SEQ ID NO:492  
 SEQUENCE LENGTH:489  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00548  
 SEQUENCE DESCRIPTION:

GATCTTGACG AGGCTGCGGT GTCTGCTGCT ATTCTCCGAG CTTCGCAATG CCGCCTAAGG 60  
 ACGACAAGAA GAAGAAGGAC GCTGGAAAGT CGGCCAAGAA AGACAAAGAC CCAGTGAACA 120  
 AATCCGGGGG CAAGGCCAAA AAGAAGAAGT GGTCCAAAGG CAAAGTTCGG GACAAGCTCA 180  
 ATAACCTAGT CTTGTTTGAC AANGNTACCT ATGATAAACT CTTAAGGAA GTTNCCAAC 240  
 ATANACTTAT AACCNAGCT GTGGTCTCTG AGAGACTGAA GATTCGAGGC TCCCTGGCCA 300  
 GGGCAGCCNT TCAGGAGCTC CTTANGTAAA GGNCTTATCA AACTGGTTTC AAAGCACTGA 360  
 GCTCANGTAA TTTACACCAG AANTACCANG GGTNGAGATG CTCCAGCTTG CTTGTGAAGA 420  
 TGCATGATTA GGTCCACCAG CTGTACATT GGAAGAANTA NANCTTNTGT TAAATCAATG 480  
 GNGTNNAAA 489

SEQ ID NO:493  
 SEQUENCE LENGTH:487  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00549

SEQUENCE DESCRIPTION:  
 GATCCTCTGN CACGGGATAA ATTTNCAGGN GAAGAGTGAG GTTGTCATGG CCTCAGCTAT 60  
 GCTTCCNGGC TCTCCCTCAA GAGTGCAACC TTGGCTAGAG AACTCACAGC TCTGGGAAAA 120  
 AGAGGAGCAG ACAGGGTTC CTGGGCCAG TCTCAGCCCA GCCACTGATG CTGGATGACC 180  
 TTGGCCTGAC CCTGGTCTGG TCTCANAATC ACTTTTCCCA TCTGTAAAAT TGAGATGAAT 240  
 TTTNGTGTTG AAAGTNCTTC CNNGAGCAGA TGTCTTAGAA GGTTTTAGGA ATAGTGACAG 300  
 AGTCAGGNCA CCCNAAGGGC CATGGGGAGC CAGCTGACCT GCTTNGCCGA AGGATTTCTG 360  
 ACAGACTATC TTTGGGGATG TTTTCAAAGA AGGGATATAG GTTATTGACN TNNGGGCATT 420  
 TAAAGNAAAT TNTNTCTCGG GGATTAANTT TTTAGGANAA TNAAAGCTTT NGTGTCTANN 480  
 GGCAAGN 487

SEQ ID NO:494  
 SEQUENCE LENGTH:481  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00551

SEQUENCE DESCRIPTION:  
 GATCCCCAGC TGCCACTGAA TCTGGCTGCC CTTCAGGCC ACCTGGCCCA GGAGAACCGT 60  
 GTGGTGGCCT TCTTCAGCCT GGCTCTACTG CTTGCCCCAC TGGTGGAGAC GCTTATTCTA 120  
 CTGGACCGGC TGCTGTACCT TCAGGAACAG GGTTCATG CTGAGCTCCT GCCCATCTTC 180

AGTCCTGAAC TCTCTCCCAG AAACCTGGTT CTGGTGGCCA CCAAGATGCC CCTGGGTCAG 240  
 GCTCTTTNTG TTCTGGAGAC TGAAGACAGC TGATGCAGCC TGAGGAGACA TCTCAGACCC 300  
 CATCATCTGA AAGTGNCCAG AGAGCACAGT GGCAGAGTAC ATCTNATCCA GAGAAACAGC 360  
 ATCCTGCATC CTCCAGAGTC CTGGTTCCTT CAAGTTTCAT CNCTTTTNTC TCCTTTCCAT 420  
 GGGNTTATGT AAATACAATT GTAAAGTTTT AATTAAATTA AAAAATTGGG TTATCTGGAA 480  
 A 481

SEQ ID NO:495  
 SEQUENCE LENGTH:472  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00552

## SEQUENCE DESCRIPTION:

GATCTAAGCT CCAGGCACGC CTGAAGATGT GTTGCTACTC TNACATCCCG AGTTTCTGTC 60  
 CACACATTGC ATGCACAGCG CCCACACAT TGGATACTGT TGTTCACGAT AATTTCTCCC 120  
 GTTTTCCAGA GCATTTAACA TAGCTTGGAG GCGTAAATG GCTCTGTATT TTAATAACAC 180  
 AGAAACATT GAGCATTGTA TTTCTCGCAT CCCTTCTCGT GAGCNCTTAG ACCTTTTNCCT 240  
 ATTTTAGTCG GATTTTGTG TGAATTTTG CTTNGTATG AACACTCAGC AGAAAAGTAC 300  
 TTACTTCTNG CCAGTTATCT ATTAACCAAA ACCNTTGATT TGTAGTTTAA AAGNTTAAAC 360  
 GNCAAAGTTC TNTNCATAAC TGCCTTGGCC AGTNNGGGT NGTNCCGGTN CTGGTTAATN 420  
 GCCTGTGGCN TTTNGGTGG TTTGTGNTG GTNTTACNT GNGCANTTAA GN 472

SEQ ID NO:496  
 SEQUENCE LENGTH:461  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00553

## SEQUENCE DESCRIPTION:

GATCAACCAA TTTNCTAAA AGTTCAGTCG AAAGCTTTTA AGTATAGCTT CCTCCCTTGA 60  
 AAAAAAATGT AAACATGAC TGCTGAGTGA TAAACACTG TGGTGTGAAA GTNTCATCTT 120  
 CACTGCCAAT CAGGCAAAGA CCGGAAAGAT TTGCATTTTA TTATGTCTGT CTTATCATGC 180  
 AATGGAAATN ATGCTTTTNG TAAGTATGCA TCTTACCAAT GATGTAACGG TTTAATACCN 240  
 TTGAATGTTT TAATAACCAA GTNGCTGCTG AACTTATACT AAATCAGGGG CCAAAAAACT 300  
 NGCTCTNATC NNCTCAAATN GTATNCNATA TCCATTAAATG TATCAGTTAT NCCAAAGCCT 360  
 TCAGGTGGAG GGGTTTACCA CCNTCCTAGG TCGTTCAACC AGGTTTGTG AGGAATGCAT 420  
 TCAAAGTGGC TNTATAAAAG ANGATTTTCT TTAGCATGAA A 461

SEQ ID NO:497  
 SEQUENCE LENGTH:459  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00554

## SEQUENCE DESCRIPTION:

GATCCCAAAA TTCCACTTTT CAACACAGAT GTGGACAACC TAGAAGGGAA GACACCACCA 60  
 GTTTTNTCTT CTAAGGCAA ATACAGGGCT CTGAAATGG ATTTTCTCTT ACCCCCTTCT 120

ACTTACGNCA CCATGGCCAT TCGAGAAGTG CTA AAAATGG ATACCAGTAT CAAGAACCAG 180  
 ACGCAGCTGA ATACAACCTG GCTTCGCTGA GCAGTACCTT GTCCACAGAT TAGAAAACGT 240  
 ACACAAGTGT TTGCTTCCTG GCTCCCTGTG CATTTTTGTN TTAGTTCAGA CTCATATATG 300  
 GATTTCAAAT CTTTGTAAATA AAAATTATTT GTATTTTTAA GTNTTTATTA GCTTAAAGAA 360  
 ATAATTNGCA ATATTNGTAC ATGTACACAA AATNCNGGAG GTTCTTANTT TTAGCTCAGG 420  
 NTATAAATNA GTCAAATNCN NNGGTNNNGG NTNNGNTGN 459

SEQ ID NO:498  
 SEQUENCE LENGTH:481  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00555

## SEQUENCE DESCRIPTION:

GATCCAGCAG AGAAGGATGA AAAGGGCATG CCTGTGACAG CTCGTGTGGT GTTTGTTTTT 60  
 GGTCTTGATA AGAAGCTGAA GCTGTCTATC CTCTACCCAG CTACCACTGG CAGGAACTTT 120  
 GATGAGATTC TCAGGGTAGT CATCTCTCTC CAGCTGACAG CAGAAAAAAG GGTGCCCACC 180  
 CCAGTTGATT GGAAGGATGG GGATAGTGTG ATGGTCTTC CAACCATCCC TGAAGAAGAA 240  
 GCCAAAAAAC TTTTCCCGAA AGGAGTCTTC ACCAAAGAGC TCCCATCTGG CAAGAAATAC 300  
 CTCGCTACA CACCCAGCC TTAAGTCTCT TGGAGAAGCT GGTGCTGTNA GCCAGAGGAT 360  
 GTCAGCTGCC AATTGTGTTT TCCTGCAGCA ATTCCATAAA CACATCCTGG GTGTCATCAC 420  
 AGCCAAGTTT TTTANGGTTN CTATACCAAT GGGTTTATTT AAATGAAAAT GGGCACTTAA 480  
 A 481

SEQ ID NO:499  
 SEQUENCE LENGTH:453  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00556

## SEQUENCE DESCRIPTION:

GATCCAGATG CAGAGGCCAG GATGTGGGCC CAGCCCTGTG CCAGGAGGCT GGCTGGAATA 60  
 AAGGTACAGA TAGAGGCCTC ACCCCCTCTG GGACCACTGG CACTCAGGGT GTTTCAGGCC 120  
 TCAGAGCCCA CCTGCCCCCA GGGCCACAGC TGCATCTCCT GCCCTGCTGT CATTACAGGG 180  
 ATGGGCAGGC TGGCATGGGG GCACCCGCTG CCCCTGCCTG GNTGTTGCTG TGTATTCCTG 240  
 CCGGCCAGGG GCACTGCCAG GACCACGCCT CCNTTTTAT ATCCNGATTC TTAAGTTCTG 300  
 CTATTGTGGT ATTCTGGTGG AGAAAAAAGA CCGNGTGGCT GTTTTTGAAC TGCCTGGAAC 360  
 CTAAGACCCT GAATTCTTTT CCCCCAAGG GAAAATCTAT ATGGAAACAT TTATTTAAAT 420  
 ACAGGATGAA GTAATTAAAA GNTTTAATTC AAA 453

SEQ ID NO:500  
 SEQUENCE LENGTH:446  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00557

## SEQUENCE DESCRIPTION:

GATCAAAGTT GGCAAGGTGC GGAAGTGGG CATGGGCGGC TACAGACCAC AACCGACTTC 60

ATCAAGTCTG TCATCGGTCA CCTGCAGACT AAAGGGAGCT AGAGCCCTTT ATTTCTTCCA 120  
 ACCTTGCAAG GACCACACTN CCCATACCNT TCAGTGCAGT GTACCAGGGA AGAGCCTTGT 180  
 GCCTCTAAGC AGTGGACCAT GGTACACCTG CTGGGTAGAG CCTAGGTTGT CCTTGGGCCG 240  
 GCTTCCTTAG GGGACAGACT NTTGGGTGGT GATGGGGATT GTAGGATGGA GCCAGGCACA 300  
 TGGATGATGA TGATTCTCCC NCACAGGTTG GAACCTCTGA CATGGGTGGC TATGCTACTN 360  
 GCNATGCTTA NTGAGGNTGT CATTGCTGCT TTNCCNAACC ATAGGCCTGT CATACNNTGT 420  
 AAGNGTCAA TAAGGACATG ACCAAA 446

SEQ ID NO:501

SEQUENCE LENGTH:434

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00558

SEQUENCE DESCRIPTION:

GATCCAATTC AGGTTAGGCT TGTTTGATTT TTTTTCAG AAAATGTATT CCATAAAGTT 60  
 TGTAAGTAGA CCAGACGGGT GACTAAGAA TCATTCATGA GTAAATGTGT GTTGAATATC 120  
 TACCCTTGAC CTTTTTTGA GAAATAGAGT AAACACAGTC CCTGTAGTCT GACAGCTAAT 180  
 GGGGAGAGAG GGTAGACTTT TCATCGAATT AAATTTCTAC ATGCACCTTT CCCCAGAAA 240  
 TCTTACTCAT GGCTGGTCTC AAGTAAGTCT TTATTGAAA ATATNGACAT ATCTNCTTCC 300  
 TCTTCTTCT CCTCACTGTC TTCCTTTAG TAGTTAGGCA GAGTTAATAG GTAAGAAAAA 360  
 TTATCTGCAT TTATGTGTAG TTTGTAATCT ACTAAAGGGG TTCTAGAATA AATGTNGNCA 420  
 TNTNGTAACN GAAA 434

SEQ ID NO:502

SEQUENCE LENGTH:430

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00560

SEQUENCE DESCRIPTION:

GATCAAACAG GTTCAAAGTA AAACGTTAAA TTTCACATTT NTTTTAAAGA ACTCTTAAAG 60  
 TGTAACAGTT ACGCCATACT TCATAAGTGG TAAAGAAAGG TATAAAATTT GGAAACATTT 120  
 TGTTGGGCAT AGTAGTGATT GGGTGAAAAG GATAAATTAT ATCAAAATGA GAATGTNCTG 180  
 TAATTGGAAG TAGGGAGCTA AAGGATGTTT CTTTCAGTTT AGTAGAACTG GAACGTTTTA 240  
 CTATTAAACA TGGCTTTTAT AAATNCATGG TCCAATAATT TTATTCACGT TTAGTATTTA 300  
 ATTCAGTGC AGCTTATTAA TGTTTTCTGT ACCCATTAAT GAATTTTAA TTACAAAAA 360  
 TTGTCTAGCA GCTTCCAGTT TAANAAATGG AACCTAGGCC ATTAAAATTA AATTTGGTAA 420  
 ATTTTTTAAA 430

SEQ ID NO:503

SEQUENCE LENGTH:428

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00561

SEQUENCE DESCRIPTION:

GATCCTAAAT GTGTTGCTGA AATCAGGCAG CCCGAGCCTC TGGTCTCTCC AGAGAGCCCG 60

TNTTCACATT TGTNTATTCC TCAGCACTCA CCCGAAACTG AACAGATGGG GAGTGGTCTT 120  
 GATTGTCAAG ATAAACTGG TGAAGAAAGC TAAATGCTGA GAAACTGAGC ATCTATTGTG 180  
 GTGTTTAAGC TTAGCTGGGT CCTTTCTAGT TTGTTTTTAC AGCTTACTAG GTGAAGTAGT 240  
 TTGCACTATT TTNGCAATAA ATTCATGGAA AACCTAACAG TTACTNGTNT NGTTTCTNAC 300  
 TGTGTGTATA TAANCTAATA CTAAANGTNT GGCATAGTGT TTNTGCACCT NCNTACATAA 360  
 CCNCTAACAT GCACAGAATG CTGGTAAATN TGATAAANTA TGANGTGANT GATGATNNGA 420  
 TANAGTGN 428

SEQ ID NO:504  
 SEQUENCE LENGTH:422  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00562

## SEQUENCE DESCRIPTION:

GATCCTCACC CTCCTGAGGC CCAGTGGGGA AGAATGAACA TGGCTTCATC CAGGTAACT 60  
 NATGCTGCCA TTTGCCAGC CTCTTCCATC CCAGCCCTGT CAGTNAGCCC AGGTCTGGTG 120  
 CAACTNCTGC AGGATGCCTG TAGTAGGGAA CTCTGGAAGT GTATTGGGCT GAGGTGGGAT 180  
 TTTCCCTCCC CACAGTGCAC TGAGCAATGG AGGGTGGTGA GGGAGCCATG CTGCTGAATT 240  
 CTGGTTGGCA TTTCCCATC ATGTAAATG GGGTGTGGG TAGGGCAGAC TCTGCTGGG 300  
 TTTGGTTGTA AGATAAACCT GGAGGAGAAG CACAGTTGTC CCATTGAATT ATTTGAGCAA 360  
 AAATACTGT AAATAACTTT TTTGGGCTNT TGTCAAATAA AATTTTTTTT TGTNTNTTA 420  
 AA 422

SEQ ID NO:505  
 SEQUENCE LENGTH:417  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00564

## SEQUENCE DESCRIPTION:

GATCTGATTC AGAAGGGCGT CATCCAACAC AAAGAGAAAT GCAACCAATG AAGAATCAAG 60  
 CCACTGAGGC AGGGCAGAGG GACCTTTGAT AGGCTACGAT ACTATTTTCC TGTGCATCAC 120  
 ACTTAACCTCA TCTAACTNNT TCCCGGACA CCCTCCACCT CTAGTTGTTA CTAAGTAGCT 180  
 GCAGTAGGCA TTGCTGGGGA AGAAACAAAC ACACACCAA CAGTACTGCT ACTTAGTTTC 240  
 TAAGGCTGCA CAGGGAAGGG AAAGACTGGG CTTTGGACAA TCTAGAGGTA ATTTATATCC 300  
 GCCCCAGGT GGAGCAACAT GCGATTNTGG AGGCACGGGG GTAAGTAAA GTGAGTACAT 360  
 ATAGTNTTTC TGGTTTCTGG GGATAACCCA TCAATAAAAG CTGCTTCCTC TNGTAAA 417

SEQ ID NO:506  
 SEQUENCE LENGTH:421  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00565

## SEQUENCE DESCRIPTION:

GATCTTCTTT ATAATTCTAC TTTGAGTGCT GTCTCCATGT TTGATGTATC TNAGCAGGTT 60  
 GCTCCACAGG TAGCTCTAGG AGGGCTGGCA ACTTAGAGGT GGGGAGCAGA GAATTCTCTT 120

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ATCCAACATC AACATCTTGG TCAGATTTGA ACTCTTCAAT CTCTTGCACT CAAAGCTTGT 180  
 TAAGATAGTT AAGCGTGCAT AAGTTAACTT CCAATTTACA TACTCTGCTT AGAATTTGGG 240  
 5 GGAATTTTA GAAATATAAT TGACAGGATT ATTGGAAATT TGTTATAATG AATGAAACAT 300  
 TTTGTCATAT AAGATTCNNT ATTTACTTCT TATACATTTG ATAAAGTAAG GCATGGTTGT 360  
 GGGTAAANCT GGGTTTATTT TTNGTTCCAC AAGTTAAATA AAATCCATAA AACCTTGGAA 420  
 A 421

10 SEQ ID NO:507  
 SEQUENCE LENGTH:413  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 15 CLONE:HUMGS00567

SEQUENCE DESCRIPTION:  
 GATCCCANAC TGGTCNTTGA ACAGACAGAA GGANGTAAAG GNTGGAAACT ACAGCCAGGT 60  
 GTGTACTGAA ATNAGGGCAG GATTAGAGGA AGGGTGGAGG GTCCTAACAG AATTGGGCAT 120  
 AGGAGGTCAG GGGATAAAAC ATCCCTTGCC CCCTCCTCTG AATCCAGGNC CTAGCCAATG 180  
 20 GNCTGGACAA CAAGCTCCGT GAAGACCTGG AGCGACTNAA GAAGATTCGG GCCCATAGAG 240  
 GGCTGCGTCA CTTCTGGGGG TGAGTGGGGG GTCTCATCTC CCTGCCTACC TCGACTCAGC 300  
 ATTCTCCTA CTCGNTCTTC TTNTTTTCCC AACCTTTTTG TTTCTTGCTT GTNCATGACC 360  
 TNGTGACTTN TTCNTNTTTT TACNTGTCAN GCCTTTNGTN GTCCTAGGGA CAN 413

25 SEQ ID NO:508  
 SEQUENCE LENGTH:407  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 30 CLONE:HUMGS00568

SEQUENCE DESCRIPTION:  
 GATCTNAGGG TGAACCACTT CATTCTGCAG GGTTCCTCCCT CCCACCTTAA AGAAGTTCCC 60  
 CTTATGTGGG TTGCCTGGTG AATGGCCTTC CTTCCCGCCA NAGGGCTTGT AAACAGACCG 120  
 GAGAGGACAG TGGATTGTTT ATACTCCAGT GTACATAGTG TAATGTAGCG TGTTTACATG 180  
 35 TGTAGCCTAT GTTGTGGTCC ATCAGCCCCT CACATTCCTA GGGGTTTNG AGTCTGTAGG 240  
 TGGTATGTGA CACCAAAGCC ACCTCTGTNA TTTGTNGTGA TGTCTTNTCT TGGCAAAGC 300  
 CTTGTGTATA TTTGTATATT ACACATTTGT ACAGAATTTN GGAAGATTTT CNAGTCTAGT 360  
 TGCCAAATCT GGCTCCTTTA CCAAAGGAN ATTACCCTTG NGGNAAA 407

40 SEQ ID NO:509  
 SEQUENCE LENGTH:402  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 45 CLONE:HUMGS00569

SEQUENCE DESCRIPTION:  
 GATCAAACAG TTTCTGGAGT GTGCCAGAA CCAGGGTGAC ATCAAGCTCT GTGAGGGTTT 60  
 CAATGAGGTG CTGCANCAGT GCCGACTTGC AAACGGATTG GCCTAATGAA GAAGTTCAAC 120  
 50 CTGGAGAGAT GGAAAATCAG CTCTCATAAC TANGTTAATT TAGTATAAAA NTAGAATTGA 180  
 TAGTGAGGGT ATAAAGTGTA ACCATCAGTT AAACCTCTCC TGTCATTCTT GGCTTCCTTG 240

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CTTCAGANTT GAAATGGAAG TGGGGGTGTC CCTACTCTGT AGAATCTGGG NCTGGGCAAA 300  
TGTGTTGTTG GCCTCCTTAA ACTAGCTGTT ATGTTATGAT TTTTNTTCTT TGTGAGTTAA 360  
TTAGGAATAA AGTCATTTTC TTTCCAAGGG TATGGTTCCA AA 402

SEQ ID NO:510

SEQUENCE LENGTH:396

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00571

SEQUENCE DESCRIPTION:

GATCATGAGA AGGAATGGAA ACTAGGCCGG TGCATTTTAC GGTTCCTGA GATTCTGCAA 60  
AAGATTTTAG ATGACTTATT TCTCCACACT CTCTGTGATT ATATATATGA GCTGGCAACT 120  
GCTTTCACAG AGTTCTATGA TAGCTGCTAC TGTGTGGAGA AAGATAGACA GACTGGAAAA 180  
ATATTGAAGG TGAACATGTG GCGTATNCTG CTATGTGAAG NAGTAGCTGC TGTCATGGCC 240  
AAGGGGTTTG ATATCCTGGG AATAAACCT GTCCAAAGNA TGTAATCCTT CATAGGTTTG 300  
ACACTGTGTG TTTTACCCAA GTGGCCATTG GNACTGTTTG CTTTTTACA ATCATGTGGG 360  
CACAAGCNTA AGAAAGGAAA TTNGCAACCA GGGAAA 396

SEQ ID NO:511

SEQUENCE LENGTH:384

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00572

SEQUENCE DESCRIPTION:

GATCCAATCA GATGCAGAGA ATGTGGATAC AGAATAATGT ACAAGAAAAG GACTAAAAGA 60  
TTGGNCGTTT TTNATGCTCG ATGAATGCTG GGAATTCAGA GGAATGTNTT CACTTATACT 120  
TGGATTTGCT CTCTTCCCAT TTCTGATTGT NGTATAGCTT TCGATTTTNC TTACAGTAGT 180  
TCCCCCTTAT CTNCGGGAGA TACATTCCAA GGCCCCCAGT GAACTCCTGA AACCTCAAAC 240  
AGTACCAAAC CTTTATACAC TGTTTTTTCC ATATATATAT ACCTATGATA AAGTATAATG 300  
TATANNTTAA GCATAGCAAG AGATAATAAT AATGTNATAG NCCATTGNTA CNANCTATAN 360  
TAANNGGTTA TGTGANTGTG AAAA 384

SEQ ID NO:512

SEQUENCE LENGTH:383

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00573

SEQUENCE DESCRIPTION:

GATCAGAGCA AAACATGCAG AGCCCTTAGC AGAAACCCAC TTAAATGCAT TTTCTTCATA 60  
TCCCTAAAGT TCCTTAAAAA TATGTGACAA TGCATCAGGA AGAGGAGAAC TGAAGAGTAG 120  
AAGTTCCCTT GCAGATTTT TTATCAGTGA CATGTAATGA GCAATTCACA GATGAGCGCA 180  
GGCAGAGCTC TGTGTGCCGT GTACATATGG ACCGTGCTAT GATGTGTCTC ACATTGGATG 240  
ATATTCCACT TTGGGAATTT TAGTATTTGT ATATAGAAAA TGGGTTTAAT AACTCACCAT 300  
GGTTTNTATT NGTCTTATAT TCGTTATTTT TTAAACTCT NGTATGTGTT TTTATAATAA 360  
ANAATAAAAG TAAGCCATGG AAA 383

SEQ ID NO:513

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00574

SEQUENCE DESCRIPTION:

GATCCAAAAT CATACTGTCA AGACCATCAA AAAAAACAAA GAAGCTTAAG TGAAC TAAGC 60  
ACAGGGAAAA GTTGT TTTT CACTCGTTCA TTTTGT CATC TGCTTCTAGA TGCTGCAATC 120  
AAGAAGTAGC AAATGCCCAA GTTGCCATAG TGT TTGCAGG AAAAAAAGAG AAAAAATAAT 180  
AAAAATAAGG AAGGAGCAAT GCCAAAAATT GAAGGAAATA TTATATAATT AANGCAAGAA 240  
GNTATCTATC CATTGAGNGA AACAATTTT ATATTATTG CTTT TAGCNG CAAAGCATT A 300  
GGAATTCTGA GATTGTTATA GCACTAAGAA GGT TTNATT CTGTGTACAC ACTGGAAAAAT 360  
TAA AATTCTG GGTAAAGGAA A 381

SEQ ID NO:514

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00575

SEQUENCE DESCRIPTION:

GATCCCCCTG GAAGAGGGAC TCCAATGGGC ATGCCCCCTC CGGGAATGCG GCCTCCTCCC 60  
CCTGGNATGC NAGGCNTTCT TTNACCCTG GCCACAGAGT ATGGAAGTAG CTCCGAGAG 120  
GCGTGGGCTC GATTCTCAG GGCCACGTTA CCACAGACCT GTTTGTTTCT NATGCTGTTG 180  
TTCGTGGAGT CTCATGGGAT TGTNTGGTT CCNTTACAGG GCCNCTCCC CNGGGAATGC 240  
GCCCAACAAG GCCNTAGACT CATCTTGGCC NTCCTCAGCT CCCTGCCTGT TTCCGGTAAG 300  
GCTGTACATA GTNCTTTTAT CTNCTTGTGG CCTATGAAAC TGGTTTATAA TAAACTNTTA 360  
AGAGAACATT ATAATTGCAA A 381

SEQ ID NO:515

SEQUENCE LENGTH:377

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00576

SEQUENCE DESCRIPTION:

GATCTGCGTG GGGCTGGTGG TGGTTGGTGT CCTGCTCATC ATCCTGATTG TNCTGCTGGT 60  
CGTCTTTCTC CCTCAGAGCA GTGACAGCAG TAGTGCCCA CGGACCCAGG ATGCAGGCAT 120  
TGCTCAGGG CCTGGGAACT GACCCAGCTG GTCCTGAAGG AGAAGCCAAA TGGCTGCACT 180  
GGCCGATTCT GGTCTCCAGA GGACCTTGGT GTTTGCTCTC CCTTGACCCA CCCCAGTNAG 240  
TGCCAAAGGG CAGCCCCAAC ATGTGCACCC CTGCATTTCC TGTCATGCCA CAGACTGGCC 300  
CTTGAGGGCA GCCTGCTGTA CTGGCCATGC TGGGCCAGCC NCACCTGGAG CTCAGTAAAA 360  
ACTGCTGTTT GATTAAA 377

SEQ ID NO:516

SEQUENCE LENGTH:375



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00577

SEQUENCE DESCRIPTION:

GATCACACCA GTTCAGAGAG CTACACTTTA TGGGTAACAG TTTCACCTGT NATACAGTTC 60  
 CCTAGAACAT TTTCCCAAAA GTAGTGAAGT GCAAAGTGCT TAGGTTTGAC ATTTATTGTA 120  
 GCAGAACAGT AATATCACAG TATGGGACAA AGGTTTACAC TTTGCAGGGT ATTCTTTGGG 180  
 GGAATGTTAA ATACTGTAAT AAAACATGT TCAATCATGG TAAATGTTC AACTNGTTAA 240  
 ANTTACAAAT GGNCAAAAAA NATTTTTTTC CTNATATATN GCCTAANTAC CAAATGAAGN 300  
 GCTTAANCTT AAGNTTCAAT GTGAAANCGA GTAAATNTGT TCCTAAATTT GCAGNAATAA 360  
 NAGATANCCN GTANN 375

SEQ ID NO:517

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00578

SEQUENCE DESCRIPTION:

GATCCATGTA CTGTTCATGTT TTTTTCAGG AACAAGCACA TCATGATTGA TTTGGGGACT 60  
 GGCAACAACA ACAAGATTAA CTGGGCCATG GAGGACAAGC AGGAGATGGT GGACATCATC 120  
 GAGACGGTGT ACCGCGGGGC CCGCAAAGGC CGCGGCCTGG TGGTGTCCCC CAAGGACTAC 180  
 TCCACCAAGT ACCGCTACTG AGGCGCCTCA GTCTGCGCGG ATAAATGTCTG TGGAGCCCTT 240  
 TTTGTATGGA AACGTTTAA GCTATTTAAA GCCTTTGGAA AATACAGGAN GTNCAGGGCT 300  
 GGAGCACCTC TGAGATGGAA TTGATAACAT GGTCTTAACT CACCGAAATA AACAAGCACG 360  
 TNGTGAGNGG NAAA 374

SEQ ID NO:518

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00579

SEQUENCE DESCRIPTION:

GATCTCACCG TGGGTCCGAT TAGCCTTTNC TCTGCCTTGC TTGCTTGAGC TTCAGCGNAA 60  
 TTCGAAATGG CTGGCGGTAA GGCTGGAAAG GACTCCGAA AGGCCAAGAC AAAGGCGGTT 120  
 TCCCGCTCGC AGAGAGCCGG CTTGCAGTTC CCAGTGGGCC GTATTCATCG ACACCTAAAA 180  
 TCTAGGACGA CCAGTCATGG ACGTGTGGGC GCGACTNCCG CTGTGTACAG CGCANCATCC 240  
 TGGAGTACCT NACCGCAGAG GTACTTNAAC TNGGCAGGNA AATTGCATCA AAANGACTTA 300  
 AAGGTNAAAN GGTTTTACCC CTNNGGTNANT TGCAACTTTG GTTATTNGN TGGGGGATGA 360  
 AGGNTTTGGG TTNN 374

SEQ ID NO:519

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00580

## SEQUENCE DESCRIPTION:

5 GATCAGAGAG ATTAGGATTG TATTTTGACA TAGGATTGG AACCCATCTA AATGTTGAAG 60  
 TTCCCTGAGA CAGCTCTCCA GCTGCTNNGC CTGCGCCAGG GGCTANGCAG CCCCTAATGA 120  
 GAGGCTCTGC TCCCTTTCCC ACCTCGCCAA TGTGTGTGTT GCTGCCTTTT TGATTGTAT 180  
 CCTCTGTTAT AGACATTTT NAAAAACGAT TTCCTCTTC ATTGTGCACA AGTGCTGAGA 240  
 GTCTNAGGCC CCATTTCTGC TGTGTATATA TATCCTGACT CGGGGCTTTT ATTCAGCAAA 300  
 10 CTGTTCAATC TTCTGTCAGA CAATGTCATA TTCAACTCTG TTCATATTAA ACCACTTGTN 360  
 AAGCANTNNA AA 372

SEQ ID NO:520

SEQUENCE LENGTH:371

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00581

## SEQUENCE DESCRIPTION:

20 GATCTGGTCG CTGCCCCAGG GGGACTGATG GGCAGNGTCG CCCCTGTGGC TGGACTGTNA 60  
 CCATCCCTGA TGGGGCCTGA CCGCGGGAGC TGAGGAAGCG CCGCTCCACC GTCTGCCCTC 120  
 CAAGGACCCG CATGGAGGCA GTGGGCTGGC AGCTTCCTGC TGCTCCGTGT NAGAGTCAAA 180  
 GCACAAATCC TCAGGACGGG CTCAAGGGCC AGGGCAGCCG AGGGAAGTNC AGGTGGGGAC 240  
 CACGTCTTCC TGAGGTTGGT GCCACTGCTT GGNACGTTT GCAGTGGGGT GGCCTCCCCCT 300  
 25 CTGTTTG CNT GGTGNAGNNA GCGTGGCGTG GGGACGTGAC TGAATAAAGC ACCATGGGTG 360  
 ATGTGTTGAA A 371

SEQ ID NO:521

SEQUENCE LENGTH:382

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00582

## SEQUENCE DESCRIPTION:

35 GATCTNTGGG ACGTCAGCTG CTGAGAGGAG CAAGCGGTAG TACCACCCCT TAGTTGAGGG 60  
 AGTCAGCACA GTCCTTTCTG CAGCTTCTAA CCCAGGACCA TGAATCAGG TGCCTAGAGA 120  
 AGCCAGGCAG CNNAAGGACA AGGAATGCTG GGGGCTGTGG GAACAGGAAT GCAGATACCC 180  
 TTTGAAGGAG CATTCTGCT AAAAGAAGCT GAAAATGTAG ACCTATGTGA AGTGCTCTGA 240  
 TTTCTAAATA TTGTGAAGGT TAAGAAAAAC ATANATTTN GGGTCTATGG GCTAGGATTN 300  
 40 AGNCCCACAG TTGGCCANTT TNTAGNGGT NCCCAAATGG ANTGGTTAA CCNNNGGTTT 360  
 NGNTTCCTAG CCTAGGGTA AA 382

SEQ ID NO:522

SEQUENCE LENGTH:382

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00583

## SEQUENCE DESCRIPTION:

50 GATCAAGAAC AATGCCTCCA CTGACTATNA CCTATCTGAC AAGAGCATCA ACCCTCTGGN 60  
 TGGCTTTNTC CACTATGGTG AAGTGACCAA TGACTTTNTC ATGCTGAAAG GCTGTGTGGT 120

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GGGAACCAAG AAGCGGGTGC TCACCCTCCG CAAGTCCTTG CTGGTGCAGA CGAAGCGGCG 180  
GGCTCTGGAG AAGATTGACC TTAAGTTCAT TGACACCACC TCCAAGTTTG GCCATGGCCG 240  
NTTCCAGACC ATGGAGGAGA AGAAAGCATT CATGGGACCA CTGAAGAAAG ACCGAATTGC 300  
ANAGNGAAGA AGGAGCTTAA TGCCAGGNAC AGATTTTGCA GTTGGTGGNN GTCTCAATTA 360  
AGNGTTATTT NNCCACTGGA AA 382

SEQ ID NO:523

SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00584

SEQUENCE DESCRIPTION:

GATCTCCAAG CNAACTCAGC CTCCANCCAA NCTCCCTGTG GGTCCTAGCC ACAAGCTCTC 60  
CAACAATTAC TATTGCACTC GCAATGGCCG CCGGGAATCT NTGCCCCCTT CCATCATCAT 120  
CNCGTGCGAG AAGTCGCTGG TGTCAGGCAA GCCAGCAGAG AGCTCTGCTG TAGCTGCCAC 180  
TGAGAAGAAG NCGGTGACTC CAGCTCCTCC CATAAAGAGG TGGGAGCTGT CCTCGGACCA 240  
GCCTTACCNG TNACACTGCA CCCTNACGGC ACCNGACTAC TTTGCCTGCT TGGATTTCT 300  
CCAGGGGAAT GTGACCTAAT TTATGNCAA TACGTAGAGT CAGGTATCAC TTCTAGTTTA 360  
CTNTAAA 367

SEQ ID NO:524

SEQUENCE LENGTH:365

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00585

SEQUENCE DESCRIPTION:

GATCAAGAGG AAAGAGAACG TAACAACCAG AACCCTGGA CATTTGAGCG AATAGCCACT 60  
GCCAACATGC TGGGCATACG GAAAGTACTG AGCCCATATN ACTTGACCCA CAAGGGGAAA 120  
TACTGGGGCA AGTTCTACAT GCCCAAACGT GTGTAGTGAG TGTAGGAGAT AACTGTATAT 180  
AGGCTACTGA AAGAAGGATT CTGCATTTCT ATTCCCCTCA GCCTACCCAC TGAAGTCTTT 240  
GGGTAGCTCT TAAGCCATAA CTAAGGAGCA GCATTTGAGT AGATTTCTGA AAAACAATGT 300  
TATTTGTTGA TTTAAAAAGA AAAGTGTATT NTTATTAAAT AAAATTTAAA CATCACTTCA 360  
GGAAA 365

SEQ ID NO:525

SEQUENCE LENGTH:396

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00586

SEQUENCE DESCRIPTION:

GATCTATGGG TTGACTAATT AAACAATAAT TCAAGTAGAG TGTCCCAGAA AAAAACCCT 60  
TGGGCTCCCT GTTTGGAGTC TGGCTGGCTC TGAGCATTGC CAATGGCCCC TACTCACCTG 120  
ACTTTGTATC CTCTCCTTTT AGAGGCTTTG CATTCTGCAC CCAGCTTCAC TAACAGTGGG 180  
CTGAAAACAT CCTTGGGTTG AGTGTTTCAT TTGGGAGTTA TTTGGCCAGG GCCTTTTGAA 240  
CAGTAGTGTC CCCATGAAGT GCTAGATAAT ATATGTGTAA GAGTCAGCTT TTTTTTTTTT 300

TAAACTNTAA CACCNTTNAG AANTTTCTAA CTACTIONGNA ACTGNATGGT TTANCCCGGN 360  
 GNTAAAAGCN GTTTTAAAA GTNTANGTTT TCCAAA 396

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SEQ ID NO:526  
 SEQUENCE LENGTH:360  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS00589

SEQUENCE DESCRIPTION:

15

GATCCGCGGG CTTCCACTNC ACCATCGGAT GTTTGCCACT CAGACTGAGG GGGAGCTCAG 60  
 AGTGACCCAA ATTCTCAAAG AAAAGTTTCC ACGAGCTACA GCTATAAAG TCACTGACAT 120  
 TTCAGGCACT AAAAGAAGAA ATCAAAGAGA TGCATGGATT GCGGATATTT ACCTCTGTCC 180  
 CCAAACGCTG ACCACGGCCT GGCTGCATAG ATGCTGCTGC TTAAGACCTT GGATGAACTT 240  
 CACTGACATC ATTCTTCCCT AAGCAGTCAC CAAAAATTT ATATATNTNG CTCATATACA 300  
 NTNCCATATN ATANTTATAG AAGATGTATA ATCTATTTTA GATGTNANTN AAAGGGTAAA 360

20

SEQ ID NO:527  
 SEQUENCE LENGTH:267  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

25

CLONE:HUMGS00590

SEQUENCE DESCRIPTION:

30

GATCGGGTTT GGCCCCCAGC CCCGCTCAGC CCAGTCCCTC TTCCTCTGCC GGGAGGGTGT 60  
 TTTCAACTCC AAACCCCAAG GAGGGGTGT AGATTGGGTC CAGCTTTGCT TCAGTGTGTG 120  
 GAAATNTCTC GTGGGGTGGC ATCGGGGCTG CGGGGTGGGG ACCCAAGGC TTTCTGGGGC 180  
 AGACCCTTGT CCTCTGGGAT GATGGGCACT GCTATCCACA GTCTCTGCCA GTTGGTTTTA 240  
 TTTNGAGGTT TNTGGGCTTT TTTTAAA 267

35

SEQ ID NO:528  
 SEQUENCE LENGTH:352  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00591

SEQUENCE DESCRIPTION:

40

GATCAATCAC CTTCTGCTGC TTGGATGGGT GGATTGGTG CTCAGCCTCC CCAAGGACAA 60  
 GCTCCTCCCC CTGTAATACC TCCTCCTAAC CAAGCCGGAT ATGGTATGGC AAGTTACCAA 120  
 ACACAGTGAG CCGGGACTCT AAAAAAAAAAT TGTAAATCAT GATAGGCTTC GATTTCTGT 180  
 GACACTCTGA AGACATGAAA GTAGACATCG GAAATGNAA ATATTTATTT TAAAAATTGA 240  
 AATGTTTGA ACCTTTAGCA CAGATTTGCT TTGGTGAAGG ACACGTGTCT TCTAGTTCTG 300  
 CCTTTTNAAG GTTTNTTGT CATGNTGGAT NTTGAACATN GNTTTTNTT TN 352

45

SEQ ID NO:529  
 SEQUENCE LENGTH:351  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

50

55

CLONE:HUMGS00592

SEQUENCE DESCRIPTION:

5 GATCAAGCCT TTCTTTCATT CCCTCTCTGA AAAGTATTCC AACGTGATAT TCCTTGAAGT 60  
 AGATGTGGAT GACTGTCAGG ATGTTGCTTC AGAGTGTGAA GTCAAATGCA TGCCAACATT 120  
 CCAGTTTTTT AAGAAGGGAC AAAAGGTGGG TGAATTTTCT GGAGCCAATA AGGAAAAGCT 180  
 TGAAGCCACC ATTAATGAAT TAGTCTAATC ATGTTTTCTG AAAACATAAC CAGCCATTGG 240  
 10 CTATTTAAAA CTTGTAATTT TTTTAATTTA CAAAAATATA AAATATGAAG NCATAAACCC 300  
 AGTTGCCATC TGC GTGACCA ATAAACATT AATGCTAACC ACTTTTTTAA A 351

SEQ ID NO:530

SEQUENCE LENGTH:348

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00593

SEQUENCE DESCRIPTION:

20 GATCCAGAAAT ACCCTGACCT CGCCCCAGTT CCAGCAGGCC CTGGGCATGT NCAGCGCAGC 60  
 TTTGGCCTCG GGGCAGCTGG GCCCCCTCAT GTGCCAGTNC GGTCTGCCTG CAGAGGCTGT 120  
 GGAGGCCGCC AACANGGGCG ATGTGGAAGC GTTTGCCAAA GCCATGCAGA ACAACGCCAA 180  
 GCCCCAGCAG AAAGAGGGCG ACACGAAGGA CAAGAAGGAC GAAGAGGAGG ACATGAGCCT 240  
 GGA CTGAGCC ACGCGCCGTC CTCCGAGGAA CTGGGCGNTT GCAGTGC GTT GCACACCTTN 300  
 25 ACCTTCNACN TACTGATTAT TAATAAAGTT TTTTCTTTA CCTGCAA 348

SEQ ID NO:531

SEQUENCE LENGTH:347

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00594

SEQUENCE DESCRIPTION:

35 GATCCTGAAG AGATTGAAAA AGAAGAGCAG GCTGCTGCTG AGAAGGCAGT GACCAAGGAG 60  
 GAATTTCAGG GTGAATGGAC TGCTCCCGCT CCTGAGTTCA CTGCTACTCA GCCTGAGGTT 120  
 GCAGACTGGT CTGAAGGTGT ACAGGTGCC TCTGTGCCTA TTCAGCAATT CCCTACTGAA 180  
 GACTGGAGCG CTCAGCCTGC CACGGAAGAC TGGTCTGCAG CTCCCACTNG CTCAGGCCAC 240  
 TGAATGGGTA GGAGCAACCA CTGACTGGTC TTAAGCTGTT CTTGCATAGG CTCTTAAGCA 300  
 40 GCATGGAAAA ATGGTTGATG GAAAATAAAC ATCAGTTTCT ATTTAAA 347

SEQ ID NO:532

SEQUENCE LENGTH:346

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00595

SEQUENCE DESCRIPTION:

50 GATCCGGTNT TGGTGCCAAT GTCTCCAAT TCACTTTTGC TCCTAGCACG ATTATATTTT 60  
 ACCTGGGACA TGCTGTATG CTGGGACTCA TGTATGTCTA CTGGACTCAG CTCAACATGT 120  
 TCCAGACCTT GAAGTACCTG GCCATCTTGG GCAGTGTGAC GTTCTGGCT GGCAATCGGA 180  
 TGCTGGCCCA GCAGGCAGTC AAGAGAACAG CACATTAGTT CCAGAAGAAA GATGGAAATT 240

55

CTGAAACTG AATGTCAAGA AAAGGAGTCA AGAACAATTC ACAGTATGAG AAGAAAAATG 300  
GAAAAAATA CCTTTATTTA AAAANGAAAA AAGTCCAGNT TGTAATA 346

5 SEQ ID NO:533  
SEQUENCE LENGTH:346  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS00596

SEQUENCE DESCRIPTION:

GATCTTGTAG CCTAGATAGG ATAGTNTGAC CTTCTAGCAT AGTCTTTTGG GCAAATNATT 60  
TGTGTTTTCA GTGTGTGGGG AAGCTGTCCT GGGGGCTGGG GCGACAGATA GCACATAGGC 120  
TGTTCCTGGG GCTGCAGGGG CTTCCNTGAG CTGGATGTTG TGGGTNTTGC CGTGCTTCAG 180  
15 GAAGTNTGGC GACCAGAAAG CGTAGACCCG GGGCCCAGGG TCTGCCCCGCC CCTGCAGCNT 240  
GGCCTCCCCG CACAGGCTGT GGCTTGCACT CCAGCCGNTC TAGTNTCTNA GGAATTTNCT 300  
TGTNACTTGT ACTGTGTAATA TAAAGCTTCC TGTTCAATA CCNAAA 346

20 SEQ ID NO:534  
SEQUENCE LENGTH:345  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00597

25 SEQUENCE DESCRIPTION:

GATCCTATGG CCATGACCCA GAAGTATGAG GNGCATGTNC GGGAGAGCAG GCTCAAGTAG 60  
AGAAGGAGGA CTTCAAGTAC ATGGTGGCTG AGCAGCGCTGC CAAACAGAAG CAAAAAATAC 120  
GGAAAGCTCA GCCCCAGGAC AGCCGTGGGG GCAGCAAGAA ATATAAGGNG TTCAAGTTTT 180  
30 AGGTCCCCTC AACTAGCCC TTTTTTTGGC CCTACGTCTG GATGCCTGGG CTTACACAAA 240  
GAACCACTC TCCCGCAGTT CCAAGGNTC TGTCATTTCA TGTTCTTATT TTAGACCTGT 300  
TTTGTAATA AAGCTGTTTC CCAAGGAAAG AGATGAATAT TTAAA 345

35 SEQ ID NO:535  
SEQUENCE LENGTH:354  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00598

40 SEQUENCE DESCRIPTION:

GATCGTGTTT ATGGTGAATC CAAGTTGGGA GGAAATGAAA TAGTATCTTT NTTGAAAGGA 60  
ATATTGACTC TTTTGCTAC TACATAAAAG AAAGATACTC ATTTATAGTT ACGTTCATTT 120  
CAGGTTAAAC ATGAAAGAAG CCTGGTTACT GATTTGTATA AAATGTACTC TTAAAGTATA 180  
AAATATAAGG TAAGGTAAAT TTCATGCATC TTTTATGAA GACCACCTAT TTTATATTTT 240  
45 AAATTAATA ATTTTAAAGT TGCTGGCCTA ATGAGCAATG TTCTCAATTT TCGTTTTCAT 300  
TTTGCTGTAT TGAGACCTAT AAATAAATGT ATATTNTTTT TTGCATAAAG TAAA 354

50 SEQ ID NO:536  
SEQUENCE LENGTH:343  
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00599

SEQUENCE DESCRIPTION:

5  
GATCCGTGAC AAGCGCACAG GCAAGACCAA GGGCTACGGC TTCGTCAGCT TCAAGGACCC 60  
CAGCGACTAC GTGCGCGCCA TGCCTGAGAT GAATGGGAAG TATGTGGGCT CGCNCCTCAT 120  
CAAGCTTCGC AAGANCATGT GGAAGGACCG GAATCTGGAC GTGGTCCGCA AGAAGCAGAA 180  
GGAAAAGAAG AAGCTGGGCC TGAGATAGGG TCTGTGGCCA GGCACCCGCT CCCACCTGGC 240  
10 CGGGCGCTGG CTCCTCCCTC AGTTCTCTTT GGGAAAACCC CCAGCTNGTC CACCCATCCN 300  
NTGCCCCAAA ACCAGTTTCA GTAAATTTAC GTTCATTTCC AAA 343

SEQ ID NO:537

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00600

SEQUENCE DESCRIPTION:

20  
GATCGAACGG ACTGTGAAAT CCGCTCTTTG TCGGAAGCTG AGCAAGCTGT GGCTTTTTTC 60  
CAACTCCGTG TGACGTTTCT AAGTGTAAGT TGGTAGGACC CCGGCGGGTG TGGCAGCAAC 120  
TGCCCTGGAG CCCCAGCCCC TGCNTCCATC TGTGCTGTGC GCCCCACAGT AGACGTGCAG 180  
ACGTCCCTGA NAGGTTCTTG AAGATGTTTA TTTATATTGT CCTTTTTTAC TGGAAGACGT 240  
ACGCATACTC CATCGATGTT GTATTGTCAG TGGCTGAGGA ATTCTTGTAC GCAGTTTTCT 300  
25 TTGGCTTTAC GAAGCCGATT AAAAGACCGT GTGAAATGAA A 341

SEQ ID NO:538

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00601

SEQUENCE DESCRIPTION:

35  
GATCCTCGGG TGTTCTTCCC ATCAGATAAA ATAGTTCAC TACAGACAGAT GTTTTTATCT 60  
ACTGAACTAC AAAGAGTAGA AGAGCTTTAT GATTCATTAT TACAAGCTGT TGCCTTCTAT 120  
GANTTAGCAG TGTTTGA CTCAGCCTTAG AATTCTGAGG TTAACGTGCT AAAGTATAAT 180  
TNTTAGCTCT AACGTAACAC CAACTGTTGT GAACATCCAT GTTATTGGAA AAGAACACAT 240  
TTTCAGTGTA TTTTAGATGT TTAANTTCTG ACTTTTGGCT ATTAAATGGT TTACACAATA 300  
40 AGCCAAGACC AAATCAATAA ACATTTTNTG AGAACGAAA 339

SEQ ID NO:539

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00602

SEQUENCE DESCRIPTION:

50  
GATCATCATC CGAGTGCAGA CCACGCCGGA CTACAGCCCC CAGGAAGCCT TTACCAACGC 60  
CATCACCAGC CTCATCAGTG AGCTGTCCCT GCTGGAGGAG CGCTTTCGGG TGGCCATAAA 120  
AGACAAGCAG GAAGGAATTG AGTAGGGGCC AGAGGGGGCT CTGCTCGGCC TGTGAGCCCC 180

55

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GTTCCCTACCT GTGCCTGACC CTCCGCTCCA GGTACCACAC CGAGGAGAGC GGCCGGTCCC 240  
 AGCCATGGCC CGCNTTGTGG CCACCNTCA CCCTGACACC GACGTGTCCT GTACATAGAT 300  
 TAGGTTTTAT ATTCCTAATA AAGTATAGCG GAAGAGAAA 339

SEQ ID NO:540  
 SEQUENCE LENGTH:339  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00603

SEQUENCE DESCRIPTION:  
 GATCGTTATG AATATCAAAAT GTCCATTTCT ATNGTAATGA ATTCAGTGGA ACCATCACAC 60  
 AAAAGCACAC AAAGACCTCC TCCTCCACAG GGGAGACAGA GGTGGGGAGG CTCTCTTGGC 120  
 TCACATAATC GTGTCTGTGT CACAAATAAT CATTAAATTA GCTATTTTCA GCTAACACAT 180  
 TTGTNGTTGC ACTTGAAAAA GAGTTAGTGA GCCTGTCTTG GAGTTTAAGT AGTTTCAAAT 240  
 AAAAAAAGGC TACAGTGCCT CACAAAGGAT GTTCCCAGCA AGTNGTTTAA ATTCCCAGCA 300  
 AGTTGTAAAA GTGTAAATAN AANTATATGA ANTTGTAAA 339

SEQ ID NO:541  
 SEQUENCE LENGTH:355  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00604

SEQUENCE DESCRIPTION:  
 GATCCTGAAA TCTACTAGAG ACACCCCTAA GCCATGAATG AACTACATCC AAATACCTGA 60  
 NTTTTTGGAA TCTGTTTCAT GGATTTTNCA TCTTCTACCG TATGTNAAAT TGCAAGTNTT 120  
 TGAAGATTTA TAAGTACAAA TTTGGGAACA TACAAATCTT TTAGGTAGTA GAGTTTAAACG 180  
 TGTATAAGCT AAAAGTGAAA GTAAGTGAAG GTTCTCTTGT TTCTTTGCAT TAATGTAACT 240  
 GTGTGGTTTG CCTTTGTCCC CCTGGATAGA ACGTGCATTT AAAGAATATA TTGTACTTAC 300  
 TGTGACAGCA GATAATAAAC CAGTCTCTTG GAGGGCACAA CCCTTATTTG ACAA 355

SEQ ID NO:542  
 SEQUENCE LENGTH:331  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00606

SEQUENCE DESCRIPTION:  
 GATCTTTTTT ANATAAANNT TATGTATTGT GGCATAATCC TTTTTTTGAG CTCTACAGAG 60  
 AACAGTCTTT TGTAATAGT GGCAGGTATT TATCCTTCT GAATATATAC CCCATTATAG 120  
 GAATAACTGT TACTTATTTA GGATTCCATC ATTGAAAATT TTNACCCAAG GCACAGCAGT 180  
 GAANTTTATA GTNCTCANTT TAGTTGNCA TATTGACAGG CATTGGNATT ATTAGTCATT 240  
 GCTAAGCAAC TAAAACTTCA TCAGTTCAAN TAAGTTTTAN TTGTCANATG GCNGTATAAN 300  
 CACATGANCT TTCTAGGAAA TATTCCTCN N 331

SEQ ID NO:543  
 SEQUENCE LENGTH:330



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00607

SEQUENCE DESCRIPTION:

GATCGGTGTG CCCCCTGCG AGGGGCCCC CATGGGGCTG NTGGCCNTC CGCAGTCAGG 60  
 ACATCCCAAC CCCTGGNTGG GACTGAACCA CCCAGAGCGG AGGGCNTCCC TTTNAGCCT 120  
 TGTNAGTCAC CTGGCAGGCC CCAGCTGGGC TGGCTGTCCG TGTCCCTCAG CCTGGNTGGT 180  
 GATTCCTTGC AGGCCAGAAA TNAAGAGTCC CTGTAGGTTT TGGTTTTGTT TGTTTTATTT 240  
 TGTTCCTTCA CCTTTTTTCC TCATTAAAAA AAAAANGNCC CTGNGGAGTG TACTNATTNA 300  
 TTTTTTGATN AAAGGGANGT AAAATGNAAA 330

SEQ ID NO:544

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00608

SEQUENCE DESCRIPTION:

GATCCAGACT GTAAGATGTT GTTTTAGGGG CTAAAGGGGA GAAACTGAAA GTNTTTTACT 60  
 CTTTTCTAA AGTGTGGTC TTTCTAATGT AGCTATTTN NTGTTGCAT CTTTCTACT 120  
 TCAGTACACT TGGTGACTG GGTTAATGGC TAGTACTGTA TTGNCNCTGT GAAAACATAT 180  
 TTNTGAAAAG AGTATGTA GTTCTCTTTT GAACTGTTAG ATGCTGAATA TCTGTCCACT 240  
 TTTCAATCCC AATTCTGTCC CAATCTTACC AGATGCTACT GGAATTGAAT GGTTAATAAA 300  
 ACTGCACAGT GCTGTTGGTG GCAGTNAAA 329

SEQ ID NO:545

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00609

SEQUENCE DESCRIPTION:

GATCACTAGA TTTATGGAGG AATTNGTCAC AAATNACTTN TAGAAAAATG CTGTCATATA 60  
 GTTCATTTCA TCATTTTCTG TTGCAGGAAG CCACTCCACC ACAGAATGCT AATATGCCAG 120  
 TGGTACCCAG TACCTCTTGT ATATAGGTTA TTGCAAAATAT TGTNCTGAAA TGCTTAACTT 180  
 CAGAATTACA TTTTTTAAAG TAAATAATTG TTTTAAATCT ATTTTGTAAGT GNTATAAAGT 240  
 ACAATAGAAT TTCTGGAGTA CAGATTAAAC TATTTGCACT AACACACGTG CCGTGCATGA 300  
 TTTAATAAAA TANCTNNACT CTCNTAAA 329

SEQ ID NO:546

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00610

SEQUENCE DESCRIPTION:

GATCACCGTG TGCTCAGGCC AGGTGTGAAT CCTGAGGTCC ATGGAGGTGC AGAGATGAGA 60  
 TTACTCCTAT TCACGTTGAA GTGATTTGCT TTGTAAACAA AAAATTGCAG CTATTGTCTA 120

GCTTTCATTT TTTACTGAG AACTTTAAAT TAGTCCCCTA TTAGAATAGG GTTGCTACTC 180  
 ANCTNTTTTN AAAAACCGAA TTTCATCATT TATCTAAAGA GNAAATATGC AGANTAAGTG 240  
 GTCTTGTTAA GAGTGCAATA TTATATNNNN ANGTAAGT AAAANTNAAT TTGGGGGGAT 300  
 TATTTATNCA GCATGANACC TANTNTGN 328

SEQ ID NO:547

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00611

SEQUENCE DESCRIPTION:

GATCCCNNGG ACGTGAGACT TANNCTTCCA GCCAGTGTGA ATCATTGTAT TTTGTCTCAT 60  
 AATCACAGCA CNCCTGCATG ACACAACAAC GTGCAGCATT TTTACATAA AAATATGGTA 120  
 GANTTAATTT ATGACATGGA AATGCCTTAC GTGGTATCAC ACTTAGTCTT GAAAAAACA 180  
 CCNAGGTGAC GTTTAAATTT TTTAGTACAT ATCCTCAAAT TGGAGCTAAG TTATACTTCT 240  
 TTTATAACCT TTTGGGCATC TGGTCGAGAG AAGACAAGAT TTTNTCTATT TACAGTGATG 300  
 CAATAAATAT GTTTGCCACC TTTGGA 328

SEQ ID NO:548

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00612

SEQUENCE DESCRIPTION:

GATCTTGAAG AGACCGCTGG CAGCACCAGT ATTCCTCAAGA GGAAGAAGTC TACACCCAAG 60  
 GAGGAAACAG TTAATNACCC TNAGGAGGCA GCCACAGAAG TGGCTCCAAG AAAAANAGGA 120  
 ATTNTCCAAA GAGGAGCCGG TCAGCAGTGG NCCTGAAAGA GCGGCTGGC AAGANCAGCT 180  
 CCAAGAAGAA GAAAATGTTT CATAAAGCAT CCCAGGANGA TTAGAATCAA ATGGACANTC 240  
 TCTNGGAGGT GGGNATACCA TAGNCCAAGG TNCATTTCCC ACCNTGTGCC GTGTTCCCAA 300  
 TAAANACAAA TTCACAAGGA AA 322

SEQ ID NO:549

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00614

SEQUENCE DESCRIPTION:

GATCCACCTA GCCTCAGCCT CCCAAAGTGC CGCCGGGATT ACAGGCGTNA ACACCATGAC 60  
 TGGCCTTCAT TATCTCTNTT TAAAAATGA AAAAGTTTAT AATTACATT CAGTAAATC 120  
 ACCCTTTTTA GTGTCTAGTC TGTGAATTTT GACAAATGCA TGGTTTGTG ACCAATCGAT 180  
 AGGNCAGTTC TGCCACCCAG GACATTCCCN TCTGTTCTC TGTTCCTCTC TTCTCCTGCC 240  
 CCCTAGCAAC CACTGGTGTT TTCTGTCCNT CTGGTTCATT TGACATTTAT TTTAAATAA 300  
 AATATTTTAA AATCTAAA 318

SEQ ID NO:550

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00615

SEQUENCE DESCRIPTION:

GATCCTCACC GTGGAGGACC ATNATAATNA AGGTGGCATT GGTGAGGCTG TGTCCAGTGC 60  
AGTAGTGGGC GAGCCTGGCA TCACTGTCAC CCACCTGGCA GTTAANCGGG TACCAAGAAG 120  
TGGAAGCCG GCTGAGCTGC TGAAGATGTT TGGTATCGAC AGGGATGCCA TTGCACAAGC 180  
TGTGAGGGGC CTCATNACCA AGGCCTAGGG CGGGTATGAA GTGTGGGGCG GGGGTCTATA 240  
CATTCCTGAG NTTCTGGGAA AGGTGCTCAA AGATGTACTG AGAGGAGGGG TAAATATATG 300  
TTTTGNGNAN AATGCAAA 318

SEQ ID NO:551

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00616

SEQUENCE DESCRIPTION:

GATCCCCTCT CTGAAGAGAA AGGAGGAAAG AAAAGAAAAA AACAGAAACA GAAGCTCCTG 60  
TTCAGCACCT CAGTCGTCCA CACCAAGTGA CACTACTGGN CCAGGCTACC TTCTCCATCT 120  
GGTTTTTTT TTTTNTTTT TTTCCCCAT GCTTTTGTTT GGNTGCTGTA ATTTTAAAGT 180  
ATTTGAGTTT GANCAGATTA GCTCTGGGGG GAGGGGGTTT CCACAATGTG AGGGGGAACC 240  
AAGAAAATTT TAAATACAGT GTATTTTCCA GCTTCCTGTC TTTACACCAA AATAAAGTAT 300  
TGACACAAGA GAAA 314

SEQ ID NO:552

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00617

SEQUENCE DESCRIPTION:

GATCCCTACT TGGNAGTTAA CCCTAACTAC TTGCTCGAAG ATTGAGATAG TGAAAGTAAC 60  
TGACCAGAGC TGAGGAACTG TGGCACAGCA CCTCGTGGCC TGGAGCCNGG CTGGAGCTCT 120  
GCTAGGGACA GAAGNTTNC TGGAAGNNAT NCTTCCAGGA TTTNTTTTTC AGAAACAAGA 180  
ATTGAGTTGA TGGTCCTATG TNTCACATTC ATCACAGGTT TCATACCAAC ACAGGCTTCA 240  
GCACTTCCTT NGGTGTGTTT CTNTCCCAGT GAAGNTGGAA CCAAATAATG TGTAGTCTCT 300  
ATANCCANTA CCN 313

SEQ ID NO:553

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00618

SEQUENCE DESCRIPTION:

GATCTTAGCT AGTTCATCAC TTCCTCAGGG AAACATTCCC TAATTTCTGT CACAGAGTAA 60

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GACCCGTTGT TATACGTCTC ACCTGACCAT GTACCTCTAC TTAGCATTTA ACACGTGTAA 120  
 TTTTGTATGT ATTGGTTTGA TTAATGTCAG ANCCACTAGA TTGTAACTC CATGAGGACC 180  
 GGAATTTNGT TTCTGTCATT GTCATTGTTT AACTTTGTAT TTTTATGTC TCATACAGTG 240  
 CCTGGCACAT AGTAGGTGCT CAATTAACCT NATTTGAAAG AATAAATGA ATGGATGAGG 300  
 TATCAAGAAA 310

SEQ ID NO:554  
 SEQUENCE LENGTH:310  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00619  
 SEQUENCE DESCRIPTION:

GATCTGGGGG CCACCACCCT GTGCCGGTGG CCTCTGGGCT GCCTCCCGTG GTGTNAGGGC 60  
 GGGGCTGGTG CTCATGGCAC TTCCTCCTTG CTCCCACCCC TGGCAGCAGG GAAGGGCTTT 120  
 GCCTGACAAC ACCCAGCTTT ATGTAAATAT TCTGCAGTTG TNACTTAGGA AGCCTGGGGA 180  
 GGGCAGGGGT GCCCATGGC TCCAGACTC TNTCTGTGCC GAGTGTATTA TAAATCGTG 240  
 GGNAGATGC CCGGCCTGGN ATGCTGTTTG GAGACGGAAT AAATGNTTTC TCATTCAGTC 300  
 TNCAGTCAAA 310

SEQ ID NO:555  
 SEQUENCE LENGTH:308  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00620  
 SEQUENCE DESCRIPTION:

GATCCNGTGC TGAAAGAGAA ACCAAGAAAA AAGATGACAT TCCAGAAGAA GACAAAGGAA 60  
 ATGTAAACA ATGTGAAATC AATTATGTAA AGAAATTTCA GAGCTTCAA GACCACAAAC 120  
 TTAATAAAG TAAAGANGAC AGTAAATTN TAAAAAGGC TCGAAAGAT GGATTTTGC 180  
 ATGAGACGCT TCTGGACAGG NGAGCCAAAT TGAAAGCCGA CAGATACTGC AAGTNACTGG 240  
 GATTTTNTT TCTGCCTTAT CTTNCTGTNG TTTTCTGA NTAAATATT CAGAGGAATG 300  
 CTTTAAA 308

SEQ ID NO:556  
 SEQUENCE LENGTH:300  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00621  
 SEQUENCE DESCRIPTION:

GATCTTCCTG AAGTNTCTCC CCGTTTNGTG CAGCTGGCCA TACCCAGGT GGACATNATG 60  
 AGTCAGGCTG ACTTAATTNC TCATGAGCAG ACCATCCCAG TGAATGCAA GGCATGGGC 120  
 TCCACAGCCT GGACCCTGGC ATGGAGTCCA GCNNCCTGCT CACCGGCCAG GAGGCCTGGG 180  
 GCGGGGTCAC TTACCCTTNT NAGCCTCANT TTCTNTTCT GGAAGCGGAG ATGGTAATAG 240  
 CTTTACATT NGAGGTGAAT GTNAGAATTA AACTTGGGCA CATGGAGGAA TACACCTAAA 300

SEQ ID NO:557

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00622

SEQUENCE DESCRIPTION:

GATCACTTGT CCTATTACCC TATACCTAGC ACTTGTGACA CCACCCCTAA ATCACTTTGA 60  
GCCTGGGAAA TAAGCCCCCT CAACTACCAT TCCTTCTTTA AACACTCTTC AGAGAAATCT 120  
NCATTCTATT TCTNATGTAT AAAACTAGGA ATCCTCCAAC CAGGCTCCTG TGATAGAGTT 180  
CTTTTAAGCC CAAGATTTTT TATTTGAGGG TTTTTTGTTC TTAAAAAAA AATTGAACAA 240  
AGACTACTAA TGACTTTGTT TGAATTATCC ACATGAAAAT AAAGAGCCAT AGTTTCAAA 299

SEQ ID NO:558

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00623

SEQUENCE DESCRIPTION:

GATCTGCTTC TCCAGTTTTT GAGGAGCCAG CCAGGGGTCC AGCACAGCCC TACCCCGCCC 60  
CAGTATCATG CGATGGTCCC CCACACCGGT TCCCTGAACC CCTCTTGGAT TAAGGAAGAC 120  
TGAAGACTAG CCCCTTTTTT TGGGGAATAA CTTTCCTCCT CCCTGTGTTA ACTGGGGCTG 180  
TTGGGGACAG TGC GTGATT CTCAGTGATT TCCTACAGTG TTGTTCCCTC CCTNAAGGCT 240  
GGGAGGGTGN TAAACACCAA CCCAGGANTT CTCAATAANT TTTTNATTAC TAAACCTGAA 300  
A 301

SEQ ID NO:559

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00624

SEQUENCE DESCRIPTION:

GATCAGATTT TGCTAAATGG AAATAATATA ACAATGCTGG TTCCTGGAGG AGAAGGACCT 60  
GAAGTGTGAA TGAGTTTCCT TGACTTACAC TAGATTTTGT TTTGGCTTAT AATGACAAGA 120  
AAATGGAATT TTTTTTCCC ACTTTCTAAT GTTTAAATCC CATAAAGCTA AGTTTCCCGT 180  
TAAAGGGAAG TGCTTTGAAG ATGTGTACCC ATTTTGTAA GTTAATCATG ATTATCCTGG 240  
AAAAAGAAGA AAAGAGCTTC TTCCTTGACAG ATGAAAATAA AGGTGTTTTT GGTAAAA 297

SEQ ID NO:560

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00625

SEQUENCE DESCRIPTION:

GATCTATTTG TAGATTAGGA TTAATGGA TTTAATCCAT TTTAAGGCT GTGTGAATTT 60  
TTCTAAACAA GAACCATTTG CAATATGGAT TTCTTAGAGA TTAAACCAAT TATAACTTAT 120  
TAGCAGTCGC GAGCACATGT TCATATAGTC AATGTAATAA TACACTAATG AGTATTTGGT 180

AAATCCCAGT AGGCTTTTAC CATTAGCATA ATTTTGTGTT GTACAATTAA GTTACAATTA 240  
CATCTCTAAT TTTGGATAAT ATTCATTGGT TAACANTANA GTGACAAAAG CTCATGCCTT 300  
CAAA 304

SEQ ID NO:561

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00626

SEQUENCE DESCRIPTION:

GATCTGGAAC TTTGCACATG TCACTACTGG GGAGGTGTTT CTGCTCTAGC TTCCACGATG 60  
AGGCGCCCTC TTTACCTATC CTCTCAATCA CTACTCTTCT TGAAGCACTA TTATTTATTC 120  
TTCCGCTGTC TGCCTGCAGC AGTACTACTG TCAACATAGT GTAAATGGTT CTCAAAAGCT 180  
TACCAGTGTG GACTTGGTGT TAGCCACGCT GTTTACTCAT ACAGTACGTG TCCTGTTTTT 240  
AAAATATACA ATTATTCTTA AAAATAAATT AAAATCTGTA TACTTACATT TCAAAAAGAA 300  
A 301

SEQ ID NO:562

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00627

SEQUENCE DESCRIPTION:

GATCTNAGGA GCTTTAGGGA GAAGACTTGG TGGGGCTGGA GCACACCTTG GGNCTCANTG 60  
GTTTCTGTGT CCCNGTGGTG CCANTCCTTC TGGGCAGTGC AGGCGGCTGC CAGGCCCAGC 120  
CCTGACTTCC ACTCTGGCTC AGCAACCTGG TTATTTATGT GGGGCCGTGC AGGCATGGGC 180  
CCACTGCCTG TCCATCCTGT TTCTNTTATA AATTGAACT CACCATTGCC CTATCCTTGT 240  
GTCTCCACCC GCTTCCATGT GTTGAATAAT AAAAGGTGGG AAAGTGCTGT CAAA 294

SEQ ID NO:563

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00628

SEQUENCE DESCRIPTION:

GATCTGCCAT AAGAAAATCT AGTTCAACTC TAATTTTATG TAGTAAATAA ATTGGCAGGT 60  
AATTGTTTTT ACAAAGAATC CACCTGACTT CCCCTAATGC ATTAAAAATA TTTTATTTTA 120  
AATAACTTTA TTTATAACTT TTAGAAACAT GTAGTATTGT TTAAACATCA TTTGTTCTTC 180  
AGTATTTTTC ATTTGGAAGT CCAATAGGGC AAATTGAATG AAGTATTATT ATCTGTCTCT 240  
TGTAATACAA TGTATCCAAC AGACACTCAA TAACTTTTTT GGTTGTAACT CTGAAA 296

SEQ ID NO:564

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00629

SEQUENCE DESCRIPTION:

5 GATCGACTAC AGAGTACTTN TTTCTTATGA TGATTGGTGT AGAAATGTGT GATTTGGGTG 60  
 GGCTTTTACA TCTTGCCTAC CATTGCATGA AACATTGGGG TTTCTTCAAA ATGTGTGTGT 120  
 CATACTTCTT TTGGGAGGGG GGTGTTTTTC TTCTGTTTAT TTTCTGAGAC TCCTACAGGA 180  
 GCCAAATTG TAATTAGAG ACACTNAANT TTGTTAATCC TGTCTGGGAC ACTTAAGTAA 240  
 10 CATCTAAAGC ATTATTGCTT TAGAATNNNC AAATAAAATT TTCCTGACCA AATTGTTTTG 300  
 TGGGAAA 307

SEQ ID NO:565

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00630

SEQUENCE DESCRIPTION:

20 GATCTTGCTC CTTCAGACTC TGACCTGAGT GGAGACCTTT CCACCAGACA CAGCTCGGGC 60  
 CTGTGTAATT GTAGGAGAAG ACACTCAGCA GTGATTGCCA TGGCACAGAG CCGTGGTCAT 120  
 TGTGCTGTT ACAAAGAAGA AAACCATCTG AGTTCTAACT CCTTGGTTGC TTAAGTAG 180  
 TTCCAAGAG TCTGAGAAGC TATTTCTATT TTAAAGAGTC ATTTTTGTGA ATNTTGTAA 240  
 NACAAAAGTA CCAATCTGTT TTGTAAATAA AANTCATCCT AAAATTTCGAN GTTAAA 296

SEQ ID NO:566

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00631

SEQUENCE DESCRIPTION:

30 GATCTTTNGC TAGGTGGATG ACTAGTNATA TTCAAAGCCT TTTCTCAAAG CCCTTTCAGT 60  
 TACAACCACC CCACTATGGA ATCAGTATTT AGTTATACAT TTGTATAAGA NCCTGTATTT 120  
 35 TGA AAAACAC ATTCATGTAT ATTTATTCCT GGAATTATTT GCCTGTAAAA CAGTGTCTTT 180  
 CATGTTCTCT CCCCAGATTG TAAACTCTGT AAGAAGCTGC TNGTATCTGT ATCCCTTGTT 240  
 GAAACTCTGA AAACACTGAA TAACTAAANT CTTCTTCTCA TCCNTAAA 288

SEQ ID NO:567

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00632

SEQUENCE DESCRIPTION:

45 GATCTTGATA TTCTGTACAA GTTGATGTAA TACCCTGATG CGTTTTAGAG GACTTGGCAT 60  
 AAAATNAAAG NTTGGCAAAG GCCCTTGAGG GGCTTGGGGA TGAGAGTATG GAACTGTCTG 120  
 CATTGGACCC TAAACTGGAC TAGANGAGGC ATCTTCAAGG TTCATACGTT GTCCAGCTGT 180  
 AAGTTCATTT GAGTAGCAGA GCTAACAAAT ATTTGAGGTC AAAACCCTAC CATGTTAAAA 240  
 50 CAAACAAAAA CTTATCATGT TAATAAAAGT ATTCATTGTC TTGANANANA AA 292

SEQ ID NO:568

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00633

SEQUENCE DESCRIPTION:

GATCCTGACA AGAAGAAAAT NAAGCTCAAA GTCAAAAAAT CTCGTGAAAA ACGGAGTTTG 60  
 GCCTCTCATC TCAGTGGATA TATCCCTNCC AAAAGGAAAC AAGGGCAAGG CTTATCTTTG 120  
 TGTCAAAACG GAGAGTCACC CAACTGTGTG GAAGACAAGA TGCTCTCGAC AGTTGCAGTA 180  
 CTTACCCTTG GCTAAGAACT GCACTGCTTT GTTTAAAGGN CTGCAGACCA AGGAGCGAGC 240  
 TTTCTCTCAG AGCATGCTTT TCTTTATTAA AATTACTGAT GCAGANAAAA A 291

SEQ ID NO:569

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00634

SEQUENCE DESCRIPTION:

GATCANGCTG GCTGCAAAGA AGGGACTGGA CCCATACAAT GTACTGGCCC CAAAGGGAGC 60  
 TTCAGGCACC AGGGAAGACC CTAATTTAGT CCCCTCCATC TCCAACAAGA GAATAGTAGG 120  
 CTGCATCTNT NAAGAGGACA ATACCAGCGT CGTCTGGTTT TGGCTGCACA AAGGCGANGC 180  
 CCAGCNNTGC CCCCCTNGT GGAGCCCATT ACAAGCTNGT NCCCCAGCAN CCTGGCACAN 240  
 TGAGGNACCT GCACTAAATT ACTNAAAATG TGCTGTAAAG NTTTN 285

SEQ ID NO:570

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00635

SEQUENCE DESCRIPTION:

GATCACCCTT GTAATGTGTT ACGGGTCCAT TTTTCCTGGA ATCGTTTAAAT CTAAAGCAGT 60  
 TTCCCCTGTT TTGGAGATT TNTAGTTAAT TTTAATTTTG GCTATTGTTT GGAAAAGATG 120  
 AGCTGTCTGT GTAGATATGA AGTATAGTTT TTNCCATAAA ACAGATGTTT ATTTGTATT 180  
 AAAAAATACC ACTGTACTTG TTTTACACCA TTTGTATACA TGTGGTGATA TTAATGCTAA 240  
 ACTGTAAAAT TCAGGAATTA AAATGTGACC CTGTAATTCC ATAAA 285

SEQ ID NO:571

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00636

SEQUENCE DESCRIPTION:

GATCTAACCA TTTTCATACT CTTAACTGAT TGAAACAGAT TCAAAGAAGT ATCGAGTGCT 60  
 ATGCATTGAA ACTTGTTTTT AAATGTTAGA TGGCACTATG TATATTAATG TAAANCAATG 120  
 TTAATTTACT CAAGTTTTCA GTTTGTACCG CCTGGTATGT CTGTGTAAGA NGCCAATTTT 180



NGTGTATTGT NACAGTTTCA GGTNATTNAT ATTCGATGTT TTGTAAANCT CAAATANCGA 240  
CTATACTNAT GGGNCCAAAT AAATGGGCAT CTGCATTCTN GGTAAAA 287

SEQ ID NO:572

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00637

SEQUENCE DESCRIPTION:

GATCTNTGGT GGCAATGNCT GACCAGTAGA CTGGTGGCTC ACTTCTNCCC ACCTGCCGGC 60  
AACACCAGTG CCAGGAAAAG GCCAAAAGAA TGTNTGTTT TAACAAATCC ACAAATAGCC 120  
CCGAGATTCA CCGTCCTAGA GCTTAGGNCT GTTTTCCACC CTCCTGACC CGTATAGTGT 180  
GCCACAGGAC CTGGGTCGGT CTAGAACTCT CTCAGGATGC CTTTCTACC CNATCCCTCA 240  
CAGCCTCTTN CTGCTAAAA AGATGTTTCA TTTTNTGGA AA 282

SEQ ID NO:573

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00638

SEQUENCE DESCRIPTION:

GATCTACTGG CGAGCGATGA AAATGTTGCA GGGAGAGTCA GCAGAGGCAT TTGTAGCTAA 60  
ACATGCTATG CATCAGACTG GCCATTTATG AAGATGAAGA ATACAGTCAG CTTTGTGAAA 120  
TAGTATTGCA AGCAAGCCCC GTGGGCAAAT TTGTATTGAG TCCATCTGTA ATTTGCTCAG 180  
TGATGGCAGA CAAGATGGCT GTCTGGTTTT GAGACACACT TTAATTTTAT GTTAACTTGT 240  
TAAATCTTTT TAAAAATTAA AAAATTTTGA TGATTGAAA 279

SEQ ID NO:574

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00639

SEQUENCE DESCRIPTION:

GATCATTGCA TTTTCTGTA TTTTCTAAAA TGGCTCCAAT TTTGTNTTTT AAGCTTCAGC 60  
TTAAGAGGAA GTTTATGTTT TAATTCCTGA CTGAGAATAC AGTATTGAGA TTCTNTGTTT 120  
TACAGATAAC AACTGGTTTT TATTACTCAT TAAGTTCATT TGCATCCCGT AGCCCTCTGT 180  
AAATGTTTCC CCTAGTTGTA TGTACGTAAA TGCACGCTTA TCCAGTNTAT ATTAGACATT 240  
TTTGTGCTAA AATATATTAA GTGGGATTTT TGTAGCAAA 279

SEQ ID NO:575

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00640

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTTTGCA AGGGCAAAAC TACAAGTAAC GAGTTTATA TAATTAATTT AAATTTNTNA 60  
 CAGGTTTTCA TGTTCAGGAT AAACCATACT TCCACCTTGG GTGAGAACAC TTGCAACAGT 120  
 TTATTAATGA GGTGACTTTC ACCTTAGGAC AACTGTTGCA TGCCAAGTTT TTTGTGTGTG 180  
 TGAAACACTN TCAAACTGA TTTAAAAGAT GTAAATTTAA AATTGGTTGT ATCTAATATG 240  
 CCCCAGGTTC GGTAAATAAA CAATTCTTTT TAAAAACAAA 280

SEQ ID NO:576

SEQUENCE LENGTH:300

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00641

SEQUENCE DESCRIPTION:

GATCTGCCTG TCCCTTTTTC CCCTGGGGTT TGACACACAG GCTCCTCTCA GCATGAGGTG 60  
 GAGCAGTGAC CAGGTGGAGC AGTGACCAGG ACGCCTCTGG CCCAGTGCTG CCCAGCCTCC 120  
 CCGNCCGCTC CCAGGCGCCC CATGTCCTCA CAGGCCAGGA CGCCATGNCA GGATGGAGAG 180  
 GACTTGGTGG ATTTTTGTTT CTTGCCTGAC CTCAGTTTCA TGAAAGAAAG TGGAAGCTAC 240  
 AGAATTATTT TCTAAAATAA AGGCTGAATT GTCTGAAAAA TAAATATATAT TTGTATTAAA 300

SEQ ID NO:577

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00642

SEQUENCE DESCRIPTION:

GATCTGGGAC GTGGTTCGGC GGANAGTCCC CAGCCCGGCC CCCTGCCTGG GACCACCAGG 60  
 CCCCCAGGAG AAGCCGCTG AGCCACAACC TTGCGGCATG CAAATNAGAT GGCCGCTCCA 120  
 GGCCTGGAAT GTTCCGTGGC TGGGCCCCAC GGAAGCCTG ATGTTCAGGG TTGGGGTGGG 180  
 ACGGGCAGCG GTGGGGCACA CCCATTCCAC ATGCAAAGGG CAGAAGCAAA CCCAGTAAAA 240  
 TGTTAACTGA CTTCCAGCCT CACCCGTGGG CGGTCAAA 278

SEQ ID NO:578

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00643

SEQUENCE DESCRIPTION:

GATCAGGGCC CACTGATGAT GGTGAAGAAG AGATGGAAGA AGACACAGTC ACAAACGGGT 60  
 CCTGAGCAGT GAGGCAGATG TATAATAATA GGCCCTCTTG GAACAAGTNT TGCTTTTNGA 120  
 ACATGGTATA ATAGCCTTGT TTGTNTTAGC AAAGTGAAT CTATCAGCAT TGTGAAATG 180  
 CTTAAGGCTG CTGCTGATAA TTTNNTAATA TAAGTTTGA AATCNAAATG TCAATTTNCT 240  
 ACAAATNATA AAAATAAACT CCACTCACNA TGCTAAA 277

SEQ ID NO:579

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00644

SEQUENCE DESCRIPTION:

GATCCGAGTC GTCCGGAAAT CCATTTGCCC GTNTTCTCAC AGTTATTAAC CAGACTCAGA 60  
 AAGAAAACCT CAGGAAATTC TACAAGGGCA AGAAGTACAA GCCCCTGGAC CTGCGGCCTA 120  
 AGAAGACACG TGCCATGCGC CGCCGGCTCA ACAAGCACGA GGAGAACCTG AAGACCAAGA 180  
 AGCAGCAGCG GAAGGAGCGG CTGTACCCGC TCGGGAAGTA CGCGGTCAAG GCCTGAGGGG 240  
 CGCATTGTCA ATAAAGCACA GCTGGCTGAG ACTGAAA 277

SEQ ID NO:580

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00645

SEQUENCE DESCRIPTION:

GATCAGGACC CACCTNCACT NCTTCTGAAA GTGTGACAGT GTCCAGCCGG TTCTGCAGCA 60  
 CTAGGGGAGG GGCAGATGG TGGTTGCATG GGCTTCCTGG GTCTCCACTC TCCGTCTGGC 120  
 CTAAGGTGA TGTATTTGGT GTTTGGCCCT GCAGTCCCCA CTCTTGAGGC TTAAGGCGCA 180  
 TGTGGCAGAN CACTNCTTCC AGCAGTAGTC GCTTTACTGT TACCNGTTTA GGCCTAGAAG 240  
 TTTTCNNCA TCTGTAAATG TGATTTAAAA TNTAAA 276

SEQ ID NO:581

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00646

SEQUENCE DESCRIPTION:

GATCTACTTA CTCAAGTCTN ATGAATNCTG NGCCTTTCAT CACATTCCTA GCCCACTCTC 60  
 ATCATTACTG CAGAAGGGTG TTGTGATGAC CAGTNTTATA CTGTGTTTG ATATGTCTAG 120  
 CAATAACTTA AAGAAAAAAA AACCTGGGAA ATCTTCAACA TGNNTNGGA ACATATATGT 180  
 ATGTATTAAT GNATATACAT GGCTTAACTT ATACGGTTAT GGCAGCNCCT GTATACAGTT 240  
 TGAAGTCATG NACCTGAAAA ANAATCTTA ANTTN 275

SEQ ID NO:582

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00647

SEQUENCE DESCRIPTION:

GATCGCCATC ATGAACGACA CCGTAACTAT CCGCACTAGA AAGTTCATGA CCAACCGACT 60  
 ACTTCAGAGG AAACAAATGG TCATTGATGT CCTTCACCCC GGGAAGGCGA CAGTGCCTAA 120  
 GACAGAAATT CGGGAAAAAC TAGCCAAAAT GTACAAGACC ACACCGGATG TCATCTTTGT 180  
 ATTTGGNTTC AGAACTCATT TTGGTGGTGG CAAGACAACT GGCTTTGGCA TGATTTATGA 240  
 TTCCCTGGNT TATGCAAAGA AAANTGGAAC CCNAACATAG NCTTGCAAGT CATGGCCTGT 300  
 ATGNGGN 307

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SEQ ID NO:583

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00648

SEQUENCE DESCRIPTION:

GATCTGAATT TTTTCTCCT TTTGGTTTTA TTTTGTGGT TTATTTTGTG TTTTCTTTTC 60  
 TCCTTTTTGG GGGGTATTCA GAGTGGGCTG GGCCCTGGG CGAGACACAG CTACCTCTGT 120  
 TGGCATCTTT TTAATACCAG GAACCCAGCG GCTCTAGCCA CTGAGCGGCT AAATGAAATA 180  
 AAGTGGAAAA AAAAAAANGG GAAAAACCCA AAGGNTTAAA AACCCACNGG AATTTTNTTG 240  
 TNGAAANTNG AAAATAAAGG TTTCCNNGTA AA 272

SEQ ID NO:584

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00649

SEQUENCE DESCRIPTION:

GATCTATACC AATTAAACAT TTTCATAGTT CTGCCTATTG TCCTTCCCTG AGGCTCCATT 60  
 GCTGCTTGGT GGCCATTCTC TGCCTTTTTA CAGTCACCTG AACAATGACC CATCATCTCT 120  
 TGCTTGCTTG AAATCTTGCT GAAATGTTCT CATTTCCTGT TTGCTGTATG GGCTCGGGTG 180  
 GGATGTTTGT TGGCTCTGTT GTGTTTATTC ACCAATTTGT ACATTATTTG TTGTCCTTTA 240  
 CTACTGTAAA CAGTAAATAT AGTTTGGTAT TCTGTCAA 279

SEQ ID NO:585

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00650

SEQUENCE DESCRIPTION:

GATCCCAGAC TGGTTCTTGA ACAGACAGAA GGATGTAAAG NATGGAAAAAT ACAGCCAGGT 60  
 CCTAGCCAAT GGTCTGGACA ACAAGCTCCG TGAAGACCTG GAGCGACTGA AGAAGATTCG 120  
 GGCCCATAGA GGGCTGCGTC ACTTCTGGGG CCTTCGTGTC CGAGGCCAGC ACACCAAGAC 180  
 CACTGGCCGC CGTGGCCGNA CCGTGGGTGT GTCCAGNAAG AAATAAGTCT GTAGGCCTTT 240  
 GTCTGTTAAT AAATAGTTTT ATATACCTNN AAA 273

SEQ ID NO:586

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00651

SEQUENCE DESCRIPTION:

GATCTNCCAC GTCTCCATCT CAGTACACAA TCATTTAATA TTNCCCTGTC TTACCCCTAT 60  
 TCAAGCAACT AGAGGCCAGA AAATGGGCAA ATTATCACTA ACAGGTCTTT GACTCAGGTT 120

# EP 0 679 716 A1

5 CCAGTAGTTC ATTCTAATGC CTAGATTCTT TTGTGGTTGT NGCTGGCCCA ATGAGTCCCT 180  
AGTCACATCC CCTGCCAGAG GGAGTTCTTC TTTTGTGAGA GACACTGTAA ACGACACANG 240  
AGAACAAAGNN TAAAACAATA ACTGTGTGTG TTAATA 275

10 SEQ ID NO:587  
SEQUENCE LENGTH:269  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00652  
SEQUENCE DESCRIPTION:  
15 GATCTTATGG ATAAACTCA GAAAGTGAAG GTGAAGAAAG AAACGGTGAA CTCCCCAGCT 60  
ATTTATAAAT TTCAGAGTCG TCGAAAACGT TGACGTGTTA TAGATAAGCC TTGTCATTNT 120  
GTATCAAAAA TCTGTTGTCG TTTTCTAGTA ACTTCAAATT CCATTACTCC AAATGGCATG 180  
GTTTTCCGGT TTGTAACCAT AACTAAATTG TCAGTCTGAC ATTTAATGTC TTTCTATGGA 240  
CAACATTAAA TCNCCCTCCC TTCTGTAAA 269

20 SEQ ID NO:588  
SEQUENCE LENGTH:272  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS00653  
SEQUENCE DESCRIPTION:  
GATCAAGTGG CTTTCCCTGG GACCTGCCCA GCTTTGAGAA TCTCTNCTCA TCCACCCTCT 60  
GGCACCCAGC CTCTNAGGGA AGGAGGGATG GGGCATAGTG GGAGACCCAG CCAAGAGCTG 120  
AGGGTAAGGG CAGGTAGGCG TGAGGCTGTG GACATTTTCG GAATGTTTTG GTTTTNTTTT 180  
30 TTTTAAACCG GGCAATATTG TGTTCAAGTC AAGCTGTGAA GNAAAATATA TATCANTGTT 240  
NNCCAATANA ATACAGTGAC TANCTGAACA AA 272

35 SEQ ID NO:589  
SEQUENCE LENGTH:268  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00654  
SEQUENCE DESCRIPTION:  
40 GATCGTCAAA TCTTTTNCAA ATTTAATNTA TATGTGTATA TAAGGNAGTA TTCAGTGAAT 60  
ACTTGAGANA TGTACAAATC CTTATCCAT ACCTGTGCAT GAGCTGTATT CTTCACAGCA 120  
ACAGAGCTCA GTTAAATGCA ACTGCAAGTA GGTACTGTA AGATGTTTAA GATAAAAGTT 180  
CTTCCAGTCA GTTTTTCTCT TAAGTGCCTG TTTGAGTTTA CTGAAACAGT TTTCTTTTGT 240  
45 NCAATAAAGT TTGTATGTTG CATTTAAA 268

50 SEQ ID NO:590  
SEQUENCE LENGTH:267  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00656

55

## SEQUENCE DESCRIPTION:

GATCAAAAAT AAAATGTTAT TTTAAAGTT TCTNTTTGAG ATTTNCTTA AGTTTGGTA 60  
GATATTCTTA AGTTTGTAGT ACCTCAGTTT GGGAATTAAG TAAGCTAAAC ATTGTGTCCT 120  
TATTATNAGT TATATAAAAC TATGCTTTAG ACTTTGTNAG AACTTCTGC CCCACCTGA 180  
CTGACTGCTT TNCCATTNT GGTGTACAA AATGAATTCA CACTTAAATG CTATGGCCAC 240  
CTTTAAATAA AGTACAGCGT GACTAAA 267

SEQ ID NO:591

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00657

## SEQUENCE DESCRIPTION:

GATCTAGATT CTACATGTTA CCATTGGTTT ATTCTGTGC TTTCTGTATT TAAACTTTG 60  
GCTGTACTAA GCAAAATGCAA GGTTATAATT TAGCTAATAG TAGTTTACAG ACAATTCTGA 120  
TGATTATGAT TTCATTGGT TTAATAAGC TGTACTAGTT CATTTCATAA GGAAATGATA 180  
CTGTAGACAA ATGTAAATAA AGCCTGTGAG TCAAGCATCA AGTGGTGTGTT GTTAGAAATA 240  
ANCTAGAGAT TTTTAACTC TGAAA 265

SEQ ID NO:592

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00658

## SEQUENCE DESCRIPTION:

GATCTGGGGC CAGCTCACCG CTCACGTCCC CGTCATCGAC AACTCCACCC TNTACATCAG 60  
TAGAGCATGC ACCATTTTGA ACGTGACATT TNCGGTAAAG TAACTATGC TGATTTCTCA 120  
GACTTTAAAG ATGCTCTNNT TCTGTGTGTN AAATAGGACC CAAAGTGTCT CGATTGCTGA 180  
AGTGATGAAC AAGTGGGAAA GCAGATTGA GACTATTTCC TTATCTGAAT ATTTAAATGA 240  
AATACAGCAT CTTTAAAANG CAAA 264

SEQ ID NO:593

SEQUENCE LENGTH:262

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00659

## SEQUENCE DESCRIPTION:

GATCTTTTAA AAAGATGATG CAGTCTGTGA TTTATTGTGC TGTGTCTGGT CCTAAGTGA 60  
GCCAATTAAN CAGGTTTCAT ATGTATTTN CCAGTGTGA ATCTCACACA CTGTACTTTG 120  
AAAATTTCTT TCCATCCTGA ATAACGAATA GAAGAGGCCA TATATATTGC CTCCTTATCC 180  
TTGAGATTTC ACTACCTTTA TGTAAAAAGT TGTGTATAAT TGTAAAAATC TGTGAAAGAA 240  
TAAAAAGTGG ATTTAAATTA AA 262

SEQ ID NO:594

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00661

SEQUENCE DESCRIPTION:

GATCCATCCA AAAACAAGGA CTGCAGCCTA AATTCCAAAT ACCAGAGACT GAAATTTTCA 60  
 GCCTTGCTAA GGGAACATCT CGATGTTTGA ACCTTTGTG TGTTTGTAC AGGGCATTCT 120  
 CTGTACTAGT TTGTCGTGGT TATAAAACAA TTAGCAGAAT AGCCTACATT TGTATTTATT 180  
 TTCTATTCCA TACTTCTGCC CACGTTGTTT TCTCTCAAAA TCCATTCCTT TAAAAAATAA 240  
 ATCTGATGCA GATGTGTAAA 260

SEQ ID NO:595

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00662

SEQUENCE DESCRIPTION:

GATCCCTTTA TGAACCTTG TGAATAGATG AATGNTTGA GATGGCGACT AGTGGACAAC 60  
 AGAACATAT TGGAATGGTG GTAATACGAG GAAATAGTAT CATCATGTTA GAAGCCTTGG 120  
 AACGAGTATA AATAATGGCT GTTCAGCAGA GAAACCCATG TCCTCTCTCC ATAGGGCCTG 180  
 NTTTACTATG ATGAAAAAT TAGGTCATGT ACATTTTCAT ATTAGANTTT TTGTTAAATA 240  
 NNCTTTTGTA ATAGTCAAA 259

SEQ ID NO:596

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00663

SEQUENCE DESCRIPTION:

GATCNNGGCT AAGCCAGCCA GCCCNCCCGC GCCAGGNAAA ACAGGGCTGC AGGTGTCCTG 60  
 TCTCCAGCC TCATCTGGCC GGCCTCCCA AACATTTGCC TGTCCATCAG CTCTTCCTCC 120  
 TTTCGAGTCA TGTGGAAAGG GACAGGNCCA AGTGGCCTTG GTGTTTAAAT CTGCCCCTAA 180  
 ATTGTAATC ACATGATTAT TTAAAGTCAC TAGANATAAG TAAGCACAGC AATAAAGNTT 240  
 TAATGGAATA AAAGAAA 257

SEQ ID NO:597

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00664

SEQUENCE DESCRIPTION:

GATCCCAGAA TTCAACCTGT ATTTATAAAT GTATAATGTA TTTAGCTACT TTTTGGTTTA 60  
 AATGAACTTG TTGGGTTAGC TTGGTAAATG TTATAATTTT NACTATTTTC TACAAAGAAA 120  
 ATATTTTCTA ATTTAAGTTG GAGCTATCTG TGCAGCAGTT TCTCTACAGT TGTGCATAAA 180  
 TGTTTTNCT ATAAATGAG CTAATGTATA ANATACTGCT GTATACCATA ATAANGATAG 240  
 TAATACTTGA AA 252

SEQ ID NO:598

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00665

SEQUENCE DESCRIPTION:

GATCATTAGT TGAATCGGTA TCATCTTCAC CAAATAAAGA AAGTAATGAA GAAGAGCAAG 60  
 TGTGGCACTT CCTTGGCAAG TGATTGAAAC ATCTGAAATT CTGCTGTCAA GATTCCCATC 120  
 TCTAAGGACT CCAAGTGCTA GAGACAAGGG GGTCTATGAG CATTTACTGA CTCCTGTTA 180  
 AAACCTTCATT TTTTCAAAC TTTTGAGCTA TGCAATATAT AANTAAACAG TAAGAATTTT 240  
 AAATTACAAA 250

SEQ ID NO:599

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00666

SEQUENCE DESCRIPTION:

GATCCTTCTT CCTTTCAC TGCTGCGCTC CCANNAGGTG CAGAGATTCT TAGAAGAGGA 60  
 GGTGTATCCC CTGTTAAAC CATATGAAAG CGTGATGAAG GTGAAAGCAG AATTATGTCT 120  
 GTAGAGTTGG AAGAGAATTA AACGAAAATC ATTGTTAATT GCTGAGGCAT GAAAATTGTG 180  
 TTAATAAT GCCTTATTTT ACCTCGAGAA TTGTTACCTT AAATTAGTAC AGCACTTTCT 240  
 TCTTCCCAA 250

SEQ ID NO:600

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00667

SEQUENCE DESCRIPTION:

GATCCTTCAG TTACATACAA TTTGTTTAAAT GAAATGTCAT GGCTCTGTTC ATATTTTNNT 60  
 NTTGTNCTTC CAATTGGTAT ATACAACCTT CAGAGCCTCT TGTATTTGGA AGGCTGGAAG 120  
 GGCCAGACT TTGGAATAGT GTCTTGGTTT CACTGTTTTN GTTTTGATTT TTTTTTGT 180  
 TNGATTTTTT TAAACTAAA GCTATATAAA GCTTGNGGAT TAANCAGANT AAATTCCTAA 240  
 ATTTAAA 247

SEQ ID NO:601

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00668

SEQUENCE DESCRIPTION:

GATCCAGGGT GTGTGTGAGT TGAGGGTGGG TGGAGGGGTT TGCAGTGTGG GAATGTGGCC 60  
 CTGCAGTTGA CCTGAGCTGC TTCACATGGT TGTCCATTCT GGGGCTTAAA GAACTGGGAC 120



# EP 0 679 716 A1

CAGACCAAGT AGAGGCCTTG GTGCTGNTTG GGGTGGGGCC TGCAGANTCT TAGTTACTGA 180  
TTTCATTTTC AATAAATGTA GGTGTGTTAC ATGAGTTTCC CAATTAAAAA AAAAATGACT 240  
TCTAAA 246

SEQ ID NO:602  
SEQUENCE LENGTH:284  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00669

SEQUENCE DESCRIPTION:

GATCAGAATT TCACCAGGGA GTAAAATTAC CTGAAAACGT AAGANGTTTT AAACAGCTTT 60  
TCACACAAAT TAGATGCAAC TGTTCCCATG TCTGAGTACT TATTTAAAAG AAAGGTAAAG 120  
ATTGGCCTGT TAGAAAAAGC ATAATGTGAG CTTTGGATTA CTGGATTTTT TTTTTTTTNA 180  
AACACACCTG GNGNGGNCAT TTGAAAACAC TTTTCTTACC CTCGANCCCT GATGTGGTNC 240  
CATTATGTAA ATATTCAAA TTTTAAAAAT GTATATATTT GAAA 284

SEQ ID NO:603  
SEQUENCE LENGTH:249  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00670

SEQUENCE DESCRIPTION:

GATCGAGGTG GAGAAGCCCT TTGCCATCGC CAAGNAGTAG GGCACAGGGA CATCTTTCTT 60  
TNAGTGACCG TCTGTGCAGG CCCTGTAGTC CGCCACAGGG CTCTGAGCTG CACTNGCCCC 120  
GGTGTGGCA TCTGGTGGAG CGGACCCACT CCCCTCACAT TCCACAGGCC CATGGACTCA 180  
CTTTTGTAAC AAACCTCTAC CAACACTGAC CAATAAAAAA AAATGTGGGT TTTTTTTTTT 240  
TTAAATAAA 249

SEQ ID NO:604  
SEQUENCE LENGTH:244  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00671

SEQUENCE DESCRIPTION:

GATCGGAATG GTGGAGAACT TCAACCAGGC ACTCAAGGAA ATTGGGGATG TGGAGAACTG 60  
GGCTCGGAGC ATCGAGCTGG ACATGCGCAC CATTGCCACT GCACTGGAAT ATGTCTACAA 120  
AGGGCAGCTG CAGTCTGCCC CTTCTAGCC CCTGTTCCCT CCCCCAACCC TATCCCTCCT 180  
ACCTCACCCG CAGGGGAAAG GAGGNAGGCT GACAAGCTTG AATAAACAC AAGCCTCCGT 240  
TAAA 244

SEQ ID NO:605  
SEQUENCE LENGTH:244  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00672

## SEQUENCE DESCRIPTION:

GATCCCCTTT CCGTAAAAGC GTGTAACAAG GGTGTAAATA TTTATAATTT TTAATACCTG 60  
 TTGTGAGACC CGAGGGGCGG CGGCGCGGTT TTTNATGGTG ACACAAATGT ATATTTTNCT 120  
 AACAGCAATT CCAGGCTCAG TATTGTGACC GCGGANCACA GGGGACCCCA CGCACATTCC 180  
 GTTGCCCTTAC CCGATGGCTT GTGACGCGGA GAGAACCGAT TAAAACCGTT TGAGAAGCTC 240  
 CAAA 244

SEQ ID NO:606

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00673

## SEQUENCE DESCRIPTION:

GATCTTTCCC ATNTCTACCT AAGTCAGCTT TCATCTTTGT GGATGGTGTC TCCTTTACTA 60  
 AATAAGAAAA TAACAAAGCC CTTATTCTCT TTTTNTTG TCCTCATTCT TGCCTTGAGT 120  
 TCCAGTTCCCT CTTTGGTGTA CAGACTTCTT GGTACCCAGT CACCTCTGTN TTCAGCACCC 180  
 TCATAAGTCG TACTAATAC ACAGTTTTGT ACATGTAACA TTAAAGGCAT AAATGACTCA 240  
 AA 242

SEQ ID NO:607

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00674

## SEQUENCE DESCRIPTION:

GATCCGGGTG GATGCACAGC CCGTCAAGGT CTATGCTGAC GNCTCCCTGG TCTTCCCCCT 60  
 GCTTGTGGCT GAAACCTTTG CCCAGAAGAT GGATGCCTTC ATGCATGAGA AGAACGAGGA 120  
 CTGAGCGGCT GCGGTCCCAG GAAGGTCTTA CCCCTCTNC TATTTATNAA TTTGCAGACC 180  
 CAGCCNTCC CCTACTTTT GGTCTAGTAC GNCTCTAGAA TAACNCCCGG TATCTGAAGT 240  
 CCAAA 245

SEQ ID NO:608

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00675

## SEQUENCE DESCRIPTION:

GATCTCTACC ATTTAATTAA GAAAGCAGTT GCTGTTGAA AGCATCTTGA GAGGAACAGA 60  
 AAGGATAAGG ATGCTAAATT CCGTCTGATT CTAATAGAGA GCCGGATTCA CCGTTTGGCT 120  
 CGATATTATA AGACCAAGCG AGTCCTCCCT CCAATTGGA AATATGAATC ATCTACAGCC 180  
 TCTGCCCTGG TCGCATAAAT TTGTCTGTGT ACTCAAGCAA TAAAATGATT GTTTAACTAA 240  
 ACAA 245

SEQ ID NO:609

SEQUENCE LENGTH:241

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00676

SEQUENCE DESCRIPTION:

GATCTAAAAT GTCACATTCA GATTTTNAGG AAGAAAATCT TCATTACAGT GGAGCACAAA 60  
 TTTCCATAC AAGACATCAT TGAGGNAGCA TGCTGTCCCC TTCTAACCTG AAACACATTC 120  
 TTTCCCATCC NGGTTGGGCT TCTNTACCNC CTTATTAATT TATGAACCNG AAGTTGCTTG 180  
 AAGTGTTTTG GGCTTAATAA ATGGGGTGAA AGTATAGGTA GCAGTAACAC CTACATGNAA 240  
 A 241

SEQ ID NO:610

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00677

SEQUENCE DESCRIPTION:

GATCTTCTGA GGTCAGGAGT TTGAGACCAG CCTGACCAAC ATGGAGAAAC CCAGTCTCTA 60  
 CTGAAAATAC AAAATTAGCC GGGCATGGTG GTGCACGCNT GTAGTCCCAG CACTTGGGA 120  
 GGCTGAGGCA GGAGAATCGC TTGAACCCAG GAGGCGGAGG TTGCGGTGAC CCTCCAGCTT 180  
 GGGCAACATG TTATGANTGA AACTCCATCT CAAAAAATAA AAAAAAAAAA GGGNNGCAAA 240

SEQ ID NO:611

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00678

SEQUENCE DESCRIPTION:

GATCTGTGAA GGCTTCCCTG ACCNNTGCCC AGGAAGAGTT CACTGGTTCGC TCTGTTGTGC 60  
 CCCACAGCAC TTTGTTATAC CTCTGCCACA CACTTCACGC AGCGCGTTGT AACTCATGTG 120  
 TTTACATGTC TGTCCNCCA GACTGTNAGC TCCTTGAGGG CAGGGACTGT ACATTCTCCA 180  
 GCTCTGTGTC CCCAGGGCCT GGCACATTGT AGACGCTTAA TAAATTTCTG TTAAATGAAA 240

SEQ ID NO:612

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00679

SEQUENCE DESCRIPTION:

GATCAGCTCC TTGACCTCTG AGGGGCAGGN GTGCTTCCTG GTGTGTGTAT TAGAATCCCT 60  
 TCCTGCCTTG TTTTCATGGCA GTGAAATGCC TCTTGGTCCT GTCCAAGTGT ATCTTTCACT 120  
 GATTCTGNA TCATGNTCTA GTTGCTTGAC CCTGCCANAT GGGTCCAGTG TTCATCTGAG 180  
 CATAACTGTA CTAATCCTT TTTCCATATC AGTATAATAA AGGAGTGATG TGCAATAGCA 240  
 AA 242

SEQ ID NO:613

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00680

SEQUENCE DESCRIPTION:

GATCGCAACA ATNAGCCATC CACATNCGTT TTTGAGGGTC ACACCCAAGT AATTGAAAAG 60  
 ACACTCCTCC ACTTATCCCC TCCNTAATAT GGCTCTNCGC ATGCTGAGTA CTGGACCTCG 120  
 GACCAGAGCC ATGTAAGAAA AGGCCTGTCN CCTGGAAGCC AAAGGACTCT GCATTGAGGG 180  
 TGGGGGTAAT TTTTCTTGG NGGGCCCAGT TAGTGGGCTT NCGNANTGTN TGTATGNGN 239

SEQ ID NO:614

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00681

SEQUENCE DESCRIPTION:

GATCCAAATA AACAGACCCC GTCTGGCAAG AAATGCATTG CAGCCAAAAA AATTAAACAG 60  
 TCGGTGGGAA ACAAAAGCAT GTCCTTTCCA ACTGGAAAGT CAGACAGAGG CTTCAGGTAC 120  
 AACTGGCCAC AGAGATAGTC CTGGAAGACA CGTGGCGCCT GTGGACCGGA AGCACCAAAT 180  
 GCTGGTGCTG CTTTGTACA TACATATTTT TAAACCATTA AAATTCTTCC TGAAGAAA 238

SEQ ID NO:615

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00682

SEQUENCE DESCRIPTION:

GATCCATAGT CAGAAAAGTT ACTGCAGCTT AAACAGGAAA CCCTTCTTGT TCAGGACTGT 60  
 CATAGCCACA GTTTGCAAAA AGTGCAGCTA TTGATTAATG CAATGTAGTG TCAATTAGAT 120  
 GTACATTCCT GAGGTCTTTT ATCTGTTGTA GCTTTGTCTT TTTCTTTTTC TTTTCATTAC 180  
 ATCAGGTATA TTGCCCTGTA AATTGTGGTA GTGGTACCAG GAATAAAAAA TTAAGGAATT 240  
 TTAACTTTT CAAA 254

SEQ ID NO:616

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00683

SEQUENCE DESCRIPTION:

GATCAAAGAA AGAAGGCATA CGCNGATTTC TACAGAAACT ATGATGTCAT GAAAGATTTT 60  
 NAGGAGATGA GGAAGGCTGG TATCTTTCAG AGTGTAAGT AATCTTGGAA TATAAAGAAT 120  
 TNCTTCAGGT TGAATTACCT AGAAGTTTGT CACTGACTTG TGTTCTGAA CTATGACACA 180  
 TGAATATGTG GGCTAAGAAN TAGTTCCTCT TGATAAATAA CCANTTAACA AATNCTTTNG 240  
 ACAGAAA 247

SEQ ID NO:617

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00684

SEQUENCE DESCRIPTION:

GATCTGCACC TGAGCCAAAG AAACCTGAGG AAAATCCAGC TTCTAAGTTC AGTTCTGCAA 60  
GCAAGTATGC TGCTCTCTCT GTTGATGGTG AAGATGAAAA TGAGGGAGAA GATTATGCCG 120  
AATAGACCTC TACATCCTGT GCTTTTNTCC TAGTTTCTCT CCACCCTGGA ACATTGAGA 180  
GCAATCAAA ACCTCTATCC AGACAAGACA AAATAAACT CAACATCTCC TGAAA 235

SEQ ID NO:618

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00685

SEQUENCE DESCRIPTION:

GATCTGTTCC TTGGCAGTGG ACTCAGAAAG CCAACATGTG GCTCCTCCCA GCCCATAACC 60  
AGTATTTTTC CTGCTTCTAA ATACAAATNG GTTGGTTTA ACTTCANATT GANCTTACTG 120  
TAGCCTCAAA TGATTTCCCC CCTCCGCCTC CAGGAAGAAA GAATGTNACT GCCTTAATAA 180  
AAAATGAAAA GAGAATGATG CTCAAAATCT TTCAAATAA AATGTTCCCT ATATTAAA 238

SEQ ID NO:619

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00686

SEQUENCE DESCRIPTION:

GATCCGCCCT CGAATGGACA CATTACCAGT GAAGGGGCAT TTNTNGTCAA TGTAGGTGCC 60  
CTCAATAGCC TCCTTGGGTG TNTTGAAGCC CAGACCGATG TTCTGTAGT ACCGCGGGAG 120  
CTTCTCCTTG CCAGTTTCTC CCAGCAGGAC CCTCTTCTNG TTTTGAAAGA TGGTCGGCTG 180  
CTTTTGGTAG GCACGCTCAG TCTGAATGTC CGCCATCTTC CCGGCCGGCT GAAA 234

SEQ ID NO:620

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00687

SEQUENCE DESCRIPTION:

GATCCCAAG CCTGGCAAGG GAATTTNTTC AACTCCCTGC CCCCAGCCC TCCTTATCAA 60  
AGGACACCAT TTTGGCAAGC TCTATACCA AGGAGCCAAA CATCCTACAA GACACAGTGA 120  
CCATACTAAT TATACCCCT GCAAAGCCCA GCTTGAAACC TTCACCTAGG AACGTAATCG 180  
TGCCCCCTAT CCTACTTCCC CTCCTAATT CCACAGCTGC TCAATAAAGT ACAAGAGCTT 240  
AACAGTNNA A 251

SEQ ID NO:621

SEQUENCE LENGTH:241

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00689

SEQUENCE DESCRIPTION:

GATCCATCAT CCGNCAATGT TAAAAGGCC CGTGCGCGAG GGCGACGTGC TCACCCTTTT 60  
 GGAGTCAGAG CGAGAAGCCC GGAGGTTGCG CTGAGCTTGG CTGCTCGCTG GGTCTTGGAT 120  
 GTCGGGTTCG ACCACTTGGC CGAGGGGAAT GGTCTGTAC AGTCTGCTCC TTTTTTTGT 180  
 CCGCCACACG TAACTGAGAT GCTCCTTTAA ATAAAGCGTT TGTGTTCAA GTTAACTCAA 240  
 A 241

SEQ ID NO:622

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00690

SEQUENCE DESCRIPTION:

GATCCTCCTG CCTNGGCCTC CAAAAGTGCT GGGATTACAT GCATACCTGA NCTACTGAGC 60  
 ACTTNNATCT TGAATGAGTG TTGGATTTTG TCAAATGCTT TTCCTGTACC TATTAATACA 120  
 ATCATGATTT TNNCTCTTT AGTATGTTGA TATGATGGGT TACATTAATT GATNNTCAAA 180  
 TGTGGAATCA GTCTNGCATA CCTGGAATAA ATCCCACTTG GTCATAATAA A 231

SEQ ID NO:623

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00691

SEQUENCE DESCRIPTION:

GATCTATGAA ATCTGTGTAG GTTTTAAATA TTTTAAAAAT TATAATACAA ATCATCAGTG 60  
 CTTTGTAGTAC TTCAGTGTTT AAAGAAATAC CATGAAATTT ATAGGTAGAT AACCAGNTTG 120  
 TCNCTTTTGT TTAAACCAA GCAGTTGANA TGGCTATAAA GACTGACTCT AAACCAAGAT 180  
 TCTGCAAAATN NTGATTGGNA TTGCACAATA AACATTGCTT GNTGTTTAA A 231

SEQ ID NO:624

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00692

SEQUENCE DESCRIPTION:

GATCCCATTT AGGAANCGGC ATTCACTTCA GAAGGTACTT TTAACTGCT CAGTTTTTGA 60  
 CTATTTTAAA TAGTTTGCTG AAAACTCCTG ATAACACTTG CTACATATCA TGTTTTAATT 120  
 GCTTGACAG TTAACCTTTA ATTTTATTTA GTAAAGTGTA TCAAAGTAGG ACTTTTTTGA 180  
 ATTGTAAATA GGTGGTTTAA TTAATAAAAA GTCAATGTAA AAATTGTAA A 231

SEQ ID NO:625

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00693

SEQUENCE DESCRIPTION:

GATCCGGAGG GAAATGTGTT AGAGGGTCTG GAAAATTCAG TGCTTTTGAG TTACTTGTTT 60  
 TTATTAAAAA TTTCCTCACA AAAGAGAGTC CTCAAGTTGT GGCTGTTCTT GGGAAAGGGG 120  
 TCACCGTGTC TGACAAAGTG TAACTTTAAA AAGCACGTTG ATTTTTTACA AATGTAAGTG 180  
 TGCTTGGGAA TTCCTTAAAT TTTGTGCAAT AAACATATTT TTGGAAGAAA 230

SEQ ID NO:626

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00694

SEQUENCE DESCRIPTION:

GATCCAATCA TATTTNCTGT AGGGTGGAGG AGGTTTCAGA CCATCCCGCT CTGTTATATC 60  
 GAAGACCACA ATGGAAGACA AAGGCTTCTA AAGTATACCC CACAGCACGT GCATCGCGGA 120  
 NAGCCTNCTT GGGATAAAAT ATGTTTACAA TAACTGCCT ATTGCTGAGA TTAAACCTTA 180  
 CAGGCTGCGT TATTTTAGCA AA 202

SEQ ID NO:627

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00695

SEQUENCE DESCRIPTION:

GATCCATTGT ATCAGTACCT CACAATCAGA GTTGGCAAAT GATGGATGAG TGATTCAAGC 60  
 AGTGCACCCG GTGGAAGCTG AAATCCATCT GTGAATGGAA CTGAAGTGAA CGTGAATATG 120  
 CTGACTATAT CCTGGAAGCA TTTTATACC ATCTTGAAAT TTCAACANAC TGGCTTTTGC 180  
 CAGTTAATCC AGCTGTCTTT CAAGAATAAA AGTTGGGGTT TTCAAA 226

SEQ ID NO:628

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00696

SEQUENCE DESCRIPTION:

GATCACCTGA GGTGAGGAGT TCGANACCAG CCTGGCCAAC AGGGTGAACC CCGTCTCTAC 60  
 TAAAAGTACA AAAATTAGCT GGGCGTGGTG GCGGACGCTG TAATCTCAGC TACTTGGNAG 120  
 GCTGAAGCAG GAGAGGTGCT GGAACCTGGN AGGCGGAGGT TGAAGTNAGC CGAGATTGCC 180  
 CTATTGCACT CCAGCTCGGG CGNCAACTGC AAGACTCCAT CTCAAA 226

SEQ ID NO:629

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00697

SEQUENCE DESCRIPTION:

GATCTGTAA TTCCTATCT AATAAATGCC TTNAATTGTN CTCATAATNA AGAATAAGTA 60  
GGTATCCCTC CATGCCCTTC TGTAATAAAT ATCTGGAAAA AACATTAAAC AATAGGCANA 120  
TATATGTNAT GTGCATTCT AGAAATACAT AACACATATA TATGTCTGTA TCTTATATTC 180  
AATTGCAAGT ATATAATAAA TAAACCTGCT TCCAAACAAC AATAAA 226

SEQ ID NO:630

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00698

SEQUENCE DESCRIPTION:

GATCAGAGTA ATTCTTTTGT ACATTGAAAT NAGGGGCTTG GTTTAAAAAA AGACCTTTCC 60  
CTCTCCCTGC CCCTAGAACA ACCAGTATTA GAAGGTGCCA CCATTGGTGC TGCCTTCTNT 120  
TCCCACAGCC TGTAAGTCAG TGTTTGTAC TTTACTGAAT TGTGATGGNT AGAAACTTCG 180  
TGGGTAGNNN NTGGGAATCA TCCNGTTAAA CAANACGGGN TTTAAA 226

SEQ ID NO:631

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00699

SEQUENCE DESCRIPTION:

GATCCTTGGT GACTGAGCA GTTCTTTTGG GGCTTTTCT TTCTGGGAAG CGGGAGGGAA 60  
AGGAGCAAGG TGTCATCCTG CTCTTCATTT GTATTTTGGT CCCAAAATGT AAATACAATT 120  
TNTTATGTTA CTTTTTGTG GTAAGTACCG AGATGAATAT TTTAATTAGA TAAGTTATAT 180  
GAAAAGGAAA ATTCCATGTC TAAATAAAAA ACAAACTCCA AA 222

SEQ ID NO:632

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00700

SEQUENCE DESCRIPTION:

GATCTTCTGG ACAAATTCT GCGATACGAC CATCAACAGA GACTGACTGC CAAANAGGCC 60  
ATGGAGCACC CATACTTCTA CCCTGTGGTG AAGGAGCAGT CCCAGCCTTG TGCAGACAAT 120  
GCTGTGCTTT CCAGTGGTCT CACGGCAGCA CGATGAAGAC TGGAAAGCGA CGGGTAATGC 180  
GGCATTGATG CTTNCCAATA AAACCAACCA ACCAAACACA AA 222

SEQ ID NO:633

SEQUENCE LENGTH:221



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00701

SEQUENCE DESCRIPTION:

GATCCACCCA GTTCTTTAGG CAACCACTGA TAGCATTTTC TTAAGTATTC TTCCAGATAT 60  
CGTCTATGCA TATGTAAAAG TATCTGNCTT TCTCCNTTTA AAAACACAAT TGGNAATATA 120  
TCATACTNGC TGGTTTGCAC CTNGCTTTTT TTGCTTAATA TATCTAGTTT ATAATGNCCN 180  
AATGNGCAAA TTTTNGCATC NGCCCTAAAT ATCTACTGGN N 221

SEQ ID NO:634

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00702

SEQUENCE DESCRIPTION:

GATCACTCGT TTAAGTCCTT AGTTGTATGT NATCTCTTCT CTAGCAGGAA TTGGCAAAT 60  
TTTTTGTAAG GGGGTAGAAA GTGAAGATTT TAAGGCTTTG CAGGCCATAT ATCCTCTNCT 120  
GCAAAATNCTC AGCCCTGCTG TTGTAATGTA AAANCTNCCA CAGACACTAC ATGAACACGA 180  
ATGAGTGTGG CTGGTGTTC AATAAACTT TATTACAAA 220

SEQ ID NO:635

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00703

SEQUENCE DESCRIPTION:

GATCATCAAA CCAGTCCACA AGCACAGGGA GATGCGTGGG CTGACATCTG CAGGCCGAAA 60  
GAGCCGTGGC CTTGGAAAGG GCCACAAGTT CCACCACACT ATTGGTGGCT CTCGCCGGGC 120  
AGCTTGGAGA AGGCGCAATA CTCTCCAGCT CCACCGTTAC CGCTAATATA NGTAAAGTTT 180  
NGTAAATTC ATACTTAATA AACAATTTAG GACAGTCAAA 220

SEQ ID NO:636

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00704

SEQUENCE DESCRIPTION:

GATCCACATC TCAAAGAAGT GGGGCTTCAC CAAGTTCAAT GCTGATGAAT TTGAAGACAT 60  
GGTGGCTGAA AAGCGGCTCA TCCCAGATGG CTGTGGGGTC AAGTACATCC CCAGTCGTGG 120  
CCCTCTGGAC AAGTGGCGGG CCCTGCACTC ATGAGGGCTT CCAATGTGCT GCCCCCTCT 180  
TAATACTCAC CAATAAATTC TACTTCCTGT CCACCTAAA 219

SEQ ID NO:637

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS00705

SEQUENCE DESCRIPTION:

5 GATCCTCTCT CGACTNGCCA TACATTTCTT TCACAGCATT TACATAGTCC ATGATAGTTT 60  
 ACTTGTGGGA TTATTGGTT AATCTTTGCC TTAAACACCA GGGTTCCTTG GGTGAAGGAG 120  
 CTTCTTTATC TNGGTAACAG CATTATTTCA AGCATAACTN GTAATATAGT NATATTACAT 180  
 ATATANCATA TATATATATN NCANANCANA TATAN 215

10 SEQ ID NO:638

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS00706

SEQUENCE DESCRIPTION:

20 GATCTGGTTT CTTAGCAAAT TTCCAGTAG GATGTCATGT AAGTNCCTTC CCCCTCTTAG 60  
 AGATTGAAGG CTGTAAGAGT CCAGATGGTG GAGCCAGGCT GTCTGGGTTC AAATGCCATC 120  
 TTTGACACTT GCAAGCTAAA TNACATTACT CAAATTAATC GTTCTGCACT TCAGCTTCCN 180  
 TGTCTATCAA ATAAAAAGAA TAGTACCNGC CAAA 214

25 SEQ ID NO:639

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00707

SEQUENCE DESCRIPTION:

30 GATCATTGTA GATGANCTGA AGCAAGANGT TATCAGTACC AGCAGCAAGG CAGAACCACC 60  
 CCAGTGCACC TCCCTGGCCT GGNCTGCTGA TGGCCAGACT CTGTTTGCTG GCTACACGGA 120  
 CAACCTGGTG CGAGTGTGGC AGGTGACCAT TGGCACACGC TAGACGTTTA TGGCAGNGCT 180  
 TTACATGTGG GGGAATAACN TGGCTTTTCT GTAAA 215

35 SEQ ID NO:640

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS00708

SEQUENCE DESCRIPTION:

45 GATCAAACCA AGGCCCAGGC TGCAGCCCCA GCTTCAGTTC CAGCTCAGGC TCCCAAACGT 60  
 ACCCAGGCCC CTACAAAGGC TTCAGAGTAG ATATCTCTGC CAACATGAGG ACAGAAGGAC 120  
 TGGTGCAGAC CCCACCCCC GCCCCTGGGC TACCATCTGC ATGGGGCTGG GGTCTCCTG 180  
 TGCTATTTGT ACAAATAAAC CTGAGGCAGG ATTTGTAAA 220

50 SEQ ID NO:641

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS00710

SEQUENCE DESCRIPTION:

5 GATCGAGAAC CACATCCTCA AGCTCTTCGA GAGCAACCTG GTGCCCCTA AACCTGAGT 60  
GAAGGCCGCC TGCCGGGGAC TCAGACACTC AGGGAACAAA ATGGTCAGCC AGAGCTGGGG 120  
AAACCCAGAA CTGACTTCAA AGGCAGCTTC TGGACAGGTG GTGGGAGGGG ACCCTTCCA 180  
AGAGGAACCA ATAAACCTTC TGTGCAGAAA 210

SEQ ID NO:642

10

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00711

15

SEQUENCE DESCRIPTION:

GATCTGGTTT TATTCCTGTA ATTCAGCCAC CTGATTTTGT GAGGGGGGGG AATAATATGT 60  
GGTTTTTGTA CAAACATGTT TCTCAGTGTG TTGTNATTTT GGAAAAATG AGGGGAGGGA 120  
GTTTGCAAG AATGGAGAAA ATGAATGAAG AAGGCCTAAT CTCTCTCTT TTCAGTNAAT 180  
20 AAATGGAACA CCATTTCTGG ATTCTAAA 208

SEQ ID NO:643

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS00712

SEQUENCE DESCRIPTION:

GATCTGTACA TTGTAAAACA CCATTCAAGT GTCAGAATCA TTATTTTCCA CCACTTATCA 60  
TGGTGCTTGA CAAGTCTTCC CAATAAATAC TGAATGAACA AATGAATGGC AGAAACATTA 120  
30 AAATGAACAC TATGGGAAA GGGGAAGAGA GGCAGAATCA GAAATTATCC NGAATAAATA 180  
TTTATNCCAT TTGTCATCCN NCNAAA 206

SEQ ID NO:644

35

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00713

SEQUENCE DESCRIPTION:

40

GATCTATGTG GTGAAAATGC ACAGGAGCTT GGTAGACTGC GGGGGAAAGA GAGAGCTCCT 60  
TTCGCCATGT TTTACCAGTN TGCTGTTATA ACCTCTTAGG TTGTATCCTT TAATTTCCAG 120  
CCTTTTAGGT TAGTTTCTGT AACAGAACAA GTGAGTCTGG GATGAAGTCC TCAAAGTACT 180  
TCAAATGGTA ATTTTTTGT TTTTGTAAATA GCTNAACAAA TAAACCNAGG GTTTCTATAT 240  
45 TAAA 244

SEQ ID NO:645

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

50

TOPOLOGY:linear

55

CLONE:HUMGS00714

SEQUENCE DESCRIPTION:

5 GATCTATGAA TGANAGGAGG GCAGACCACA TTGCTTTTNA CATCCATTTC CCCTCCTTCC 60  
CATGGGCAGA GGACCAGGCT GTAGGAAATC TAGTTATTTA CAGGAACTTC ATCATAATTT 120  
GGAGGGAAGC TCTTGGAGCT GTGAGTTCTC CCTGTACAGT GTTACCATCC CCGACCATCT 180  
GATTAAATG CTTCTCCCA GCATAGGATT CATTGAGTTG GTTACTTCAA A 231

SEQ ID NO:646

10 SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00715

15 SEQUENCE DESCRIPTION:

20 GATCTACATC TTTTCTAAA GAAAAGTGGA GCTTGCCTCC AGTTCAATTC ACAAGAGCAT 60  
TTTCCCTCCC ATGCCACCT TTTCTTGTGG CTGTCGCTAG GAAGGATGCA GAGGCTGTGT 120  
GGTTTACCAA ATGCCTTAAC TTAGCAGTGA ATGACAACTG TCAAACACAT GTTGAGGGGA 180  
AATTTTACT GATTCACAAA 200

SEQ ID NO:647

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS00716

SEQUENCE DESCRIPTION:

30 GATCTGCCGC AAGTGCTATG CTCGCCTTCA CCCTCGTGCT GTCAACTGCC GCAAGAAGNA 60  
GTGTGGTCAC ACCAACAACC TGCCTCCCAA GAAGNNGGTC AAATAAGGTT GTTCTTTCCT 120  
TGAAGGGCAG CCTCTGCCC AGGCCCCGTG GCCCTGGAGC NTCAATAAAG TGTCCCTTTN 180  
ATTGACTGGG GNNGNANAAA 200

SEQ ID NO:648

35 SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00717

SEQUENCE DESCRIPTION:

40 GATCCAGAAG GGGTTTGGTC TGGGACTTCC TTGCTCTCCC TCTTCTCAAG TGCCTTAATA 60  
GTAGGGTAAG TTGTTAAGAG TGGGGNAGAG CAGGCTGGCA GCTCTCCAGT CAGGAGGCAT 120  
AGTTTTTACT GAACAATCAA AGCACTTGGA CTCTTGCTCT TTCTACTCTG AACTAATAAA 180  
TCTGTTGCCA AGCTGGAAA 199

SEQ ID NO:649

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS00718

55

## SEQUENCE DESCRIPTION:

GATCTTTTGT CCTCACTGCT TTCTAATGGG GAGGGCTGAG GGTTCCTGT CCCCACAGCA 60  
 GGTATGTTGG GNTCTGCCCC AGCCCCACAC TTGCTCTGAA AACCAAGTGN NAGAGCCCCT 120  
 TCCCCTTGTT TTTATTTTAC TGTATAATA ATTATTAAC TCCTTGTAAT AGAAATAAAG 180  
 TTTGTAAGTTG GAGTTCAGCT CAGAAA 206

SEQ ID NO:650

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00719

## SEQUENCE DESCRIPTION:

GATCCTCGTT TTCTNGGTTT TGGTGATGTT GGAGGAGTAC CCCCAGCCC ACCGCCCGA 60  
 TTCCTTTTGG CTTCTGGTTT GGAGCTCCGG ACCAGGACCT TCGTCCTGGT CAGTTTTTAA 120  
 ATAATNATTT AGCAGTGTA CTTTAAACC TGCCTGACAT CTACANNNG CCAATAAAG 180  
 AAAGAGGAAG CCACGGTCAA A 201

SEQ ID NO:651

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00720

## SEQUENCE DESCRIPTION:

GATCTGTTAT CTAGCTGAGT TCATTTTCATC TCTCCCTTTT TTATATCAAG TTTGAATTTG 60  
 GGATAATTTT NCTATATTAG GTACAATTTA TCTAACTGA ATTGAGAAAA AATTACAGTA 120  
 TTATTCCTCA AAATAACATC AATCTATTTT NGTAAACCTG TTCATACTAT TAAATTTTGC 180  
 CCTAAAAGAC CTCTTAAA 198

SEQ ID NO:652

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00721

## SEQUENCE DESCRIPTION:

GATCTTAAAC ATCGGTCAGA TGAGTCATAC ATTGGGTTAT TTTTATATA CATGTATACA 60  
 CAAAATATTT CAAATTGAAA GCAACATCTT AATGGATTCA AAATATTAC AAGCTGTTGT 120  
 CTAAACAGG TGAGAAAAAA ATTTATAACT GTAAANCAA ATGCACATAT TGATATTTAA 180  
 AATGCGTAAT TAAGAAA 197

SEQ ID NO:653

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00722

## SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTGGACT GTCCTGGCAT CGAACTCTCC CTCTGTGTGT AATTGGAGGA GACCACAAGC 60  
 TGTGTTTTG GGTGACTGAA GTATAAAGTG TTTNCTGTAC CTTAGATTCA CAACTTTGT 120  
 ATTTNAGTA CATATTTNNA AGAATTCTA TAGTACATAT NTNNAAGAAT TTTNATATCA 180  
 AATATACCGT ATACTNN 197

SEQ ID NO:654

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00723

SEQUENCE DESCRIPTION:

GATCACCGCC GCGAGTAAAA AAGGCTCCAG CCCAGAAGGT TCCTGCCCAG AAAGCCACAG 60  
 GCCAGAAAGC AGCGCCTGCT CCAAAAGCTC AGAAGGGTCA AAAAGCTCCA GCCCAGGNNN 120  
 GCACCTGCTC CAAAGGCATC TGGCAAGAAA GCATAAGTGG CAATCATAAA AAGTAATAAA 180  
 GGTCTTTTT GACCTGTTAA A 201

SEQ ID NO:655

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00725

SEQUENCE DESCRIPTION:

GATCTGCAGT TTAAGTTGCC ATGCTGCTAG GAAATTGTCC TTTNCTTTC TAGCTGTAA 60  
 CCTACTTCTT GGAAGAAAGTA GTAGCTCTCT GTAGCATTAT GGAGTTTCAG TGGAACCAAA 120  
 TTTTGGCCAT TAAAACTGG CATTATACTG AACTATACAT TGAGAAATCA ATCAAAATAA 180  
 AANTTTTAC TTTACAAA 199

SEQ ID NO:656

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00726

SEQUENCE DESCRIPTION:

GATCTGGTTT CTAGCAAATT CCCAGTAGGA TGTCATGTAA GTCCTTCCCC CTCTTAGAGA 60  
 TTGAAGNTGT AAGAGCCAGA TGGTGGAGCA GGCTGTCTGG GTTCAAATGC ATCTTTGCAC 120  
 TTNAAGCTAA ATGACATACT CAAATTAATC GTCTGACTCA GTTCCTTGCT ATCAAAATAA 180  
 AAGATAGACC TGCAAA 196

SEQ ID NO:657

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00727

SEQUENCE DESCRIPTION:

GATCTGCCTG CCTCAGCCTC TCAAAGTGTT GAGATTACAG GCGTGAGCAN CCGCTCCCTG 60

CCCAACACAT ATACCATCTG AAAATGTTAG AATTCTGAGT TGTGATTTTA TTGACTTGTT 120  
 GCTTGCTTTT CCTNAGGCTT TGTAACTTGT AATATGTAA AGTGACTAT CCTAATAAAC 180  
 TGAATACTTT GGTATCTTAA A 201

SEQ ID NO:658

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00728

SEQUENCE DESCRIPTION:

GATCCTCCAT TGGAGTGGCC CAAATCTTTC CATCTAGGGC AAGTCCTGAA AGGCCCAAGG 60  
 CCCCTCCCC AGTCTGGCCT TGGCCNCCAG CCTGGAGAAG GGCTAACATC AGCTCATTGT 120  
 CAAGGCCACC CCCACCCAG AACAGAACCG TGTCTCTGAT AAAGGCTNTT GAAGTGAATA 180  
 AAGTTTTAAA ANCTAAA 197

SEQ ID NO:659

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00729

SEQUENCE DESCRIPTION:

GATCGTNTTT GTTTTGTTTT TAAAGAAAGG TGAGATTGGC TTGGTTCTTC ATGAGCACAT 60  
 TTNATATAGC TCTTTCCTG TTTNCCTTG CTCATTTCTG TTTGGGGAAG AAATCTGTAC 120  
 TGTATTGGGA TTGTAAAGAA CATCTCTGCA CTCAGACAGT TTACAGAAAT AAATGTTTTT 180  
 TTTGTTTNNC AGAAA 195

SEQ ID NO:660

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00730

SEQUENCE DESCRIPTION:

GATCTCAAAC TCCAGGCTCA GAACTGTGAA GACTGTTTCC AGCCTGGCTG TGAGCCAAGA 60  
 CCTGGTTCCT GGTGGACCTT GAGGACAAAG TGTGATAAAA CCTCTGGCTC AGACTTGCTC 120  
 TACTGAAGGC TTCTTGGTTA TAAGATGCAT AAAGTCACTG GGGCTAGCTA AACAATAAAG 180  
 AGTTTATTGT GAGAAA 196

SEQ ID NO:661

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00731

SEQUENCE DESCRIPTION:

GATCTAATGT ACTGTAACCT TATCAGTGAA AGGTAAAATC TCAAATAACA AGTACAAACA 60  
 TTGAACAATT ACCTATAAAG ATTTNTAAAA GTAAAATTTT TCCAATAGAT TTCATTCTTG 120

TCATTTTGTGTA AGACGACCCT GCAGTCCACC NGTTTGTAAC TTTTAAATA AAATAGACAT 180  
CTGTATTACT GAAA 194

5 SEQ ID NO:662  
SEQUENCE LENGTH:246  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS00732  
SEQUENCE DESCRIPTION:  
GATCAAGAAA ATAAGGACAA CGTGAAGTTT AAAGTTCGAT GCAGCAGATA CCTTTACACC 60  
CTGGTCATCA CTGACAAAGA GAAGGCAGAG AAAGTGAAGC AGTCCCTGCC CCCCAGTTTG 120  
15 GCAGTGAAGG AACTNAATAA ACCAGACACA CACAGAACAG GCGATTATTT ATTTGTTTTT 180  
AATTTATTTT GTCATATTTT TGTAACACCG CAGAAATGCA ATAAACCTA TATTTCAACA 240  
GTGAAA 246

20 SEQ ID NO:663  
SEQUENCE LENGTH:192  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS00733  
SEQUENCE DESCRIPTION:  
25 GATCATATTT TATACATGTG TAATAGATAA AAATAAACCA GATTGCAAAT CCTTTTTTAA 60  
AATCCTAAAC CATGTACCAA GTTTTGGTC CAAATTATGT AGGATAAGTT AAAGTTAAAT 120  
TGCATTCTAT TAACCAATAT GAGTGTATTT CTGTAAGCAT AGTTATGTTG AAATAAGTT 180  
TTAAAAACCA AA 192

30 SEQ ID NO:664  
SEQUENCE LENGTH:191  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

35 CLONE:HUMGS00734  
SEQUENCE DESCRIPTION:  
GATCTTCACA CTAATGATGA GTGTGTGGCT ACATACAAAG GAGTCCCTT TGAGGTGAAA 60  
GGGAAGGGAG TATGTAAGGG CTCAAACCAT GAGCAACAAG TGGAATCAAA TAAATGCTT 120  
40 CCACNACCAA AAGACATTAG AGAAACCTT AAAAGTAATA AAGNGAAATA TATTTNTCAC 180  
TTATACCTAA A 191

45 SEQ ID NO:665  
SEQUENCE LENGTH:188  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS00735  
SEQUENCE DESCRIPTION:  
50 GATCTGAATC TNCGGGGGCC CCAGCCCACT CCACCCTGCC AGCAGCTTCC AGCCAGTCCC 60  
CACAGCCTCA TCAGCTCTCT TCACCGTTTT TTGATACTAT CTTCCCCCAG CCCCAGCTAC 120

55



CCATAGGGGC TGCAGAGTTA TAAGCCCCAA ACAGGTCATG CTCCAATAAA AATGATTCTA 180  
CCTACAAA 188

5 SEQ ID NO:666  
SEQUENCE LENGTH:186  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS00736  
SEQUENCE DESCRIPTION:  
GATCTNAAAC CCAAGGGTCT GAGGCCAGGG CCGACTGCCG TAAGATGGGT GCTGAGAAGT 60  
GAGTCAGGGC AGGGCAGCTG GTATCGAGGT GCCCATGGN AGTAAGGGGA CGNCTTCCGG 120  
15 GCGGATGCAG GGCTGGGGTC ATCTGTATCT AAAGCCCCTC GGAATAAAGC GCGTTGACCG 180  
NCGAAA 186

20 SEQ ID NO:667  
SEQUENCE LENGTH:184  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00737

SEQUENCE DESCRIPTION:  
25 GATCTGTAAA TAATCATTGC CAGTNTGACT TTTGTTCAAC AAAAGGATTG TACTGTATTA 60  
AGAACCGATG AAAAAAATTN TCCTGTAACA TTTTITTAAG AAAACTTTGT TTGTTTAAAG 120  
AAAAAGTATT GTATAANTNA TAATTTTAAT TTAAATAAAC CTAAAATGCT TTGTGCTAAG 180  
GAAA 184

30 SEQ ID NO:668  
SEQUENCE LENGTH:180  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00738

35 SEQUENCE DESCRIPTION:  
GATCCCAGAA AAGTTCTAAT TTTCATTAGC AATTAATAAA GCTATACATG CAGAAATGAA 60  
TACAACAGAA CACTGCTCTT TTTGATTTTA TTTGTACTTT TTGGCCTGGG ATATGGGTTT 120  
40 TAAATGGACA TTGTCTGTAC CAGCTTCATT AAAATAAACA ATATTGTAA AAATCATAAA 180

45 SEQ ID NO:669  
SEQUENCE LENGTH:179  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00739

SEQUENCE DESCRIPTION:  
50 GATCTATCCA AGGTTTGGAC ATGTATCGAG AGTTTATTCC TTTTATTGC TGAATAGTAT 60  
TAATATTCTA TAGTATGGAT GTAACATAGT GTGTTTAAAC ATTCGCCTGT TGAAGGACAC 120  
TTGGGTTGTT TCCAGTTTCA GGTCTTACA AATAAAGCTA CTCTGTGTGT TCATGTAAA 179

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# EP 0 679 716 A1

SEQ ID NO:670

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00740

SEQUENCE DESCRIPTION:

GATCAAATGC CAGTGTTCATT TTGTACTTAA GTTCCAAAGT AGGAACATTN TATACTTTTT 60  
NCTGTATTGT AATAGGTAGT TTTGTATGAA ATCTTTTCTC CTCTCCCGTT GTACCGCATT 120  
CTTTCCAGCA TTGTGCTTTT TCCCTGGNCT TATTTGAAAA TTTTACTGTT TTATACAAA 179

SEQ ID NO:671

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00741

SEQUENCE DESCRIPTION:

GATCCAAGAA ACCAGGGCCA TGACCAGGTC CACTGTGGAG CAGCCATCTA TCTACCTGAC 60  
TCCTGAGCCA GGCTGCCGTG GTGTCATTTT TGTCATCCGT GCTCTGTTTC CTATTGGAGT 120  
TTCTTCTCCA CATTATNTTT GTTCCTGGGG AATAAAAACT ACCATTGGAC CTAGAAA 177

SEQ ID NO:672

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00742

SEQUENCE DESCRIPTION:

GATCTGCAAG TCCCGGAGAG CAACAGCACA GCTCTGCCTG ACGCTCTCAT TAAAATCTAT 60  
GCAGCCAAGC TCGGCACTTT GTAGCAGCCG GCCTTGCGAA GCCTCCTCAG CTCGGGGGGC 120  
CGGGGACCCA GTGAGCCGAG AGCCCTCTGG NCTCCACTTA TGCATATGCA CCAAA 175

SEQ ID NO:673

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00743

SEQUENCE DESCRIPTION:

GATCCGGAGA ATAGGGCENN AATATGTGCC GCCAGTGTTT CCGTCAGTAC GCGAAGGATA 60  
TCGGTTTCAT TAAGTTGGAC TAAATGCTCT TCCTTCAGAG GATTATCCGG GGCATCTACT 120  
CAATGAAAAA CCATGATAAT TCTTTGTATA TAAAATAAAC ATTTGAAAAA ACCCTTCAA 180

SEQ ID NO:674

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00745

## SEQUENCE DESCRIPTION:

GATCTATTCA GATGGTTCTG ATGAAGTGAA ACGNGCCATG AACAAATCCT TTATCNNNGT 60  
 CGGGTGGTAC AGTTTTGAGT ACCAACTGGT CTGATGTAGG TAAAAGGAAA GTTGAAATCA 120  
 ATCCTCCTGA TGATATGGNN NGGAAAAAGT ACTAAATAAA TTAATTTGCT CTCAAA 176

SEQ ID NO:675

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00746

## SEQUENCE DESCRIPTION:

GATCAAAACC AGTTTGATTT GGGAAATCTTC CCCTTTCCAA ATGAAATAGA GATGCAGTAC 60  
 TTAACCTTCC TTGGTGTTC TAGATATTGC CTTGTGTATT CCACTTAAAA CCGTAATCTA 120  
 GTTTGTAAAA GAGATGGTGA CGCATGTAAA TAAAGCATCA GTGACACTCT AAA 173

SEQ ID NO:676

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00747

## SEQUENCE DESCRIPTION:

GATCCTAGCA TCCCTTTTCA CATGGTTTCT CCATGTATAT AACAGAATCA AGAAACAAAT 60  
 TTNAATTTAA CAATCTGTAA CAGAATCAAG AAACAAATAC ATTTTAATTA AACAATCTAT 120  
 ATGGAACAAA CATCCCAA TNCTAAGAAT AANTNTTCNT NTAAGTTTTC AAA 173

SEQ ID NO:677

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00748

## SEQUENCE DESCRIPTION:

GATCCAAATA ATTTATTAAA TGAAGGTCT CAGAACTGA ACTCATTAAAT GTCTCTGGTT 60  
 AACAAACTA CGCATCTCAT AGCCAAAGAG GAGATGATAC ATAATCTACA ATAAGGGTCT 120  
 TAGTGCTTTA GAAAAAGTT AAAATTGGAA GTCATTAAAA AAAGACTGTT ATAATGGTGA 180  
 AA 182

SEQ ID NO:678

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00749

## SEQUENCE DESCRIPTION:

GATCTTATGA GAAGAGGAAG GAGAGANGTC TCTNCCTATG CTCACACACA AAGGAAAGTC 60  
 CACATGAGGA CACAAGGAGA AGCCAAGAGN GCCCTTACCA GGANTTAAAC CTGCTAATCC 120  
 CTATTTTAAAT TAGAACAGTG AGAAANTAAA TATCTGTATT TAAGCCTCAC AAA 173

# EP 0 679 716 A1

SEQ ID NO:679

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00750

SEQUENCE DESCRIPTION:

GATCCAGAGA AAGCCAAAGC TCTTAGTAAA CACTTGCCAT CGTCAGTNTN ATGTCTCTAA 60  
AAGTAGATGT TGAGGCTCTT NAAAAATNCTC CTGGTGCTAC ATACATTCGG AAGAAGGGTG 120  
GAAAAGTTAC TGGAGATAGT CAACCAAAGG AACAAGGACA GGNAGATTG AAA 173

SEQ ID NO:680

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00751

SEQUENCE DESCRIPTION:

GATCCAATCC ATTCAGCAGT CCATTGAAAG GCTCTTAGTC TAAACCTGTG GCCTCTGCCA 60  
CGTNGCTCCC TGCCAGCTTC CCCCTGAGG TTGTGTATCA TATTATCTGT GTTAGCATGT 120  
AGTATTTTCA GCTACTCTCT ATTGTTATAA AATGTAGTAC TAAATCTGGA AA 172

SEQ ID NO:681

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00752

SEQUENCE DESCRIPTION:

GATCAAATTT AAACCTCATT TTGGGGGGTA TTTTGGTACT GTAATGGGGT CATCAAATNA 60  
TTAATCTGAA AANAGCAACC CAGAATGTAA AAAAGAAAAA ATTGGGGGGA AAAAGACCAG 120  
GTCTACAGTG ATAGAGCAAA GCATCAAAGA ATCTTTAAGG GAGGTTTAAA 170

SEQ ID NO:682

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00753

SEQUENCE DESCRIPTION:

GATCGGAACA GCTCCTTACT CTGAGGAAGT TGATTCTTAT TTGATGGTGG TATTGTGACC 60  
ACTGAATTCA CTCCAGTCAA CAGATTGAGA ATGAGAATGG ACGTTTGGTT TTTTTTGTGTT 120  
TTTGTTTTTG TTTTTCCTT TATAAGGTTG TCTGTTTTTT TTTTNNAAA AATNGCANCA 180  
GTNCATGGCC CCCATCATT ANANGNGAGG ANTNCANCAG AAAATAAAAT ATNCACTCN 239

SEQ ID NO:683

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00754

SEQUENCE DESCRIPTION:

GATCCAGACA GCCATCAGGG AAAGCTTGTN TTTAACCGAA CTGTCACACT GAAGGAAGAC 60  
CCAGGAAAGG TGTGAGCTGG AAGCACTGAA CCTACCTCAT CCTCCTGGAG GGTGTGGCTA 120  
CCCTCGCCAC CCCAAATTCC ATGTCAATAA AGAACAGCTA AATTCTCAA 170

SEQ ID NO:684

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00755

SEQUENCE DESCRIPTION:

GATCTTTCCA TTGGAATATA CTGGAAGTGA AGAGGTTTTG TTGCTTGAC AGTGTGAGAT 60  
GAGGAACACC ACTATCTTAA TTTTGTGATA CACTGCATTT GCTGGTGCTA TTTNATACA 120  
GTGAAGCAAC AGCTTTGCAG CAAAATAATA AAATACTTCT ANGTAAA 168

SEQ ID NO:685

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00757

SEQUENCE DESCRIPTION:

GATCCATCGT NATGTCTTAT TTAAGGGGAA CGTGTGGNCT ATTTAGGCTT TATGGCCCTG 60  
AAGTAGGAAC CAGATGTCGG ATACAGTTCA CTTTAGCTAC CCCCAAGTNT TATGGGCCCG 120  
GAGCGAGGAG AGTAGCACTC TTGTNCGGGA TATTGATTTC ACGGAGAAA 169

SEQ ID NO:686

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00758

SEQUENCE DESCRIPTION:

GATCTGCTAC TAAACAGAGT TCAAAAACTT TCCAGAGTAA TTAATATGTA AAGCCANGTA 60  
ACTAACAAAN GATTGCTTT AGAGATAATT ATTTGGAATT TTTATAGCTN ACTTCACAAT 120  
GTGCCAGGT CAGCTGTATA AAATAAATAC TGCATTNTNG TTTCTTTCAA A 171

SEQ ID NO:687

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00759

SEQUENCE DESCRIPTION:

GATCCTGACA CTAAGGAAAT GCTGAAGCTT TTGGACTTCG GCAGTCTGTC CAACCTTCAG 60  
GTCACTCAGC CTACAGTTGG GATGAATTTC AAAACGCCTC GGGGACCTGT TTGAATTTT 120

NCTGTAGTGC TGTATTATTT TCAATAAATC TGGGACAACA GCAGAAA

167

SEQ ID NO:688

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00760

SEQUENCE DESCRIPTION:

GATCAGCGAT GAAGAGGAAG AAGATGATGA TTGAAGTATG AAATATGAAA ACATTTTATA 60  
TATTNNATTG TACAGTTATA AATATGTAAA CATGAGTTAT TTTGATTGAA ATGAATCGAT 120  
TTGCTTTTGT GTAATTTTAA TTGTAATAAA ACANTTTAAA AGCAAA 166

SEQ ID NO:689

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00761

SEQUENCE DESCRIPTION:

GATCTATTTG GTCTTTCTCA TGTCCCCAC TGGTCTGTAC CCCAGGGAGC GGGTGCTTGT 60  
ACTGTGTGAA TCCAGTGTTT ACATTCACAC TTAATGACTT CTTGGCACC AATCATGTAT 120  
TTCACCGTTT GCACTTNTTG TATTTCAATA AAAATGTTGA TGCAAACTG CTAAA 175

SEQ ID NO:690

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00762

SEQUENCE DESCRIPTION:

GATCGACTCT ATCATCCAAC GCTCCGAGGA CAGCCCATGT CCCACCCCN GNGACCCGGA 60  
CCCGGCCAGC AGGACCCACT GAGANGGGCT GCCCGGGNCT NCTCAGCTGC CCACACCCAC 120  
ACTGTCCAGC ATCTGGCACA ATAAACATNC TCTGTTTTGT AGAAA 165

SEQ ID NO:691

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00763

SEQUENCE DESCRIPTION:

GATCAAGAAA TAAACATAAA CATCTCAGAA TGCTCCTTCA TTACCAGAGT CACTACCTGA 60  
TTATGTCTTA ATGGGTTACA TAATGACAGA GGGTATCTCA TATATGTNCT TTTCCAAACA 120  
TAAAATAACT TTTGTTTTG TTTGATTGAA AAAAAATTTA GAAA 164

SEQ ID NO:692

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00764

SEQUENCE DESCRIPTION:

5 GATCCAGATT CTCACCTAAT GGGGTTTATA TGGACTTTCT TCTCATAAAT GGCCTGCCGT 60  
CTCCCTTCCT TTGAAGAGGA TATGGGGATT CTGCTCTCTT TTCTTATTTA CATGTAAATA 120  
ATACATTGTT CTAAGTCTTT TNCATTAAAA ATTTAAAACT TTTCCCATAA A 171

SEQ ID NO:693

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00765

SEQUENCE DESCRIPTION:

15 GATCGACTCT ATCATCCAAC GCTCCGAGGA CAACCCNTGT CCCCACCCCC GGGACCCGGA 60  
CCCGGCCAGC AGGACCCACT GAGAAGGGCT GCCCGGNTCA CCTCAGGGGG NCACANTTTA 120  
CACTCTCCAG CATCTGGCAC AATAAACATN CTCTGTTTTG TAAA 164

SEQ ID NO:694

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00766

SEQUENCE DESCRIPTION:

25 GATCTAATGG TCTAAAACT GGAGTTTCCG GACACAAGCT CTCCCTTTNC CTGCAACCAT 60  
CCATGCAAGA TGTNACTTGC TCCTCTNTGC TTTCTGCCAT GATTGTAAGG CCTCCCCAGC 120  
TACATGGAAC TNTAACTCCA TTAAACCTCT TTNTTTTGTA AATTGAAA 168

SEQ ID NO:695

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00768

SEQUENCE DESCRIPTION:

35 GATCCGCCCC CCTCAGCCTC CTAAAGTGCT GGGATTACAG CTGTGAGCCA CCCTGCCCGG 60  
CCACTTTTGT ATGATTTCTA ATGTATTTGT AATTTACCTA ACAAATTGCC TAATCTGCTA 120  
TGTTAATGTA TTTATGAATT AAAATAAATA CGACTGCAAA 160

SEQ ID NO:696

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00769

SEQUENCE DESCRIPTION:

50 GATCCGTAGC GGCATGTTCT GGCTGCGCTT CTAGGCGGGA AGCCTATGTA AGCAAGAGGG 60  
CAGGGCCGGG GTTGTGGTC CCCCCCCCAC CACAAACACA GCACTTCGGC TCCTCTAACC 120

TGTGCCACAG GTGACCACCA ATAAAAATCCT CTGCTGAGAA A 161

5 SEQ ID NO:697  
 SEQUENCE LENGTH:159  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00770  
 10 SEQUENCE DESCRIPTION:  
 GATCTCCCTG CCCCCACCCC AGTTCCCCAA CCCACTCCCT TCCAACAACA ACCAGCTCCA 60  
 ACTGACTCTG GTCTTGGGAG GTGAGGCTTC CCAACCACGG AAGACTACTT TAAATGAAAA 120  
 AANGAAATTG AATAATAAAA TCAGGAGTCA AAATTCAAA 159

15 SEQ ID NO:698  
 SEQUENCE LENGTH:159  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00771  
 SEQUENCE DESCRIPTION:  
 GATCTTTTNN TTTTTTTTAA GTCTCACAAG ACATGGGGCA TCTCCACAAA TTAAAGTTCC 60  
 TGTCCATTG GAAATTTGTT TCTATGTGTA CAGTTTGTCA GAGAAAAACA AAGTTTTTGT 120  
 25 ATGANTACAG AATGTGATTT ACGCAAGATT TGACAGAAA 159

SEQ ID NO:699  
 SEQUENCE LENGTH:161  
 SEQUENCE TYPE:nucleic acid  
 30 TOPOLOGY:linear  
 CLONE:HUMGS00772  
 SEQUENCE DESCRIPTION:  
 GATCTACCTA TCTTCAGGAT GGAACCTTGG GGAAAAATAA AATTGAGGGG AAGTAAAAAG 60  
 35 TATGTAACAC TTCCAGTTGT GAGCCAAGAT TGTAACCAGA GAGCAGCCAG GAGCTTCCTG 120  
 TCAGTAACCA TTTTTTCAAT AAATACTCTT TCATGTACAA A 161

SEQ ID NO:700  
 SEQUENCE LENGTH:157  
 SEQUENCE TYPE:nucleic acid  
 40 TOPOLOGY:linear  
 CLONE:HUMGS00773  
 SEQUENCE DESCRIPTION:  
 GATCTCTCA CCTCAGATTT CCAAAGTGTT GGATTATAGG TGTAAGCCAC TGAGCCCAGT 60  
 45 TTGAATGCTT TTTTATATAT TTTTGGCCA TTTGTATGTC ATCTTTGGAG AAATGTCTAT 120  
 NCAATCCNT TGCTCATTAA AATNATTNC TGATAAA 157

50 SEQ ID NO:701  
 SEQUENCE LENGTH:160  
 SEQUENCE TYPE:nucleic acid

55



TOPOLOGY:linear

CLONE:HUMGS00774

SEQUENCE DESCRIPTION:

GATCTGGCCG TNAGCCGCGA NCCGCTGNGA ACTCCACTCG GGGAACTCCT TTCCAAGCTG 60  
ACCTCAGTTT TCTACAAGA ACCCAGTTAG CTGATGTTTT ATTGTAATTG TCTTAATTG 120  
CTAAGAACAA GTAATAAGTA AATTTTAAA AAGCCTTAAA 160

SEQ ID NO:702

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00775

SEQUENCE DESCRIPTION:

GATCAAATTG TGCAGTACTT TGTGCATTCT GGATTTTAAA AGTTTTTNAT TATGCATTAT 60  
ATCAAATCTA CCACTGTATG AGTGGAAATT AAGACTTTAT GTAGTTTNA TATGTTGTAA 120  
TATTNCTCCA AATAANTCTC TCCTATAANC CACCAGGGAA A 161

SEQ ID NO:703

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00777

SEQUENCE DESCRIPTION:

GATCAGAGCT TATACTTAAT TAAGGTTTTA TACACACCAG TTCCCCAGTA AATNCAAATT 60  
TAACAAGAAA ATCAGACATG TCATATGTNC AAAATGCTCA TGGCAAACAA TCATTTTGCA 120  
TTCCTGCAAA TAAAATTGTT TTATACTGTA GAAA 154

SEQ ID NO:704

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00778

SEQUENCE DESCRIPTION:

GATCTGTTTG TTCCCTGAGC TTTTAAATA CCCTGTGAAA ATTTNTTTC CTCCCTTGGT 60  
CATCATGCAT CTAATTGTGG GGAAATGTTT GTCAAACCAA CCTGCAAAGC AGCATGGTGT 120  
AGTTGAGAAG AATAAACAGA GAAGACTGGG AAA 153

SEQ ID NO:705

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00779

SEQUENCE DESCRIPTION:

GATCTTTGGA CAGAAGCAGC TCTTTCCCGA ACACTTGTGG CGTCTGGNAC GGCCCCACCC 60  
NTCCCCCACC ACTCCCTCCC ACGGGGCTCC GGGAGACAGG CCGGCCCTGC ACCTNACCCC 120

ACCGTGACCT CAATAAACGT TGAAACTNCA AA 152

5 SEQ ID NO:706  
SEQUENCE LENGTH:152  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00780  
10 SEQUENCE DESCRIPTION:  
GATCTATCCT TTA CTGAAA GCTTTTGAAA AGTGGAAAGG TCATTTTGGT GCATTTCCCC 60  
ATTTCTTGTT TTAAAAGAC CAACAAATCT CAAGCCCTAT AAATGGCTTG TATTGAACTT 120  
TTACATTTGA ATTAAAGATG TTAAACATGA AA 152

15 SEQ ID NO:707  
SEQUENCE LENGTH:151  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS00781  
SEQUENCE DESCRIPTION:  
GATCTAGTAT GCTCCTGGTC TAATGCATTT ACATTGTTTA GGTAAGTGGT TCCTAATAAA 60  
AAGAATTATA AAATACCCTC AAATTAACAA TTCAATNGCA TATAATAGCC TAACTCAGTA 120  
25 AGANTATTAA AACTTACTAT TATNCTTCAA A 151

SEQ ID NO:708  
SEQUENCE LENGTH:152  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS00782  
SEQUENCE DESCRIPTION:  
GATCTANTCT GTGCTACCTG ATTAACCTAC AGCAGGCTTA CTGANTGGCT TCATTTTCAGA 60  
35 TTTAGTTGAT TTCTCCACCA AATNCATGTC ATGTATTCTC AATAGGCTGT ATTCCCAGCA 120  
GNCAATAAAT GGAACACCCG TANAANCNCA AA 152

SEQ ID NO:709  
SEQUENCE LENGTH:147  
40 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00783  
SEQUENCE DESCRIPTION:  
45 GATCCCCAGG GTTCTTTTGT CTTATTTATG GAGAAAAACC GGTCACCTTG TCCAGCGCAC 60  
TGTGAGGCCC CCACTCAGGC CAGCCCTGGC CCCCCTTGG TACTTGGAAC CGAAGTTACA 120  
GATTATATTA AAATAATAAT GTACAAA 147

50 SEQ ID NO:710  
SEQUENCE LENGTH:146  
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00784

SEQUENCE DESCRIPTION:

5 GATCTTATAA AAGGAAATTC TAGCAGTTTT AGAAATAGGT GGGAAAAACT CAAATATTCC 60  
 TCCTATCTGC ACCAAAAAGT TTATTTGTGG TATATAAAAT GAATATTGTT TTATAATAAC 120  
 TTGTTAATAA AGTACTTTCT AATAAA 146

SEQ ID NO:711

10 SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00785

15 SEQUENCE DESCRIPTION:

GATCAATGAA GTGAGAAATT GTTGAGAAGG ATACAGTTTG TTTTATAGATG TCCTTTGTCC 60  
 AATGTGAACA TTTATTCATA TTGTTTTGAT TACCCTCGTG TTACTACAAG ATGGCAATAA 120  
 ATACTATGGG ATTGTTTGTA TTAAA 145

20 SEQ ID NO:712

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS00786

SEQUENCE DESCRIPTION:

30 GATCTCCCTT CAGCAACTTA TTTTGCTTTA ATTGCTTTAA ATCTTAAGCA ATATTTTAA 60  
 TTCAGTAAAC AAATTCTTTC ACAAGGTACA AAATCTTGCA TAAGCTGAAC TAAAATAAAA 120  
 NTGAAAAGGA GAGATTAANG GTAAA 145

SEQ ID NO:713

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS00787

SEQUENCE DESCRIPTION:

40 GATCTAGAAG CAGAGGAATC CCAGCGCCTT TAAAAAGTTG TTATGTGGTT TTCTTTTAA 60  
 AAGCTCCTGT TTTTGAAAG TAGAATTAT GGTACAACG TATGTTTATT ATTTGTACAT 120  
 AAAATAAAAC CATTTAATAA GTAAA 145

SEQ ID NO:714

SEQUENCE LENGTH:154

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00788

SEQUENCE DESCRIPTION:

50 GATCTATGCC TAACAGAGCC CCAGTACAAC TATTTTNCAG AATGGCTGTT ACCCTAGAAT 60  
 TACTATAGCA CATATTGAGA TATAGTTGTA CTCCCTAGTA GATAGGAACT GACCCCAACA 120

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ATAAACTTTG ATAATAAAGA AAAAAAANCN NAAA 154

5 SEQ ID NO:715  
SEQUENCE LENGTH:144  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00789  
10 SEQUENCE DESCRIPTION:  
GATCAACCTT AAAGGAACT GCTATCCGAA CTTGGCTATC TCACAGCAGA GCCAGTTTGA 60  
CGAATGGGTA AACCTAAGG ACATGCTGGG TCCAAAGTGA TTTACATAAA TNTATAATGA 120  
AAATAAACAT GTATAANATT TAAA 144

15 SEQ ID NO:716  
SEQUENCE LENGTH:149  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00790  
SEQUENCE DESCRIPTION:  
GATCCGTGAT GCCACTTACC TGTGTGTTTG GTAACAACAA ACCAACATCA TGGAGGTCCC 60  
TGGATTGAAA AAGGAGCCTC TCCCACTCCT CCTACCACCA AAGTGGTTAG GACNCTATAT 120  
25 AANTAAAAAC AAGGCTTTTG GAAAATAAA 149

SEQ ID NO:717  
SEQUENCE LENGTH:147  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS00791  
SEQUENCE DESCRIPTION:  
GATCTGGCTG AACCAGTTCC ACAAGGTTAC TGTATACATA GCCTGAGTTT AAAAGGCTGT 60  
35 GCCCACTTCA AGAATGTCAT TGTTAGACTT TGAAATTTCT AACTGCCTAC CTGCATAAAG 120  
AAAATAAAAT CGTTTAAAT CAAGAAA 147

40 SEQ ID NO:718  
SEQUENCE LENGTH:115  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00792  
SEQUENCE DESCRIPTION:  
45 GATCTGGGGC AGCCACCTTG CTACCATGAA GGAAAGGCCA AGACAATCAT CCACAGCTAT 60  
TCCCTCCAGC ATCTGGTTCT GTACAAAAAT TAAATGCTTA TTTNTTTAAG TCAAA 115

50 SEQ ID NO:719  
SEQUENCE LENGTH:142  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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# EP 0 679 716 A1

CLONE:HUMGS00793

SEQUENCE DESCRIPTION:

GATCGCCACT GTAAAGGTCC TAGAGTTGCC TGTGTCTC TGGAGATGGA ATTAAACCAA 60  
ATAAAGAGCT TCCACTGGAG GCTTGTATTG ACCTTGTAAC TATATGTAA TCTCNTGTTA 120  
AAATAAAATA TAGCTTGTGA AA 142

SEQ ID NO:720

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00794

SEQUENCE DESCRIPTION:

GATCTGTGCC TACNTTTTAC CACCCTCTTG ATTGGAGCTT TTGTNATGCA GCTACCATNN 60  
TTCAAAAAA TTAAAAATTA AAAAAAAAAA ATCTGCCACT TATCCAAGTC CACTAGAGGC 120  
CACTGTCTTC AAAGNTTNTN TN 142

SEQ ID NO:721

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00795

SEQUENCE DESCRIPTION:

GATCCAGGTG ACTCTGAACA TCATTAGAAG CATGCCAGAA CAGACTGGTG AAAAGTAAAC 60  
CTTTTCACCT ACAAATTTT ACCTGCAAAC CTAAACCTG CAAAATTTT CTTAATAAA 120  
ATTTGCTTGT TTAAANAACA NNNGAAA 147

SEQ ID NO:722

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00796

SEQUENCE DESCRIPTION:

GATCCAGAGC CTCCCGGCC TTCTCCGGTG TCCTGTACCA ACTCTTCTAT TTAAGAGAAC 60  
CTCAGATGAT GTACCTGAGC CTCAGGGTTT TGTTTCAGAG GGATATAAAT NATTTAAAA 120  
TTAAATGAAA ACGTTGCAAA 140

SEQ ID NO:723

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00797

SEQUENCE DESCRIPTION:

GATCGGCCAC TACCTGGGCG AGTTCTCCAT CACCTACAAG CCCGTAAAGC ATGGCCGGCC 60  
CGGCATCGGG GCCACCACT CCTCCGCTT CATCCCTCTC AAGTAATGGC TCAGCTAATA 120  
AAGGCGCACA TGACTCCAAA AAAAAATAAA 150

# EP 0 679 716 A1

SEQ ID NO:724

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00798

SEQUENCE DESCRIPTION:

GATCAGGGTA AGGCAGTCAG GCGGGTGTTT ACCACTGCCT TTCCTTCCTC TGAGCGTGAG 60  
 AACACTGAAC CCAGCCACTG CCCCTGGGTC CCTGTCTCTG AAATNGTCTA ATAAATCCTT 120  
 TNCCCTTCTT GAGCTACAAA 140

SEQ ID NO:725

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00799

SEQUENCE DESCRIPTION:

GATCCGAATC GAGGCCAACG AGGCCCGGGA TGAAGGCCCN GGAGTAGGCG AGCCAGACGA 60  
 CAAGGTTGAC CTCAGCTTCG GAGCCACCTC TGGATGAACT GCCCCAGCC CACGNCCNAT 120  
 TAAAGACCCG GAAGCCTGAA A 141

SEQ ID NO:726

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00800

SEQUENCE DESCRIPTION:

GATCAGCTTT ACCTATGGTG CTTTGCCTTT AACTAGAGTG TGTGATGGTA GATTATTTCA 60  
 NATATGTATG TAAACTNTT TCCTGAACAA TAAGATGTAT GACCCGGAGC AGAAATAAAT 120  
 NCTTTTCCTA ATTAAA 136

SEQ ID NO:727

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00801

SEQUENCE DESCRIPTION:

GATCATGTCA TTCAATTCCA GTCACCTCTT CTGCAATCAT GACCTCTTGA TGTCTCCATG 60  
 GTGACCTCCT TGGGGGTAC TGACCCTGCT TGGTGGGGTC CCCCTTGTA CAATAAAATC 120  
 TATTTAAACT TAAAA 135

SEQ ID NO:728

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00802

SEQUENCE DESCRIPTION:

5 GATCTTAAAC ATTGTTTTGT AGTGTATATT ACTTGTCAT TCCTTTAAGG GGAGCAGCCT 60  
 GCACTCTTTT GTAGATTACT TTTGGGGGAT ATATTNNAG AATNATGAAA CGGAATAAAA 120  
 TTGTAAAAAA CTAAA 135

SEQ ID NO:729

10 SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00803

15 SEQUENCE DESCRIPTION:

GATCATGTTA CCATATCAAG CTGAAAATGT CACCACTATC TGGAGATTTC GACGTGTTTT 60  
 CCTCTCTGAA TCTGTTATGA ACACGTTGGT TGGCTGGNTT CAGTAGGGGG NTATTNAGG 120  
 CCTTCTTTT TAAA 134

20 SEQ ID NO:730

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS00804

SEQUENCE DESCRIPTION:

GATCTANGTT GCCTACCTTG AATTTTTTTT TAAATATATT TGATGACATA ATTTTGTGT 60  
 AGTTTATTTA TCTGTACAT ATGTATTTTG AAATCTTTTA AACCTGAAAA ATAAATAGTC 120  
 ATTTAATGTT GAAA 134

30 SEQ ID NO:731

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS00805

SEQUENCE DESCRIPTION:

GATCTCACTA AAGGATTCTT ATTTGCTGTC AGTTAAAAAT AAAGCCCTAA ATACATTTTT 60  
 ATTCTTTCTA CTGAGGGCAT TGTCTGTTTT CTTTGTAAT GCCGTACAAT AAACAAATTA 120  
 TTTAATAACC TAAA 134

40 SEQ ID NO:732

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00806

SEQUENCE DESCRIPTION:

50 GATCTTGCA CTCTCCATGT TCTCTACAAG AAGCTGTGGT GATTGGCCCT GTGGTCTATC 60  
 AGGCGAAAAC CACAGATTCT CCTTCTAGTT AGTATAGCGG ACTTAATAAA AGAGGAAAAA 120  
 ACTCTTGCTT CAGTAAA 137

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# EP 0 679 716 A1

SEQ ID NO:733

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00807

SEQUENCE DESCRIPTION:

GATCCTCGAA CGGAAAGCCA AATCTCGCCA AGTAAGGAAA GGAAAAGGGC AAATACAAGG 60  
AAGAAACCAT TGAGAAGATG CAGGAATAAA GTAATCTTAT ATACAAGCTT TGATTAAAC 120  
TTGAAACAAA GAAA 134

SEQ ID NO:734

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00808

SEQUENCE DESCRIPTION:

GATCAGTGGC TTTGAATGAA ATACAGATGC ATTATCCAGA ACTGAAGTTG CCCTACTTTT 60  
AACTTTGAAC TTGGCTAGTT CAAAGATAGA CTCTTCTTTT GTAAAGTAAA TAAATTCTTC 120  
AAAATGCTTA AA 132

SEQ ID NO:735

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00809

SEQUENCE DESCRIPTION:

GATCNNAACC TTTTCAATAA AAGGCAAAAC AAACCAATNT CCNAACATAG CATTACAGCC 60  
TTTAAACCA TTCACTNCTC ATAGTGATTC ACAGAGGACA AGAGATTAAA GTGCTGGATT 120  
TTAAATGTCA AA 132

SEQ ID NO:736

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00810

SEQUENCE DESCRIPTION:

GATCANATGC AACCNCACAA CCTCGGCTGA GTCTTGAGAC TGAAAGATTA AGCCATAATG 60  
TAAACTGCCT CAAATTGGAC TTTGGGCATA AAAGAACTTT TTTATGCTTA CCATCTNTTT 120  
TTTTTCTTAA N 131

SEQ ID NO:737

SEQUENCE LENGTH:383

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



CLONE:HUMGS00811

SEQUENCE DESCRIPTION:

5 GATCATACAC CTGCTCACAG GCGAGAACCC TCTGCAGGTC CTGGTGAACG CCATCATCAA 60  
 CAGTGGTCCC CGGGAGGACT CCACACGCAT TGGGCGCGCC GGGACTGTGA GACGACAGGC 120  
 TGTGGATGTG TCCCCCTGC GCCGTGTGAA CCAGGNCANN TGGCTGCTGT GCACAGGCGC 180  
 TCGTNAGGCT GCCTTCCGGA ACATTAAGAC CATTGCTGAG TGCCTGGCAG ATGAGCTCAT 240  
 CAATGCTGCC AAGGGCTCCT CGAACTCCTA TGCCATTAAG AAGAAGGACG AGCTGGAGCG 300  
 10 TGTGGCCAAG TCCAACCGCT GATTTTCCCA GCTGNTGCC AATAAACCTN GTCTGCCCCT 360  
 TTTGGGGGAA GCCCGAAGC AAA 383

SEQ ID NO:738

SEQUENCE LENGTH:128

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00813

SEQUENCE DESCRIPTION:

20 GATCCAGCTG CCAGAGGATG AGTGACCAGT TGCTAAGTGG GGCTCAAGAA GCACCGCCTT 60  
 CCCCACCCCC TGCCTGCCAT TCTAACCTCT TCTCAGAGCA CCTAATTAAA GGGGCTGAAA 120  
 GTCTGAAA 128

SEQ ID NO:739

SEQUENCE LENGTH:128

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00814

SEQUENCE DESCRIPTION:

30 GATCTGGATT ACNATGTAAA TTCACAGCAG TAAGATAATA TAAATTTTGT TGAATGTATT 60  
 AACATCATAT GGTCTGAAAA TGTGGGTTTT NATTTGGCAC ATTTAAATAA AATGTTTCTA 120  
 ACTAGAAA 128

SEQ ID NO:740

SEQUENCE LENGTH:128

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00815

SEQUENCE DESCRIPTION:

40 GATCAAGAAT GAAAAAGACA TCATATGAAN NGGGAGAAAC TATTTGCACA CCATCTATCT 60  
 CATGGTTTGG TTAATATTCA AACTATATNA GCAGAATGTG TAAGGATATC CTACAACTCA 120  
 ATAGCAAA 128

SEQ ID NO:741

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00816

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## SEQUENCE DESCRIPTION:

GATCCAAGGG GAAACTGCAG GTCAAGGGCT GATAACGGCC ATGCAGGATG CTTGATGCTG 60  
 CGTCCCCCGC TGCTTGCCGC CCCCCACCCC GCCATTTTGT ATAATAAAGC TCCCTGTGTA 120  
 TTCTCAAAAA AAANCAAA 138

SEQ ID NO:742

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00817

## SEQUENCE DESCRIPTION:

GATCCCTGAG ACTGAGGGGT TTACGGGCTG TGAATGGACC TTCAGCCCTN CCCACCCTCC 60  
 CTCCCCACTG CTGCTGAGTC TGTCTGATGT TTTGGTTGTG TGAATAAATA TAATTCCCT 120  
 CTGGA AAA 127

SEQ ID NO:743

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00818

## SEQUENCE DESCRIPTION:

GATCGGGTAG CTCAAAAGAA GGCAAGCTTC CTCAGAGCTC AGGAGCGGGC TGCTGAGAGC 60  
 TAAACCCAGC AATTTTCTAT GATTTTTTCA GATATAGATA ATAACTTAT GAACAGCAAC 120  
 TAAA 124

SEQ ID NO:744

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00819

## SEQUENCE DESCRIPTION:

GATCAGAAAT TCTCTTGCTT GAGAGATTTT TTTTGTCTT CTGTTGACTA CATAGTTTCA 60  
 AATCTCTCTN TATTTCTATG TGATATATAA ATNGCTTTTA ATTATATNAA ATNTTAATTN 120  
 NCCN 124

SEQ ID NO:745

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00820

## SEQUENCE DESCRIPTION:

GATCTCATTA CCCTGTTTCC GAATTCTGCC GTGTGTATCC CCAACCCTTG ACCCAATGAC 60  
 ACCAAACACA GTGTTTTTNA GCTCGGTATT ATATATNTTT TTCTCATTA AGGTTTAAAA 120  
 CCAAA 125

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SEQ ID NO:746

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00821

SEQUENCE DESCRIPTION:

GATCCGTGGC TTAAGACAGG AGATTATCTC TNTACTCCAG TGGCATCTCC TTAGCCAAGA 60

TGTGAAATTA AAATCATAGT TCGCCTCATT TAAAAATNCT AATAAAGCAC TCAAACCTTG 120

AAA 123

SEQ ID NO:747

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00822

SEQUENCE DESCRIPTION:

GATCCAAATC TGGTTCAAAC ATTCAAAACT TCAAAGATAA TTCATCTTTC AGCTAATGCT 60

TGTGGTTCTG TTGTTCCCTT GAAAAAAAT AAAAACAGTT GCCTTCNGGG AAAANTTNA 120

AA 122

SEQ ID NO:748

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00823

SEQUENCE DESCRIPTION:

GATCTTGTGT TTTAGNTGG GCATTTTCAC TCTTCTGCCT TAAATCCCTA ACCCCATGGA 60

GCTGACATTC TAGTGCGGCT GAGGGGAGGG GAAACATTGT AAAATAAATC ATAAAAATTA 120

AA 122

SEQ ID NO:749

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00824

SEQUENCE DESCRIPTION:

GATCTCTGGG CTGGGGACTG AATTCCTGAT GTCTGAGTCC TCAAGGTGAC TGGGGACTTG 60

GAACCCCTAG GACCTGAACA ANCAAGACTT TAAATAAATT TTAAATGCA AAAACTCGGA 120

AA 122

SEQ ID NO:750

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00825

## SEQUENCE DESCRIPTION:

GATCNTAGAA GGGCTTCCCA ACCNNATTG CAACATCCAA ATTGTCTTCA ATTNAAGGAA 60  
 GGCCTTATCA GTTCATAGAT GANCTTCATT GTAAAAATAA ATGTACTTTG CACCACTTCA 120  
 AA 122

SEQ ID NO:751

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00826

## SEQUENCE DESCRIPTION:

GATCCACTTC TGTNATTANG TAAATGGATG TNTCGTGATG CGTCTACAGT TATTTATTGT 60  
 TACATCCTTT TCCAGACACT GTAGATGCTA TAATAAAAAAT AGCTGTTTGG TAACCATAGT 120  
 TTCATTGTN CAAAGCTGTG TAATCGTGGG GGTACTATCT CAACTGCTTT CGTATTCATT 180  
 GTATTAAAAAG AATCTGTTTA AACAACTTTT ATCTTCTCTN CGGGTTTAAG AAACGTTTAT 240  
 TGTAAACAGTA ATTAAATGCT GCCTTAATTG AAA 273

SEQ ID NO:752

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00827

## SEQUENCE DESCRIPTION:

GATCAAAAAG AAACCTTTGTT TTTCCGCAAT TGAAGGTTGT ATGTAAATCT GCTTTGTGGT 60  
 GACCTGATGT AAACAGTGTC TTCTTAAAAAT CAAATGTAAA TCAATTACAG ATTAAAAAAA 120  
 AAAGCCTGTA TTAAAGAAC GAAA 144

SEQ ID NO:753

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00828

## SEQUENCE DESCRIPTION:

GATCAGAGGA AAAATCCAGT GTGACAGAGT GCAAGTNAGA AGACCTGGCT TTNATCCCA 60  
 GCTTTGAAAC TTGGAACCTT TTGATTGACA AATTAATAAA CCTCTCTATG CCTCAGGCTC 120  
 CTCATCTGTA AA 132

SEQ ID NO:754

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00829

## SEQUENCE DESCRIPTION:

GATCTAGGCT TGAGCTTGGT TGGGATTGCT NTTTTCTTCT TCTTCTTTAT AAACGATTCT 60  
 NTGTAACNTT TTGTATTGAC AGTTTCAAAC TTACAGTAAA ATTGCAACAC GAGTAAA 117

# EP 0 679 716 A1

SEQ ID NO:755

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS00830

SEQUENCE DESCRIPTION:

GATCAGTACA TAGCATTTGG CTCNTGAACN NAATTNTAAA CTTTCAGGTA TTTTGTACA 60  
 10 AATAAGGGAC TGATGTTCTG TTTCTGTAA TTAGAAATAA ACATTAATAC AGTGAAA 117

SEQ ID NO:756

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00831

SEQUENCE DESCRIPTION:

GATCTATCAT TACTGCAAAA ACCTGCTCTG TTGTGCTGGC TGGNAGGCC TGTGGCTGCT 60  
 20 GGCTGAGGGT TCTGCTGTCC TGTGGCACCC CATTAAAGTG CAGTCCCTC CGGGCCAAA 119

SEQ ID NO:757

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS00832

SEQUENCE DESCRIPTION:

GATCTGAAAT TAAATACTCA ACAGACTCCT CCTTTTTTAG CTGTATTTT CAGGTACTGT 60  
 30 GTGGTGACCG CCCCACTGGT GTCTATTACA GGCCACTTG GTAGTTGTGT ATCTGNTCAT 120  
 GTATGTGATT TGACAAACCA GTTTTTTAAA ATAAATGGCT TTTTAAA 167

SEQ ID NO:758

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS00833

SEQUENCE DESCRIPTION:

GATCCAATA GAAATGAATG GAAGATGATG GGAAATATGA CTTACCAAG GAGCAATGCT 60  
 40 GGGATTGCAA CTGTAGGGAA CACCATTAT GCAGTGGGAG GATTCGATGG CAATGAATTT 120  
 CTGAATACGG TGGAAGTCTA TAACCTTGAG TCAAATGAAT GGAGCCCCTA TACAAAGATT 180  
 TTCCAGTTT ANCAAATTTA AGACCCTCTC AACTANCAG GCTTAGTGAT GTAATTATGG 240  
 TTAGCAGAGG TACACTTGTG AATAAAGNGG GTGGGTGGGT ATAGATGTTG CTANCAGCAC 300  
 45 CACAANGCTT TTCCATATTN GCNTCCTNTT AACCATGCNT GTCCATAAAC CCNGGGGANGN 360  
 NNANTTGNGG GGTNAANN 379

SEQ ID NO:759

SEQUENCE LENGTH:121

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00834

SEQUENCE DESCRIPTION:

GATCTACTAC TNGGCCTTCA GTGCGAAGAG CCACATCCAG GCCTGAGGGC GGCACCCCAG 60  
CCCTGCCCTT GCTTCCTTCA ATAAACATCA CAGGACCTGG GACTGCACAG GNCCTGGGAA 120  
A 121

SEQ ID NO:760

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00835

SEQUENCE DESCRIPTION:

GATCGAAGCA ATTGANGTAT CATGGATTGG ATTGTTACTG ATTTTCAGTAA AGTATGTTTT 60  
GCCAATTAGA TACATATATA CAAGATAAAG GAATAGGATG GTAATATATT TGTNTGAAAT 120  
TAAATTACTG TTTTNATTAA AAAATACTGC TTCATTGGGC TGATTTTGTA AAATGTAATG 180  
AGTAAATGA ATTACTGTAT TTNCCCTTTT ATGTCCACAG AATGAGAGTC ATATGTNGTN 240  
ATATNCTAAA TNTNCATTAA ATATTCATGT CACCTTGAGT TGTCATGATA AGTATGTTTT 300  
AAA 303

SEQ ID NO:761

SEQUENCE LENGTH:373

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00836

SEQUENCE DESCRIPTION:

GATCTACTAT GTNATGTCAG GGCCTGCGTG GCAACTCATG CAGCAATTCC AGAACCCCTGA 60  
CTTCCACNC GAAGTAGAGG AACAGGATGC CAGCACCTG CCTGTGTCTT GTGCCTGGAA 120  
GAGTGGGATG AAACGCCACA GAGCAGCCTG TGCTTCGGCT AGTATTAATG TGTAGATAGC 180  
ACTCTGGTAG CTGTAACTG CAAGTTTAGC TTGAATTAAG GGATTTGGGG GGACCATGTA 240  
ACTTAATTAC TGCTAGNNNN GGAATGTCTT TGTAAGAGTA GGGTCGCCAT GATGCAGCCA 300  
TATGGAAGNC TAGGGTATGG GTCACACTTT ATCTGTGTTC CTATGGAAAC TNATTTNGNA 360  
TATTTNGNTT TGN 373

SEQ ID NO:762

SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00837

SEQUENCE DESCRIPTION:

GATCTAGGGA GATGTGGAAG AAACGTGAC TACTATAGAA ATTGATGAAG AAACATATGA 60  
AGAGATATAT AAATCAACGN AACGGAATAT TCCAATGCTC TTTGTCCGGG GAGATGGCGT 120  
TGTCCTGGTT GCCCCTCCAC TGAGAGTTGG CTGAAACAAA GAATTTGTCC TGTATGGAAG 180  
NCGNNNNNNN GGTGTACAGT GGCCTCTCTA AAAGTACAAA ACATTCATAA GAGAAACCCG 240

CATACATTTT GATATTAAGA AATAATTCCG GGGATTCTTC CACTCCTGAA ATGAGTTGAT 300  
TTGCAGATAA CTCACAACCT CTTAAGCTAA ATGGTATTTT CATTTTCTC AAGCTCTCCN 360  
ATAANTATGG CCACCNNGG NNANNGNGTG GGGAAAAAAA NAATTN 406

SEQ ID NO:763

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00839

SEQUENCE DESCRIPTION:

GATCCCCACG CCACAGCCCT TTTGTCTCTG CAAACTGCCT TCTTCGGAAA GAAGAAGGTG 60  
GGAGGNTGTN AATTGTTAGT TTCTGAGTTT TACCAAATAA AGTAGAATAT AAGACGNAAA 120

SEQ ID NO:764

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00840

SEQUENCE DESCRIPTION:

GATCTTGATG GTGTTTCTTT CCCCAAAAAT TGACTTAGAT ATTAAAAATT GGTGCTTATA 60  
AGAGAGAGTT AAAAAAAAAT AGGATTGCTT CAATTAAAAA TACAAAAGAG NCAAA 115

SEQ ID NO:765

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00841

SEQUENCE DESCRIPTION:

GATCCAGTGA CAGCAGGTGT CATGGGTCAA GCATAAATCA TATATAGCAT TTTCAGGCAT 60  
GTTCTTGTA GTTCTTTTGA GTCTGACATT CTAATAAAAT AATTTGTAGG AAA 113

SEQ ID NO:766

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00842

SEQUENCE DESCRIPTION:

GATCTTTGTG AGGATTAGGA ATTAGGTAA AAGAAATTAA GAACCATCTT CAAGCAAAAN 60  
TTAAACTTTA TTTCTNCTTA ANCAATAAAT ACACCTGANT TAGTTTTCCA AA 112

SEQ ID NO:767

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00843

## SEQUENCE DESCRIPTION:

GATCAAAGAC CCAAAGGAAT GCAACANTTT ATCTNTTATC TACCTATNAC CTGCGAGCTG 60  
5 CCCACCACCC CCANGTTGTN GGCCTTTCC AGACAGAACC AGTGATACATC TN 112

SEQ ID NO:768

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

10 TOPOLOGY:linear

CLONE:HUMGS00844

## SEQUENCE DESCRIPTION:

GATCCAAAAC TTAAATACAT CTATGAATTT CCTGGGGCTA TTGTGAGTAC TGTGTATGTA 60  
15 TTTAGCAAAT ATTTAAGACC TAGTAAGTGC TCAATAAATT GTAGCTGTTA TTGCTGTTGT 120  
NGTTTGTAAT 130

SEQ ID NO:769

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS00845

## SEQUENCE DESCRIPTION:

GATCGTGCCA CTGCTCTCCA GCCTGCATGA CGGGAGTNAG ACACCATCTC AAAAAATACA 60  
25 TATAATAATA TAAATAAAAA TATCTTTTNN GAAAATAATT TAATATNNCN N 111

SEQ ID NO:770

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS00846

## SEQUENCE DESCRIPTION:

GATCNAGTAN TGNAGGGGCT GTTAGGAGCT TCCTGCAAAT CCCTGAGAGG GCAGAAGATA 60  
35 GCTTCTGTTA ATTCATTATT CTTCCAATAA ATGTTGATTG AGTACCTAAA 110

SEQ ID NO:771

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00847

## SEQUENCE DESCRIPTION:

GATCACCGNC CAGTAATGGG CTCAGAGCAG GTCTTCATCA TGCCTTGTCCT TTTTAACT 60  
45 GAGAAAGGAG ATTTTTTGAA AAGAGTACAA TTAAGGAC ATTGTCAA 109

SEQ ID NO:772

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS00848

SEQUENCE DESCRIPTION:

GATCTTCTTC AATATGTGAA TTTGGGCTCA CAGAATCAAA GCCTATGCTT GGTTTAATGC 60  
 TTGCAATCTG AGCTCTTGAA CAAATAAAAT TAACTATTGT AGTGTGAAA 109

SEQ ID NO:773

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00849

SEQUENCE DESCRIPTION:

GATCAACAAG GTTGGCCACT GCTTGATTA CCAGGGACTG GTTACAACCA TTATTTCTNT 60  
 TCATTTGCTT GGCTTATCTC ATATTAAAGT GAGTTTGAG TTCTCCAAA 109

SEQ ID NO:774

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00850

SEQUENCE DESCRIPTION:

GATCCAGTTC TAAACTTTGG GATATTTTTT TTCAATTTTG AAGAGAAAAT GGTGAAGCCA 60  
 TANGAAAAGT TACCCGAGGG AAAATAAATA CAGTGATATT CTTACGCAA 110

SEQ ID NO:775

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00851

SEQUENCE DESCRIPTION:

GATCTGTGTG CTCTTATCAC CAATCAGTTC AGACCTGGTT GATTTGTAC TTTGGAAGCTG 60  
 TACCTGGAT GGTTTTGTTT ATTTAAAGAG AAACCTGAAG TACTCAA 108

SEQ ID NO:776

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00852

SEQUENCE DESCRIPTION:

GATCACCATC TTAAATTTA CTTCAAAATA AAAGCATGTA AGTNACTGTT TTTCAAGAAG 60  
 AAATGTGTTT CATAAAGGA TATTTATATC TCTNTNGCTT TGACTNNN 108

SEQ ID NO:777

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS00853

SEQUENCE DESCRIPTION:

5 GATCCCCCTC GGAAGAGGGA CTCCAATGGG CATGTCCCCT CCGGAAATNC GGCCTCCTCC 60  
CCCTGGAATG CNAGGNCCCC CTCCCCCGGN AATNCGCCCA CCAAGN 106

SEQ ID NO:778

SEQUENCE LENGTH:130

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00854

SEQUENCE DESCRIPTION:

15 GATCCCATCA TGAATTCATT GGAATTTGTG TTGCATGTAA GGCAATCTTT TCCNTGTTGT 60  
AAATCTTCCG TTTTITAATG TACATATATT TTGAAAAATA TGAATAAACA TGAAATTTTA 120  
AAAGCTGAAA 130

SEQ ID NO:779

SEQUENCE LENGTH:104

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00855

SEQUENCE DESCRIPTION:

25 GATCATGGTG GGTCAGCTGT ACTGATTGTN ATCCTGACTT TGGCATTGGC AGCTCTTATA 60  
TNCCGACGAA TATATCTGGC AAACNNATAC ATATNTAACT TTAN 104

SEQ ID NO:780

SEQUENCE LENGTH:107

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00856

SEQUENCE DESCRIPTION:

35 GATCTTTTTA CAGTATCCAT TTATTATGTA ATNCTTNTNA GAAAAGAATC TTATAGTACA 60  
TNTTANTATA TGCAACCAAT TAAAATGTAT AAATTAGTGT AAGCAAA 107

SEQ ID NO:781

SEQUENCE LENGTH:109

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00857

SEQUENCE DESCRIPTION:

45 GATCAAAATG AAAGAAAATC ACAGAAATTA TCCTATGTGT ACTCCTCATC CCTCCTGCTG 60  
TATATNTTCT NATTTTTTGC GTAATAAATN ATGTTAATTA CCAAATAAA 109

SEQ ID NO:782

SEQUENCE LENGTH:125

50 SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS00858

SEQUENCE DESCRIPTION:

GATCTCCAAT GTTTTGGGGA TGCTTTGAGT CTCAAAAAAA ATTGATAATC AGAAAAGTAA 60  
TTTTTGTGTTG TTTGTTTAAT GTATCCCTGT TCTGTTTTTA ATTAAACTCC AAGTCTCATT 120  
TTAAA 125

SEQ ID NO:783

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00859

SEQUENCE DESCRIPTION:

GATCGAGGTG ACAAATANTC AGTCNTANG TCCCCACAAT GACCTCACCA NNATGGCTTT 60  
GGGGAGCTCT TCACCCTAAA GATTCGGTCT GGTTCGTAA TGN 103

SEQ ID NO:784

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00860

SEQUENCE DESCRIPTION:

GATCTGGAGG CAAGATGCCA GGCCCCACAG GTGTTCTCAG GGCAGTTCTT GGTGTCTGCT 60  
TCTCAGATAC CAAGGACTGG AATTAAAACC TTTCTGGGA AA 102

SEQ ID NO:785

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00861

SEQUENCE DESCRIPTION:

GATCACAGCC GAAGAGTGAA AGGTGCTGCA ATGAATGTTA GCTGTGGCCA CTGTGGATTT 60  
TTCGCAAGAA CATTAATAAA CTAAAAACTT CATGTGAAA 99

SEQ ID NO:786

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00862

SEQUENCE DESCRIPTION:

GATCAAGTTA TTTTNAATTT GGTTCACACA TTGGAAACAA GTCAGTCATT CAGATATGAT 60  
TCAATGTCT ATAAACCGAA CTGATGTAAG TAAA 94

SEQ ID NO:787

SEQUENCE LENGTH:102

# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00863  
 SEQUENCE DESCRIPTION:  
 GATCTCTTCT TCTCCCTGTG GCCCCTGCGC TGTGCCCCG TCCCCGTCAC CCCGCCCNN 60  
 ACTGAAATNT ATAATCTGAC TTCCTGTACA GAAACCTGCA AA 102

10 SEQ ID NO:788  
 SEQUENCE LENGTH:93  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00864  
 SEQUENCE DESCRIPTION:  
 GATCTTGTTA GCAATGCTGT TTTNCTGTT AGTCGGGTTA GAGTTGGCTC TACGCGAGGT 60  
 TTGTTAATAA AAGTTTGTTA AAAGTTTAAT AAA 93

20 SEQ ID NO:789  
 SEQUENCE LENGTH:100  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00865  
 SEQUENCE DESCRIPTION:  
 GATCTTCAAG TGAACATCTC TTGCCATCAC CTAGCTGCCT GCACCTGCCC TTCAGGGAGA 60  
 TGGGGGTCAT TAAAGGAAAC TGAACATTGA ACCCTTTAAA 100

30 SEQ ID NO:790  
 SEQUENCE LENGTH:92  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00866  
 SEQUENCE DESCRIPTION:  
 GATCAGAATT TAAAATGTGT GATTCTTTTT CTTTCTGTAA GTATGTATTG CTATGATAAA 60  
 TAAAAAATGG CAGGACCATT NTTTTATNA AA 92

40 SEQ ID NO:791  
 SEQUENCE LENGTH:93  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00867  
 SEQUENCE DESCRIPTION:  
 GATCTCCAAC CAGGCCAGAG AAGATTCTCA CAGAAGGTTT TGAACCTAA GAAATAAATT 60  
 GGTTTGGTAA TAAATGGCTT CTGGTCAGAT AAA 93

50 SEQ ID NO:792  
 SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00868

SEQUENCE DESCRIPTION:

GATCTTGAT CTTTGATATA CGGATGTNAT TTGTACGAAG GGCAGTTCGT AAACAGCACT 60

TGTNCTTTTA ATAAAAGAAT GTTTTGCAA AAAAAAAAAA AAANCCCNAG GAAA 114

SEQ ID NO:793

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00869

SEQUENCE DESCRIPTION:

GATCTGTTTT GTACTTTTGA TACTGTTGGA TACTTATAAT CAAAACTTTT ACTAGGGTAT 60

TGAATAAATC TAGTCTTACT AGAAAATAAA 90

SEQ ID NO:794

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00870

SEQUENCE DESCRIPTION:

GATCCATTTT ATAAAGTATG ATTTGCCCAA ACCTGTACCA TTTCCGTATT TCTCCTGTAG 60

AAGTAAGAAA TAAATTCCT TAAATAAA 88

SEQ ID NO:795

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00871

SEQUENCE DESCRIPTION:

GATCTGGCGC TTGGGGGTAA GTGGNATGAT TTGCTAATAT TGAGNATCTG TTGTATCAAA 60

CATAATAAAC TTTTTTTTGA GATGTGAAA 89

SEQ ID NO:796

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00872

SEQUENCE DESCRIPTION:

GATCAGGGTG TCTCCTTGTC CTTCTNAGAT GTGGAGAAGA GGCTGCTGGC TACCCTAAAA 60

NTTGAAATAA AAGATTTTGG CCTTTGAAA 89

SEQ ID NO:797

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00873

SEQUENCE DESCRIPTION:

GATCCATTGA GCCCAGCAGT CCAACCTGGG CAAAATAAGT GAGAGACCCT GTATCTGAAA 60

GTAATAATAA AAATAAAAAA TATAAA 86

SEQ ID NO:798

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00874

SEQUENCE DESCRIPTION:

GATCCTTTTT GATAATCTCA TTCCTAGAAA TTAACTTA ATGAAATCCC TAATAAACT 60

CAGTGCTGTG TATTTGTGC CTCAAA 86

SEQ ID NO:799

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00875

SEQUENCE DESCRIPTION:

GATCGAACAT TTCACCTCTC ATATTAAGTC TGGCAATGAT GACTATATGT ATTCCTGCCT 60

AAATAAATCA TCTATTAATC ATTAAAA 87

SEQ ID NO:800

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00876

SEQUENCE DESCRIPTION:

GATCTCCGAG TCAGGACGGT CGGCCAGACC CACGGGGTAA CGGGTCTAAT CGTGTAGGAA 60

TAAAGCTGTA TTCCAGTGCT TCCAAA 86

SEQ ID NO:801

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00877

SEQUENCE DESCRIPTION:

GATCCCCGCG ATACTTCAAC GCCTTCTGAC TTCCAGGTGA TGACTGGGCC CCCAATAAAT 60

CCCGTCTTTG GGTCTCTCTG CAAA 84

SEQ ID NO:802

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00878

SEQUENCE DESCRIPTION:

GATCCCTCAA AACCTCACTA ACTGGAAGGA TGATTTTGTC TCAGTTTGTA CTCCTAAATA 60

AAAAGTAAAC ATGACACCTC TAAA 84

SEQ ID NO:803

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00879

SEQUENCE DESCRIPTION:

GATCTGTGAA GAAATGAAAT AAAATGGTAT TTAGTAAGAA ATCTCTATTT TAAGAAAAAA 60

AGTAAACCT GTTATAAACA CATGCAAA 88

SEQ ID NO:804

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00880

SEQUENCE DESCRIPTION:

GATCGTGCCA TTGTGATATG AATATGCCTT ATATGCTGAT ATGAATATGC CTTAAAATAA 60

AGTGTTCCTT ACCCCTGCCA AA 82

SEQ ID NO:805

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00882

SEQUENCE DESCRIPTION:

GATCTTAAGT CATACATTTN AATTGTNTAG AGGTTGTTCA ACTGAAGGAA TAAATGTCTA 60

TNAANCTAAA ACAAATGGAA A 81

SEQ ID NO:806

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00883

SEQUENCE DESCRIPTION:

GATCAAGTTT GTACATAACA CTAGTGGCAT TTCTTATCAA AAGGATTGGA TAATAAAAAAT 60

AAGTTTCTAC TGGGTAAA 78

SEQ ID NO:807

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00884

SEQUENCE DESCRIPTION:

GATCCCCCA GCAAGGATAN CATTCAAAGG AGCTCACATT TATGGAATGG ATGAATCAAT 60  
AAATTAATTC ACTTTAAA 78

SEQ ID NO:808

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00885

SEQUENCE DESCRIPTION:

GATCCCATTT CTGATGGATG TGTCACACCT TTTCTGTCAA AATAAAATGT CTTGGAGGTT 60  
ATGACTCCTT GGTGAAA 77

SEQ ID NO:809

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00886

SEQUENCE DESCRIPTION:

GATCTGTGTT AATCTGAGTA ACTTATTGCC TAGCCTATAA ATAAATTCCA AAATATCCAA 60  
TTCATTCTT CTTGAAA 77

SEQ ID NO:810

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00887

SEQUENCE DESCRIPTION:

GATCATCCTT CCTGGCAAAT AAATTCCCGT TTCTATCCAA AAGAGCAATA AAAAGTTTTC 60  
AGTGAAATGT GCAAA 75

SEQ ID NO:811

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00889

SEQUENCE DESCRIPTION:

GATCTGAAAG CCTGAGTGTG TGTACGTGCG CGCGTGCGTG AAGGCCCTGC CACGATTAAA 60  
GACTGANACC GGCAA 76

SEQ ID NO:812

SEQUENCE LENGTH:129



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00890

SEQUENCE DESCRIPTION:

GATCTTTAAT ACAATATAGA AATTGTGTAA TAGTTATTAT AAATGTTAAT ACACAAC TTT 60  
CAGGTAATTT TAACTGATTA TTTCTTTTGC TCTTTTAACT TAAGTTATTA AAGTTTAAAA 120  
GTTTCGTAAA 129

SEQ ID NO:813

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00891

SEQUENCE DESCRIPTION:

GATCTGGTCT CGGTGGTCCT TCCCCGCAGG CAGGTGTCAG GACCGGCCTA ATAAACATGT 60  
GTGGCCTCCT CAAA 74

SEQ ID NO:814

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00892

SEQUENCE DESCRIPTION:

GATCCAAATC CCATTACAGT TGTATAAAGA AATAAAATTT TGTACTNATA TTATTAAAAA 60  
TCACATTTTT AATATTTGTA AA 82

SEQ ID NO:815

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00894

SEQUENCE DESCRIPTION:

GATCCCCAGA GACCCCATTT GCCTCTCAAC ACTCAGACCT TCAACTGTTT TTNAATAAAT 60  
CTACTTTTAA AA 72

SEQ ID NO:816

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00895

SEQUENCE DESCRIPTION:

GATCCTACAC CCNGAGCCTC AGAGCACTGC TACTTTTAA AATACTTCTT TCTCTTAAAA 60  
GTCTTTACCA AA 72

SEQ ID NO:817

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00896

SEQUENCE DESCRIPTION:

GATCAGATGT TAAGACTGAC ATTTCCAAGG TTGGCTACTA TGTAATAA AAATTACACA 60

AATTGTGCAA A 71

SEQ ID NO:818

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00897

SEQUENCE DESCRIPTION:

GATCTGAAGT AATTGTGCTG TATTTATGTT TATTCACCAG TCTTTGATTA AATAAAAAGG 60

AAAACCAGAA A 71

SEQ ID NO:819

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00898

SEQUENCE DESCRIPTION:

GATCTAGCTC TCTGATTCCA TACATTCCAG ACTTCTCAGT GGATTTGTAA TAAACTATAA 60

ATAAAAATAG CTCTCATTTA TAAA 84

SEQ ID NO:820

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00900

SEQUENCE DESCRIPTION:

GATCATGTCT TTTCCATGTG TACCTGTAAT ATTTTCCAT CATATCTCAA AGTAAAGTCA 60

TTAACATCAG AAA 73

SEQ ID NO:821

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00903

SEQUENCE DESCRIPTION:

GATCTGATTA TTTACTTTGT TTATTGTCTA TATGCCTTTT AAAAAAATAA ACTTGTTATG 60

CAAAATAAA 69

SEQ ID NO:822

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00904

SEQUENCE DESCRIPTION:

GATCCAGTTG TAGCTGCCAT CAGATGCCGG AGACTCGCCC NTCAATAAAA AAATCTCTTC 60  
TAGCTGAAA 69

SEQ ID NO:823

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00905

SEQUENCE DESCRIPTION:

GATCACTGTA AATGGTAATC AGTTGGAATT CTCCTAAATG TCTTCCAGAC ACTAGTAAAA 60  
AACGACCTGA AA 72

SEQ ID NO:824

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00906

SEQUENCE DESCRIPTION:

GATCTTTCTA CCTGCCTTTC CATGTCATGA GAGGAAGAAA CAAGAATGAC AAGTGTATGA 60  
CTNCCAAA 68

SEQ ID NO:825

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00908

SEQUENCE DESCRIPTION:

GATCACGTAC CTGTGCAGAA ACCGCCTCTG TGGCTGCATT TGAAATAAAA CCCGACCCAG 60  
CAGCAAA 67

SEQ ID NO:826

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00910

SEQUENCE DESCRIPTION:

GATCATATTT TATGAACAGA AAGACTCAGG ACATATTAAA AAATAAACTG AACTAAAACA 60  
ACTTTTGCCC CTGACTGATA GCATTTTCAGA ATGTGTCTTT TGAAGGGCTA TGATACCATT 120  
TATTAAATAG TGTTTTATTT TAAAAACAAA ATAATTCCAA GAAGTTTTTA TAGTTATTCA 180  
GGGCACTATA TTACAAATAT TACTNNGTTA TTACACAAAA AGTGATAAGA GTAACATTTG 240

EP 0 679 716 A1

CTATACTGAT GNTTGTNTAC TCAAAAACCT CNGNTNAACN GTATGTAATC TNAGTTCACT 300  
GCACTTAAGT TCACCNAACA TNNATNAATG TCAATGNAGA AA 342

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SEQ ID NO:827  
SEQUENCE LENGTH:72  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS00911  
SEQUENCE DESCRIPTION:  
GATCTAAGAA GTTGTGAATG TTGTTAATCA TTAGCCGTT GCAATAAATG TAGAGGAAAT 60  
GCAGTGTGCA AA 72

15

SEQ ID NO:828  
SEQUENCE LENGTH:65  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS00912  
SEQUENCE DESCRIPTION:  
GATCACCTGA GGCCATGAGT TTNAGACCAG TCCTGGTAAC ATAGCAAGAC CTCCATCTCT 60  
ACAAA 65

25

SEQ ID NO:829  
SEQUENCE LENGTH:65  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS00913  
SEQUENCE DESCRIPTION:  
GATCCTAGAC AGCGCCTTAT CTATGATTGA GTGTCCGTGT AAATAAATC CTACTTAGAC 60  
TTAAA 65

35

SEQ ID NO:830  
SEQUENCE LENGTH:65  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40

CLONE:HUMGS00914  
SEQUENCE DESCRIPTION:  
GATCTGGGAA CTTTTNCTG TACAAATCTG TTAAAAAAA AAAAAAGGNA CCNCATTGAT 60  
TTAAA 65

45

SEQ ID NO:831  
SEQUENCE LENGTH:63  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

50

CLONE:HUMGS00915  
SEQUENCE DESCRIPTION:

55

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GATCCAAATT AAAACCTGGT AGAATCTAAT ACATTGACTG CAATTAAAAT GTTTCCTGG 60  
AAA 63

5 SEQ ID NO:832  
SEQUENCE LENGTH:68  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00917  
10 SEQUENCE DESCRIPTION:  
GATCCAGTTC TAAGTGTCAT CTTTATNAT NAAGACAATA AAATCTTGAG TTTATGCTTC 60  
ACTTNAAA 68

15 SEQ ID NO:833  
SEQUENCE LENGTH:63  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00918  
20 SEQUENCE DESCRIPTION:  
GATCCACGGT TGTNACCATG TATTACCACA AATTAAACAA TAAAAAATTG TTTAAGAGT 60  
AAA 63

25 SEQ ID NO:834  
SEQUENCE LENGTH:109  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00919  
30 SEQUENCE DESCRIPTION:  
GATCTACTGT CATTTGNATG CAATTCCTG TTACCTTGAA AAAATAAAAA TGTTAACAGG 60  
AATGCAGTGT GCTCATTCTC CCNAAATAGT AAANCCCACT GTATACAAA 109

35 SEQ ID NO:835  
SEQUENCE LENGTH:62  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00920  
40 SEQUENCE DESCRIPTION:  
GATCCAATTA CACACATTCTG TTCACAACTC AACACAAATT CCTATTAAAT ATTAAAAGTA 60  
AA 62

45 SEQ ID NO:836  
SEQUENCE LENGTH:61  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00922  
50 SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

GATCTTAAAC ATAGGAAAAC CATACGTGTT CATGATAATA AAATGCTTTC TATGAAATAA 60  
A 61

5 SEQ ID NO:837  
SEQUENCE LENGTH:56  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS00924  
SEQUENCE DESCRIPTION:  
GATCATACCA CTGCTCTCCA GCCTGGCTAT CAGAGTGAGA CTCTGTCTCA CAGAAA 56

15 SEQ ID NO:838  
SEQUENCE LENGTH:56  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00925  
20 SEQUENCE DESCRIPTION:  
GATCAGACAC TTAACCCCTTA TAANTTAAAG TCAATAAAGC ACCTTTTAA AGGAAA 56

25 SEQ ID NO:839  
SEQUENCE LENGTH:57  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00926  
SEQUENCE DESCRIPTION:  
30 GATCAAAGTG AAACAATGTT TGGATGCAAC GCAGAATAAA AGAATATAAG AAATAAA 57

35 SEQ ID NO:840  
SEQUENCE LENGTH:52  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS00929  
SEQUENCE DESCRIPTION:  
GATCTAATTA AAAGACCTTC TGCACAGCAA AAGAACTAA CAACAGAGTA AA 52

40 SEQ ID NO:841  
SEQUENCE LENGTH:52  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
45 CLONE:HUMGS00930  
SEQUENCE DESCRIPTION:  
GATCCCGGCA GAAGCTATGA AAGGGAATAA AGAGAAAAGA AGTACCCAGA AA 52

50 SEQ ID NO:842  
SEQUENCE LENGTH:52

55

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00931  
 SEQUENCE DESCRIPTION:  
 GATCTTTTAG TTTCAACTCA GCTTTTACAA TAAAANGGAT TTGTATTGCA AA 52

SEQ ID NO:843  
 SEQUENCE LENGTH:58  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00932  
 SEQUENCE DESCRIPTION:  
 GATCTCTTTT CAGAAGTGTC TATAGAACAA TAAAAATCTT TNACTTCTGA CCTTGAAA 58

SEQ ID NO:844  
 SEQUENCE LENGTH:53  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00934  
 SEQUENCE DESCRIPTION:  
 GATCCTAAAT CATGACTTAC CTGCTAATAA AAACCTATTG GAAAAGTGAG AAA 53

SEQ ID NO:845  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00935  
 SEQUENCE DESCRIPTION:  
 GATCAAGCTG TAAAAAACN AAAAAATTAA TAAAAATTTC GAGAAATANA AA 52

SEQ ID NO:846  
 SEQUENCE LENGTH:51  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00936  
 SEQUENCE DESCRIPTION:  
 GATCAGCATT GTGACTTGGA GATAATAAAA TTAGACTAT AAACCTGGAA A 51

SEQ ID NO:847  
 SEQUENCE LENGTH:62  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00937  
 SEQUENCE DESCRIPTION:  
 GATCTGAGGT AAACTTTGAA GTAAAATAAA AGCTGTGTTT GAGCATCATT TGTATTTCGA 60

AA

62

SEQ ID NO:848

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00938

SEQUENCE DESCRIPTION:

GATCCTCCCT CCCCTAATTA AAGTCTCTTT TTGCCCCCTT GGGCTGNCAT GAGGTCAAA 59

SEQ ID NO:849

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00955

SEQUENCE DESCRIPTION:

GATCAGAATT TTAAATNAAA GGTTTTTTCT TTAAATNATT TGTATTACTT TATTA AAACT 60

CTGATATTAA A 71

SEQ ID NO:850

SEQUENCE LENGTH:661

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00972

SEQUENCE DESCRIPTION:

GATCCGGTTC TGGGACAGCA GGGGGCCCCA CTGCACCCAG GTCATCCCTG TGCAGGGCCG 60

GGTCACCTCC CTGAGCCTCA GCCACGACCA ACTGCACCTG CTCAGCTGTT CCCGAGACAA 120

CACACTCAAG GTCATCGACC TGCCTGTCAG CAACATCCGC CAGGTGTTCA GGGCCGATGG 180

CTTCAAGTGT GGTCTGACT GGACCAAAGC TGTGTTTCAGC CCGGACAGAA GCTATGCACT 240

GGCAGGCTCC TGTNATGGGG CCCTTTACAT CTGGGATGTG GACACCGGGA AACTGGAGAG 300

CAGACTACAG GGACCCCAT TGCCTGCCGT CAACGCCGTG GCCTGGTGCT ACTCCGGGAG 360

CCACATGGTG AGCGTGGACC AGGGCAAGGA AGGTTGTGCT TTTGGCAGTA GGGCCACGAC 420

CTGCCTGCTT GGGNTGGAGN TTTTNNCCG AAGCTNAAAG TTTCTNNGG GGCAATGAAG 480

GGGTTTGGGG TTTGGGATTN GAGNTTNGNC TTGGGATTTA ATTGGGNAAG AAGGCTTGGA 540

AAGACCTTGN CTTTTTTNTT TAAAANTNAA GTATTGGTTT GGGGGNTTAA GGTAATTTTT 600

TTTTNGAATT TTAANTTNAT NTCTAAATTT TTTCCAAAT TTTGAAAAAT TTTTTTTNAA 660

A 661

SEQ ID NO:851

SEQUENCE LENGTH:641

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00973

SEQUENCE DESCRIPTION:

GATCTTGGAT GTCTATTATA GGAGAAGTAT GTCCTGCCAA TGTACAAGAA GGCAGCATTG 60



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TAGGATTAAC ATTCTTGCTCT ACTGTATATT ATCTTGGAAG GCTCTTGTTA ATATGTTACA 120  
 CTTAATATTC TCCACAGTTA CCTTTAGAGA GAATTTATGA GAAGTTAGTT TCTGATGCAG 180  
 AGGTTTTTAG GCTGTGATTT CATCAAAAGT CCTAATAGCA TTCTACCTCA AAGGGGACACT 240  
 TAGNATGCCT AAAATTTATT CACTTAGTTT TCCTTTTTTA TTTGAAAAAA TACATGACAT 300  
 GTAATCTTTT TTTCTTGAAT TCTTTCTCAG ATTTTAAAGT ACTATATTAA AGAAAAAAAT 360  
 TAATGTCTAA AGGCCTAGCA TTCCTTGCGAG GACCCCTATA CTAACCATGG TAATGGGGGA 420  
 GAGGGGTGGG GCAGNTNNGT AGGGGNACCA GGTTCAGGC CTCAAGCTTC CCAAAGCCAT 480  
 TTTTNTAAA TGGGAAATCC NTNAANTNT GGAACCCGCT TTGNTATNGG NGCCCCTTTT 540  
 TTTAAAATTC CNGGCCTTTT TTNNTTGGT AATGGGGGT NCTGTTTGNG GTTTAACCT 600  
 NANCCTGGNC CGGGGGGGTT TAAAGGAATG CTGNCTGCAA A 641

SEQ ID NO:852

SEQUENCE LENGTH:627

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00974

SEQUENCE DESCRIPTION:

GATCTGCTNC AGTGCTCTGA GCCCTAGGAT TCATCTNTCT TTTACCGTA GNGCGCNGA 60  
 CTGGCATTGT ATTAGCAAAC TCATCACTAG ACATCGTACT ACACGACACG TACTACGTTG 120  
 TAGNTCACTT CCACTATGTC CTATCAATAG GAGCTGTATT TGCCATCATA GGAGGCAACA 180  
 TTCACTGATT TCCCTATTC TCAGGCTACA CCCTAGACCA AACCTACGNC AAAATCCATT 240  
 TCACTATCAT ATTCATCGGC GTAAATCTAA CTTTNTTCCC ACAACACTTT CTCGGCCTAT 300  
 CCGGAATGCC CCGACGTTAC TCGGACTACC CCGATGCATA CACCACATGA AACATCCTAT 360  
 CATCTGTAGG CTCATTCAAT TCTCTAACAG CAGTAATATT ANATAATTTT CATGATTGA 420  
 GAAGCCTTCG GTTTCGAAGC GAAAAGTCCT AAATAGGTAG GANGAACCT TCCATTAAAC 480  
 CTGGAGTGAC TATATGGNTT GCCCNTACCC TTACCANACA TTCNGAGGAN CCCGTATACA 540  
 TAAAAATTNT GNNAAAAAAN GGANGGNTTC GNACCCCCCA AAGGTTGGTT TNANGNCAAC 600  
 CCCCNTGGGC TCNATGGTTT TTTTAAA 627

SEQ ID NO:853

SEQUENCE LENGTH:617

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00976

SEQUENCE DESCRIPTION:

GATCAGANTG CCCCTCCACT CATGAGACTC TTCATTTTGT CCACTTTGAC AGGAAAAGTG 60  
 GGAATGTATG CAGAGCTCTC AAAAGAAACA AAAAAGGCCA AAACGGTGCC TTCAGCCACA 120  
 TCCTCTGAAT TGGCCCTGAC TTGGACTAAA NCCNCTAATG CAAAATCCCT TGACAAAAGC 180  
 GCATAGGTTA TTTCAAACCA GCATTGTTTT TTATGTAACC TGTTTTACCG CATCTTCTCA 240  
 GCAGCTTCTG ACCACTGCTC AATTTTTTCC TTTACAGCCA TTGTTCTGGT GGACAAAATA 300  
 CCTAGGTACT CCAATCCTG GCAGGAAAAA TATACAGCAT TATGAAACAG CACTCAGTAA 360  
 TCCTAAAATG GATTTTCCAA AGCTGGTTAC ACATGNCCTG CAAAGTCTTA TTTAAATTTA 420  
 AAAGGCCTTT CTCATTACC AGGGGTTTAG GTCAACGNNG GCAAACCCCT GGGGGAATTT 480  
 AAATTGGGAA GGTTANTTNC CTTTNGTAAA TTCATAGGGN CCAAANGGCN GGNAGTTAA 540  
 TTTTCCATN GGGTTGGTGG CNCCCGGNT TCATTGGTNT TNGGCCCAN GGAATTTAAT 600

TTTTTTAAAN CCTTAAA

617

SEQ ID NO:854

SEQUENCE LENGTH:602

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00977

SEQUENCE DESCRIPTION:

10 GATCCCGTGC GCGCGCTGC CCGAGGGGAG CAAGGACAGC TTTGCAGTTC TCCTGGAGTT 60  
CGCTGAGGAG CAGCTGCGAG CCGACCATGT CTTCAATTTGC TTCCACAAGA ACCGCGAGGA 120  
CAGAGCCGCC TTGCTCCGAA CCTTCAGCTT TTTGGGCTTT GAGATTGTNA GACCGGGGCA 180  
TCCCCTTGTC CCCAAGAGAC CCGACGCTTG CTTATGGCC TACACGTTTC AGAGAGAGTC 240  
15 TTCGGGAGAG GAGGAGGAGT AGGGCCGCCT CGGGGCTGGG CATCCGGCCC CTGGGGCCAC 300  
CCCTTTTNA GCGGGTGGGT AGGAACCGTA GACTCGCTCA TCTCGCCTGG NTTGTCCGC 360  
ATGTTGTAAT CGTGCAAATA AACGNTCACT TCCGAATTAA GCGGTNTATT TTTGAANGT 420  
TTAATAATTG TGTTTNTGA ATACTGAAGT ATTTGGCTTT AAATTCCTAA NTTAAAAATT 480  
20 TAATNTTTTA CTTTTTAAAT TGCTGGGTTT AAGATNGTTN AAGATTATCC TTGNAACTTT 540  
NNGGGGGANG TTNTATTTT NGAGTCTTTT NGGAANAGNC TTNAGGCTTT TNNACTTNGA 600  
AN 602

SEQ ID NO:855

SEQUENCE LENGTH:595

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00978

SEQUENCE DESCRIPTION:

30 GATCCCAGGG CTCCTGCCA TTTTAGTGTC TTGGTGAGT GTAACCATTT AGTGTTGGT 60  
GGCAACAATT TTATGTACAG GTGTATATAC CTCTATATTA TATATCGACA TACATATATA 120  
TTTTNGGGG GGGGCGGACA GGAGATGGGT GCAACTCCCT CCCATCCTAC TCTACAGAA 180  
GGGCCTGGAT GCAAGGTAC CTTGAGCTG TGTGCCACAG TCTGGTGCCC AGTCTGGCAT 240  
35 GCAGTACCC AGGCCCACCC ATCACGTGTG ATGACATGT AGGTACCCTG CCACGGCCTA 300  
TGCCACCTG CCCTGCTTCC TGCTCCTTA TCAGTGCCAT GAGGGCAGAG GTGCTACCTG 360  
GCCTTCCTGC CAGGAGCTTT NCACCCACTN ACATTCCGTC CCCGCGGCTT AACTGNAGCA 420  
AGCGTGGNCC TAGGACAGNA GGAGCTTCGG GCCCNGTTT ACCTGCGGT GGGGCTNANG 480  
GGTTGGCATT TCTTGCTGG GGCCTGCGG TTNAATTTT GGGNTGATNA TTGGGGNGAG 540  
40 GGGTGGGGTA AAAAAACCAN TTTTGGNNAA GNTTGGGANG NTTTTGNCTT TTAAA 595

SEQ ID NO:856

SEQUENCE LENGTH:581

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00979

SEQUENCE DESCRIPTION:

50 GATCTGGAAT TGCAGCCAC ATAAACATAA AGGAGGATGT CCCTGGTCTG TTCCATCCCC 60  
ACGGATGGTG TTGCTGCTGG GCAACAGTGT TGGCTTCTTT NAAGTACCCC CTTTCCTCCT 120

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CACCCACCTC CAAACTGACT AGCACTCAGA GGGACTTATG ATAAAGGTTC AGCTCCAGGG 180  
 GTAGTACCTG AGTGTGTGCC ATGCCCTTC AGACCAGCTG CTTCCATCAG AATTCCAGGG 240  
 TCACAGCCCC AACAGAAGCA GCAGTGCCTC TGTAGGAGGG GTGCTGGGCT CTGGNCTTCT 300  
 NATGCAGAGA GGTCCGGGAC AGGGTCAGTA TCGTGGGCAT GTNTATAGCT TCCCAAGTTC 360  
 TTTTACAAGT CCCNTGCTGG GACTCCCTGA NTTTACTTTT GGTNGGNTTC CTAGGTNCTA 420  
 ATTGGTTTTA CAAACTTACA NTTTTNTAGG AATTGANTT ANGATTANCT TGNTTTAATT 480  
 TAATTGTAGA NTTTNGGGGC CTTTTTGGGN CTCAAATTTT NCCATTACAA GGNNTTATTN 540  
 GGGAAANAAA GNNGTTTNA TNAAAATCCT TGGCCAGGAA A 581

SEQ ID NO:857  
 SEQUENCE LENGTH:569  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00980

SEQUENCE DESCRIPTION:  
 GATCTAAATC AGACAGGAGT TGGTCTACAT AGTAGTAATC CATTGTTGGA ATGGAACCCCT 60  
 TGCTATAGTA GTGACAAAGT GAAAGGAAAT TTAGGAGGCA TAGGCCATTT CAGGCAGCAT 120  
 AAGTAATCTC CTGTCTTTG GCAGAAGCTC CTTTAGATTG GGATAGATTG CAAATAAAGA 180  
 ATCTAGAAAT AGGAGAAGAT TTAATTATGA GGCCTTGAAC ACGGATTATC CCCAAACCCCT 240  
 TGTCATTTCC CCCAGTGAGC TCTGATTTCT AGACTGCTTT GAAAATGCTG TATTCATTTN 300  
 GCTAACTTAG TATTTGGGGT ACCCTGCTCT TNTGGCTGTN CTTTTTTTGG AGCCCTTCTC 360  
 AGTCAAGTCT GCCGGATGTC TTTTTTACC TACCCCTCAG TTTTCCTTAA AACGGGNACA 420  
 CAANCTCTAG NGNGGTGTTA NGANTAATNG TTACTNNGGT TANTGGGGTA NTTNNTGGGG 480  
 TNTNGGTTTG GGGCTAGGCA TTGTGGTAGG TTTTNAANAA TTAGNNGGTT GGNCCCCNTT 540  
 NGNTGGGGTG NTTTCANGGT NGAATNAAN 569

SEQ ID NO:858  
 SEQUENCE LENGTH:566  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00981

SEQUENCE DESCRIPTION:  
 GATCCCAACC NGGCTCTCC TGGAACTCTG AACCTGCTGT GGAAGGAATT GGCCATGACC 60  
 TTCACCTCTG GAGAGTAGGG TCTATGGCGA GGGAAAAGGG NNTTCACCAT GATAACCTAG 120  
 TGCCCTCCATA GAGGGGTTTG GAAAAATTCC AGTCCGATTT CTTTGTGTGT CAGCTGACTT 180  
 CCTTAGCTGA TTGTTCCAC TTGCACCTCT CCACCTTTGG CACTAGAACT CCTGAGACAC 240  
 CACTTCTCAT GCTTCTCCCT CCCTACCAGC GGTCAAGGCT TTGGAGCCAC TCTTTTGTAA 300  
 CTCCAGATTA TTAAAGAGA AAAGTACAAG ACAGAAATCT TCTAGCACTT TGTAACACA 360  
 GTTGATTAAC CCTCTTGGGN GTATTTTTTG GGCTTTATAT AAAANCANGG TTTTTTAATT 420  
 NGTAAAGTNT AAGTGCCATT AGGAANATGC ACCAGGGCAT ATTTTGGTT NAAGGTGGTT 480  
 TTTTCAATGG TTTTNCAGGN TTNCATTTTC AAAAAAANGG TTTTTTAAT GGAGGTGTGT 540  
 NTTNAAANNT TCNTGANTGG TGGAAA 566

SEQ ID NO:859  
 SEQUENCE LENGTH:556

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00982

SEQUENCE DESCRIPTION:

GATCTACAAT TACTAATTAA AGCTGTGAAT CTNTTCCTG CTGGAACAAA TTCAAGATGG 60  
 GAAGTTATTG CTAATTACAT GAACATACAT TCTTCCTCTG GAGTCAAAAG AACTGCCAAA 120  
 GATGTTATTG GCAAAGCAAA GAGTCTCCAA AACTTTGACC CTCATCAAAA AGATGACATA 180  
 AATAAAAAGG CATTTGATAA GTTCAAAAAA GAACATGGNG TGGTACCTCA AGCAGACAAC 240  
 GCAACGCCTT CAGAACGATT TGANGGTCCA TATACAGACT TCACCCCTTN GACAACAGAA 300  
 GNACAGAAGC TTTTNGAACA AGCTTTGAAT ACATACCCAG TAAATACANC TGAAAGATGG 360  
 GNANAAATAG CAGTAGCGGT GCCTGGCAGG NCAAGGAGG GNCTGCATNN ANCCGGTTNC 420  
 AGGGGACTTT GTCGNNTGG GTAAAGCCAA AGGAAGCTTG TTCCAGGTCN ANGTGCTGGA 480  
 TGCAAGTTGG GGCNTGGNAT TNNCNATTTT TTGTTGGGGT GTTCCTTTTT TTANTAAACC 540  
 TGNANTTCTT TTTAAA 556

SEQ ID NO:860

SEQUENCE LENGTH:555

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00983

SEQUENCE DESCRIPTION:

GATCTGGATT ATTTGTCTAA GTGAGAGATT GCGAATATCA AAATATCTGT CTCACTTCTT 60  
 CTGTGAATNA CACAGAGTAG AAATAAATTC ACTTTAAAAA TATGACTGAA TTTTGAAAAT 120  
 CAAGACTGAA TCTCACATAG CTGCAGACAG GAACTAAGCC AGCCTCTTTG TATGTGGTAA 180  
 CAAGTACAGT ATAAGANTGA AAGATTTACC ATCCTTGAAA GCTCTAATGA AAATCAAATC 240  
 CAGCAATATA TATTCAACTG TGTACAGGAT TTAAGAACTT ATTTTATGAA GGAGTAATAG 300  
 TGTGTAGATA TAGATTCTGA AGTCTTTAAA CGTGCCTTAA TAAATNAAGT TCNCTGGCAT 360  
 TGAGNTGANN ACCAGGTGAC CNTTGGGGNC AAAAACCNC ACAAGTGATT NGCACACCAG 420  
 TATACNTTCA CCANTATACT NTNTGCACAC ACANCNTTTG TTTNGGTTCA GGGTTTTGCA 480  
 AATNGGTCNN ATGTATTGGC ACTGGCGTCT TTGNATTGTG TAAGTGGNTA TTTNTGAGG 540  
 NTAGCGTGGT NNCNN 555

SEQ ID NO:861

SEQUENCE LENGTH:554

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00984

SEQUENCE DESCRIPTION:

GATCCATGTC TCAGCCTCCA CCCC GCCACA CCTGTCTGTG CAGCCCACCG GCCTTACCTT 60  
 CTACCCTGCC GTGGATGTCC AGGCCTTTGC CGTCCTCCCC AACTCCTCCC TGGCTTCCCT 120  
 CTTCTGATT GGCATGGTAA GCAGTTCCTG GGTGGACAG ATGAGGAGCC CCAGACAGTC 180  
 CCAACAGCAC TGTCTTTGGA GTCAGGAGAC CATGTGAATC CTGTCTGGAT TCAAACCTGG 240  
 ACTGTGTAC TCCGGAGCCT GAGGCTTGAG TCACTGTACT CAATGGTGCC GACTCCTGGA 300  
 GGTATTCAAT CACCAGCCA TTCACTAGTG CGTTTGTITA CTTATTCATT CAATTATTCA 360  
 TTCAGTCAAT TTCTCATTCA TTCANTTATT CATTCCATGT TGGCTTGAAA TATGTGTACT 420

GTNCCAATTN ATCCATTTAT ATCTTTAGTC ATTCAATTAT GCATTNGTGG TATTTGTTCA 480  
 TTNATTCANT TTTAATTTN ATTNAGTTAN TNNNTNGGTT GGTGNCTTGG NGTANNGTNA 540  
 TACATTTGNG GAAA 554

5

SEQ ID NO:862  
 SEQUENCE LENGTH:549  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

10

CLONE:HUMGS00985

SEQUENCE DESCRIPTION:

GATCCTATGG TTCAGGAGGC CAGAAATTC CACCTCTAGG AGGTGGTGGT GGCATAGGTT 60  
 ATGAAGCTAA TCCTGGCGTT CCACCAGCAA CCATGAGTGG TTCCATGATG GGAAGTGACA 120  
 TCGGTACTGA GCGCTTTGGG CAGGGAGGTG CGGGNCTGTG GGTGGCAGGG TCCTAGAGGA 180  
 ATGGGNCTGG AACTCCANCA GGAATATGGT AGAGGGAGAT AAGAGTACGA AGNCCAAACA 240  
 AAAAACCCCG ATTTTAGATG TGATATTTAG GCTTTCATTC CAGTTTTGTT TTGTTTTTTT 300  
 GTTTAGATAC CAATCTTTTA AATCNTTGCA TTTTAGNAAG AAGCTATCTT TTAATGGTTG 360  
 TAGCAGTTAT TGACCTAATA TTTGAAATGG CTGTTGGCAG TAAATTATGA ATCAGTTTTT 420  
 GACCAGNGA TTTTTTNCN TNTATTCCTT ANTTTCCTGT TNCTGATATN CCCCCAAGTA 480  
 TGCAGTTNCT NNNCNCNAA TTCCANGGNN CCATTTTTTT TTCNGGGTTC AANAATNGAA 540  
 TNGNTTAAA 549

25

SEQ ID NO:863  
 SEQUENCE LENGTH:543  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00986

30

SEQUENCE DESCRIPTION:

GATCAGCAGT CTTCTGCTGC CTTCTTAATG TTTCACCTAA GTTCCCATAG TTGCTCTCAA 60  
 AAAGTTTCTT GGCCCTCGTG GGCCAGTNTG GAGGGGCTGT ATCATCATTC ATNAGGAGCG 120  
 TCACTTGGTG GTTTAGGGGG AAATAATCTA TTCTNAAGAT TGAAGAGAGT GCAGGATTTG 180  
 GGGGGTTGAC TCTACATCCT TCAGTATCAG GGCTTATCTC CTTGTNTTAC CTCCTAGGAG 240  
 ACCCTCCTGT TCTTAACTGT GGGCGATGAG AAAGGTGGTG GACTCTTCTT ACTGGCAGGG 300  
 CCACCTGCGT CTGTGGAGAC CCTGGGGCCC AGGGTGGCTG AGGTCCTGGA AGGCAAAGGA 360  
 GCAGGGAAGA AAAGGCCGTT TTTCAGGGCA AGGCCACCAA GATGAGCCGG CGGATGGAGG 420  
 GCGCAGGCGG TTCTCCAGGN CTACATCAGC AACGNAGAGT NCTAAGNANT TANGGCTTTA 480  
 GGGCACTTAN CTNCTGGTTT CCACAGGAAT CTTTNGTCA ATNAAATTAG TTGCCTCAG 540  
 AAA 543

SEQ ID NO:864

45

SEQUENCE LENGTH:538  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS00987

SEQUENCE DESCRIPTION:

GATCATTTCT ATAAAAGAAA TGGTCATTTT ACTTAGATGC CAGTCTACTT TATAAAGACA 60

55

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AATGGATTAT AGACTTAAAA ATAGTCATTT TTCTTATTCA TAAATCTGAC AGGCATAAAC 120  
 CCAAATCAAA GATAATTTGG TGCCCATTTAT GAATTTGAAG TTAAGTGATA GCTCACTTGT 180  
 AAAGTGACTA CCTTAATGTG TATAGAGACC CCAGTCTACT ATTATTTGGG AAAATTGTTT 240  
 AGGTTATATG GGAAAAGTAG CTCTTTAAAA ATCATATTGC CCAACAGAAA CCTTAGGCTG 300  
 AATTTACAGG TATGATAATT TTTGTAATTA ATTTTCTTAG AATTGTGCAG GCTGGGATGG 360  
 GGATAATGNC ATACTCTTTT ACACTGTACC AGCAGCATTT ATTNCCCTNG GACCTTTTAA 420  
 CCNTTTTAGG GGTTAGGGTN CTNGGGGAAC CAACCTTAAT TNGGNCATCC TCCATTTNNC 480  
 TTNTNTNCCN NNNNCCCNNT TTTTTTTTGG GNCCCCNTN GGNCCCCCTA AACNACCN 538

SEQ ID NO:865

SEQUENCE LENGTH:533

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00988

SEQUENCE DESCRIPTION:

GATCAAAACT ATANGTGGCT ATGGCGGATA TGATTATACT GGGTATAACT ATGGGAACTA 60  
 TGGATATGGA CAGGGATATG CAGACTACAG TGGCCAACAG AGCACTTATG GCAAGGCATC 120  
 TCGAGGGGGT GGCAATCACC AAAACAATTC CCAGCCTTC CACATTGGCT TTCCCATGTA 180  
 GTCCTTAGTG TGTCTGCTNC TCCTCTCTCT CCTCATCACA GTTCCCAGCC CCCACCTTCA 240  
 ACTGAACCTA AAAAAATCTT CAACTTCATA CAGTAGTCAC ATTGTTAGTA ATAACACTGG 300  
 GCATTTTAT TTTGATANAN TAGACCGTTT AAATTTTGA GATTCTACCT TATATTTTTT 360  
 GAATTATATA CTAAAGCANA TAAGTAGGTG NTGTAATGTC CATTGGGGNC CAAGNTTTTT 420  
 AGGTGTAAAT GGNAAGGG TANCAATTT NAANCTCAAG TAAACACCCT GTAGGCTTTC 480  
 CCCATGGNTT GGGGNATNTC CGGATTAAGG NCAGGGTTTT CCNTTTTCTN AAA 533

SEQ ID NO:866

SEQUENCE LENGTH:532

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00989

SEQUENCE DESCRIPTION:

GATCTGAAGT GGTGGATTCC TTGTTTTTGC TAGTATCTCA TTTAGAGTTG AGATGGACCT 60  
 TAAAACTCAT CTGTTTTAAC TCACTTTTAA ATAGATGAGT TAAACTTAAT TTAATAAGG 120  
 ANNNNCAGTT AGAGCCTGGA ACTTCAACCA TTATTCATC CCCATGCCCT GTTCCCCC 180  
 ACTTCGAAAT TAAATGCGGT TAGCATCATA TAGTTCATTT TCCCCCTCCA TGCTGCTGTG 240  
 TGATTCTTGA CCTTGGGTAT GAGTTTTTCA TCCTTCATGC AGGGTTCTGT CAGTTCATGG 300  
 TATAGTGATT CAGTGTTAAA ATGGTGGTGT CTCAGCTGTG CTGTGCACAT TTCCAACCTT 360  
 GTCAAAATTA TAGTCCTGAG CAAGCAAGAA AAAGAGGTAA TAACATACCC ATTTTCTTTT 420  
 ATGGANTATA AGCTTAATAA TATTTTTTTC NATGNGCCTA TTTTTTACCT GNGCAAATTN 480  
 GTATGGNCTC ACATGGTTAA CCCCATNAA TTANTCTTGG NCAATTTTAA AA 532

SEQ ID NO:867

SEQUENCE LENGTH:528

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00990

SEQUENCE DESCRIPTION:

5 GATCGCAAAT NCACCTAAAC AATACATTTA CAAAGCCATC TTTACATGCA TTAAACGAGG 60  
GCTACAACAA TATTGTTTTA CAAATACTAG CACTTTTTTC CTGTTATGTA CTTAGTGTTA 120  
GAGGGTCAAA ATAATCTTTC TGCTTAGCAT CTCTTAAACC ATACCTGCAA ATATAGCAGG 180  
ATTNNTTACAT TTACAGTACT TTAATACTTG TATAANCTAT GCAGAAATTT TTAATAAAGT 240  
10 GTAATATATT TNATAAGCTA ATAAGACTGA ATGGGTAAAG GTTTTNGCA TGCCTTAGTA 300  
TACTTGCAGA TACTGAAACA TTTTGGTAAT CTTTCTTACT AAAGGATGTG AATGTTTAAT 360  
GTACCTTCTC TGTTTCTACT CTGTAGTCCA ATGGGAATTC AGTAATGNCA TTTTGNCATG 420  
TCAACCTGGG GACCATAAAN TTGGTCCTGG TCCAGGCCCT CATNTCCTAT ATCCAGTATG 480  
CAATNTTATN TNNTNTNCCT GGTNAATNAA CCCCTCCGGG NTTTAAA 528

SEQ ID NO:868

SEQUENCE LENGTH:526

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00991

SEQUENCE DESCRIPTION:

20 GATCTTTCCT CAGTATGTGC TGATGTTTGG GTTGCTTGTG GAATCACAGA CACTCCTAGA 60  
GGAGAATGCT GTTCAAGGAA CAGAACGTAC TCTTGGATTA AATATAGCAC CTTTNATTAA 120  
25 CCAGTTTCAG GTACCTATAC GTGTATTTTT GGACCTATCC TCATTGCCCT GTATACCTTT 180  
AAGCAAGCCA GTGGAACCTC TAAGACTAGA TTTAATGACT CCGTATTGTA ACACCTCTAA 240  
CAGAGANGTA AAGGTATACG TTTGTAAATC TGGAAGACTG ACTGCTATTC CATTTNGGTA 300  
TCATATGTAC CTTGATGAAG GGGATTAGGT TGGATACTTC ANGTGAGGCC TCCNCTGGGA 360  
30 AACAAGCTGC AGTTGTTTTA GNTANTCCCA TCCNGGTTGA NATTGGGNGN GGNCCTTGNN 420  
CCTAGCATTN CGCATCACNA AGGCAATGTC NGCNTCACAG TTANGGCATT GNGGGGCCGT 480  
TTNCCATGN GNACTGGGTT ATTGGGNGCT NACCAGGTCC AANTTN 526

SEQ ID NO:869

SEQUENCE LENGTH:526

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00992

SEQUENCE DESCRIPTION:

40 GATCCTGTTG CTTCTGCAGG CCATTTTCTG AAAACCCCTG TTAGGAAGGT TGGATTTGGC 60  
GTGACTTGCT TGAGCAAGAG TCCTGGGGAG AGATTTTNAG GTTTAATTTA ACGGTATATC 120  
CAGAGCTAAC AGTGAACAA CTCGTCTAGT TCTGCAAGTC AGATGTACAC TTAGAGTCTC 180  
TCTGTGAAGG GTTTGGGTCT GAGCTGTATA GTATGTCAAA CTGCCAGTAA GCCAGCCCT 240  
45 CACCNTCTGA TAGATATTC TTTAATGCAC CAGACTTCAT GTTTGATAAA TGATTAATGG 300  
TTGAAATTGT TTCTCTTCTT TTGTGTTTTT CCAGTTAATA GATGGTCACT GTTTCACAA 360  
TGTTTTTATAC TTTCCAGCTT TTNGTAACTN AACCTATAAT TACTTNAATT TTAATTTTTT 420  
TTAAAGCTTN GTTGGTGGNC CTAATGNAA GGTNTTTTTC CAGTGCATNA ATGGTTTTTT 480  
50 NTGGNGCTTC TGNNAATGN CCNTCCCAAT TGTGGGTTGG GTTTTN 526

SEQ ID NO:870

SEQUENCE LENGTH:520

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00993

SEQUENCE DESCRIPTION:

GATCAGGACG GCTGGATTCA GGTGTCGTAC GAACAGTACC TGTCCATGGT CTTCAGTATC 60  
 GTATGACCCT GGCCTCTCGT GAAGAGCAGC ACAACATGGA AAGAGCCAAA ATGTCACAGT 120  
 TCCTATCTGT GAGGGAATGG AGCACAGGTG CAGTTAGATG CTGTTCTTCC TTTAGATTTT 180  
 GTCACGTGGG GACCCAGCTG TACATATGTG GATAAGCTGA TTAATGGTTT TGCAACTGTA 240  
 ATAGTAGCTG TATCGTTCTA ATGCAGACAT TGGATTTGGT GACTGTCTCA TTGTGCCATG 300  
 AGGTAAATGT AATGTTTCAG GCATTCTGCT TGCACAAAAA TCTATCATGT GCTTTTCTAG 360  
 ATGTCTCTGG CTCTATAGTG CAAATGCTTT TATTAGCCAA TAGGAATNTT AAAATACCAT 420  
 GGACCTTACA CAAAAGGCTT TCATGNCCTT ACTTTNTNAA AAGGGGTTAT TGTATTCAAT 480  
 GGATATGTGC CGTAGCAATN NNGGGNTGTT AGCGGNTAAA 520

SEQ ID NO:871

SEQUENCE LENGTH:517

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00994

SEQUENCE DESCRIPTION:

GATCTCCGTG GCTTTGGGTT AAAAGACACA CTTGTCCACA TAGGTTTAGA GATAAGAGTT 60  
 GGCTGGTCAA CTTGAGCATG TTAGTGACAG AGGGGGTATT GGGGTTATTT TCTGGTAGGA 120  
 ATAGCATGTC ACTAAAGCAG GCCTTTTGAT ATTAATTTT TNAAGGCA AAATTATAGA 180  
 AGTTTAGATT TTAATCAAAT TTGTAGGGTT TCTAGGTAAT TTTTACAGAN TTGCTTGT 240  
 GCTTCAACTG TCTCCTACCT CTGCTCTTGG AGGAGATGGG NACAGGGCTG GAGTCAAAAC 300  
 ACTTGNANTT TTGTATCTTG ATGTCTTTGT TAAGACTGCT GAAGATTTAT TTTTTCNN 360  
 TTATAATANG GGGNTAANCC CCACCTTAT TCCTTCAATT CACCTACCA TTTTCNNGG 420  
 TTCTTNGTGT TGGGCTTGTG GCAGGNCAG CTTNTGGGT TCCCTTTTN CCATGCCAAN 480  
 NTTNTNAATT NCCCATGTAC CAGTTTGNTN CAAAGGN 517

SEQ ID NO:872

SEQUENCE LENGTH:517

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00995

SEQUENCE DESCRIPTION:

GATCAGAAAT ACAGATTTTG ATAGCAAAGC GACGTTAGNT NGANGCTCTT GTGAGGAAAG 60  
 TCATTGGCTT TATCCTCTTT AGAGTTAGAC TGTTGGGGTG GGTATAAAG ATGGGGTCTG 120  
 TAAAATCTTT CTTTCTTAGA AATTATTTT CTAGTTCTGT AGAAATGGTT GTATTAGATG 180  
 TTCTCTATCA TTTAATAATA TACTTGTTGA CTAAGAGATA TAAGTNTGT ATAAANNCNN 240  
 CCAATTATGT TAACTAGCA TATCTGCCTT TATTGTGTTT GTCATTAGCC TGAGTAGAAA 300  
 GGCCTTTAAA ATTTTTTTAG AAAGCATTTG AATGCATTTT GTTGGTATT GTATTATTC 360  
 AATAAAGTAT TTAATTAGTG CTAAGTGTGA ACTGGACCCT GTTGCTAAGC CCCAGCAAGC 420  
 AATCCTAGGT AGGGTTTAAT CCCCAGTAAA ATTGCCATAT TGCACATGGT CTTAATGGAN 480



GTTTGAATCT TAAATAAATT GGATATTCAC TTTTAAA

517

SEQ ID NO:873

SEQUENCE LENGTH:515

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00996

SEQUENCE DESCRIPTION:

GATCTGCGAA AGACCAACTT TTAGGCAGTG ATACTTTTCT CCCATTCCCT GGGGTGGGGG 60  
 GAGTATGCAG TTGGTGCTTT CTGTAATTCC CTTGTNCTGT TTTGTTCTG TAAGCTTTTC 120  
 CCCTGGTGTC ATGGAAAGGA CTTCTTAAAT AACCACATTG TGGGTGGCTG TATCCAAAGT 180  
 TAAATAAATT GGCCAGAAGT GCAGAGTATC CTTTCCTGGA TTCGTGTCAG AAAAGGGCTC 240  
 CTTGCCACAA CTGAACTTAC TGTATAAAAA CCTGGCTAGG GAGATTTAAT TTTACTAAAA 300  
 TTACAGTTTA ATGTTACCGT CTAGCCACAA ATCAAGCAGC AAAAGCTATT TTGATGATGA 360  
 AAGGGGGTCC CGTTGAGCTG GCCATCTAGT GCAGTGTGCT CTCAGATNCC ATGTTTGTG 420  
 ATTGTGTGCT TCACAAGNCC NTCTCTGGTG CTTGAATTGG ATTTGAATTC TTGGTNAGAA 480  
 GNCTCAGCAT CTCCTTGGGG TNGGCTTGGG CCAAA 515

SEQ ID NO:874

SEQUENCE LENGTH:514

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00997

SEQUENCE DESCRIPTION:

GATCAGNNA TNAAGTGCAG CAATATCATG AATTCTCAGA AGCCCTTTCA GGGAGCCAGT 60  
 NAGTCATACA GTATCCACAG TTGAGTCACT TAAAGATGTC AGTATACGAA ACATTATTCA 120  
 CAATCCTTGG GCAATCTCAT TTTTCTTCC TTCTCCCTC CTCCCTGCC CCCCATACAT 180  
 TTNTATCCTT GAGTTAGTTT TGGNGGGGCA GGAAGTACTT AACATCTCAG AAGCTAGATT 240  
 GGGAAACATG CTCAGCTATA AGAACTGAGC TTTAAATTTT GAGTTTAAAA ATGTACATCA 300  
 GGAGCAGNTG GGGAGGGTCT TTTTNTNAA AAAAATCTTT CCAATTTTGG GTTTTCTNTG 360  
 CCATATGGCC GTTTTGTAAT TNCTTTNGGG GTTTTNNATT NTTTTNGAAA GTGGNTGAAA 420  
 TCTTGTNTG GGNTTTTTTT CCCCAGAAACA TTTNNAATAT AACCNGTTT ATTTTNNAT 480  
 GNAATTAATA CCTTNTTGG GTAAAAAGGT TAAA 514

SEQ ID NO:875

SEQUENCE LENGTH:513

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00998

SEQUENCE DESCRIPTION:

GATCTTCTAT TAAANTGATT CCTCTTTATT AGAGAAGGAA AATTTAGTTG CTATACATCT 60  
 TATATTTNCA CAGTTTATTA AAGTCAGTNC CCTAAAGGTA CCTNCTTNC TTTGTGGCAT 120  
 ATATGGCATC TNCTGTCTTC AGATTTNCTT ACACTTTGT GATTTATAAT GTTAGTGATT 180  
 GGTGCCTTAT TCTCTGAGGA AAGATGGAGG GTTCATAAAG CAATGCCTTA TCCACAGCAG 240  
 ATTTNCTTGT ATATTAAGTT AAACAGAATT CTGTAAATTA TTATGAAGGG TTCAAGCTCT 300

TTAGGGGGAG TTTTTTTTC TTGTTGGTTA ACAAATTGGT TGCAATCTNT TATATTTCCG 360  
 AATTGGNTTA GATATTACAG TCTACTTATT TTTNCANGNG TAAATTAATT GTNTAAGGTT 420  
 TGGGTTNGGT ATAAATGGNT AAAATATTAA TATNGTGGG GGTAAAATTT GATTNGGNGT 480  
 TTTTTTTTTT NAAGGCCNNN GGNTTTANGG AAN 513

SEQ ID NO:876

SEQUENCE LENGTH:510

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00999

SEQUENCE DESCRIPTION:

GATCAGTATG AGANGCAATA CCTAATCCTA TGTGCTATT GTATTTTNC CTAGTTGGTG 60  
 TGCCTGCTCA GAAAAACATA TACTGTATGT GTATACATAC CTGTGTATAT ATAAAAGGTC 120  
 AATTATATA TNTNCCTATA GGAAATGGA GTAACAAGTT CCCTATCTCC CATATTTATT 180  
 TGTCCATAGT AAAATGGCCA CATTGATGAT AATTTCTAGA ACTAGTTTCT GAGATTGTCA 240  
 GCCCTTTGTC TAAATAATG GCAGTATTAA TGATTGACTT CTGTCACTGC CATAGTTACC 300  
 TGGATTGTCA GCCTNGGTAG CCTTTGTCTA AAGTCCTAAA GAGTTCCAAA AAAAATGTGT 360  
 TGAATAAATT GCTAAATAGT GGTGGGTGAT TCTTNCAGTA GGNATTTGTA ATAATTTCNT 420  
 GGCAANAAG GTTATTNCCT GCTATTGGTA TTGGATNATT NGNCTTNTAT NCNGGTATTT 480  
 TNNAAAAGGC AGGNNTATAN GGNTNNNCCN 510

SEQ ID NO:877

SEQUENCE LENGTH:504

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01000

SEQUENCE DESCRIPTION:

GATCTTCCAT CCTCAAATGA CTCTTTTTTC TTTATATGTT AACATATATA AAATGGCAAC 60  
 TGATAGTCAA TTTTGATTTT TATTCAGGAA CTATCTGAAA TCTGCTCAGA GCCTATGTGC 120  
 ATAGATGAAA CTTTTTTTAA AAAAAAGTTA TTAAACAGTA ATCTATTTAC TAATTATAGT 180  
 ACCTATCTTT AAAGTATAGT ACATTTTACA TATGTAAATG GTATGTTTCA ATAATTTAAG 240  
 ACCTCTGAAA CANTCTACAT ATAATTATTA CCCAGTACAG TTTTTTCCC CTGAAAAGC 300  
 TGTGTATAAN ATTTATGGTG GATAACCTTT TATGGTTTCC CTTTCCAAAG GCCCAGGGTG 360  
 GGAGGGGGGA TTAAGGGGGC CTAAGGTNTA TGCCTCCNNG GTTTTAAANT TAAATNCCCT 420  
 CNNGGTATTT AAATTANNTT TTNCCNANGG TTTNTNGGGG GANTGGGGGG GTTTANANTT 480  
 GCCTTNTTTN GGGGTTTGGG GAAA 504

SEQ ID NO:878

SEQUENCE LENGTH:500

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01001

SEQUENCE DESCRIPTION:

GATCTGGGCT CTGAGCACAA GTCAGGAAAC ACCAACATAT TCACACTCTC CCAGTAGGTT 60  
 CCTCAGTCCG ATGGTGAATG GCTATTCGTA AATGGCTGGT CTGGCTCTTT GGTGTTGGAG 120

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CCTTTCCAAT AGCCCCATGA AAAGAAGCAT CACCCAAGGA TATTGTAAAA AGGATGTAAC 180  
AAGGAGATAG GGTAGACATT GTACTCAGTG GGCCTTGGGG CCTAGCCCAG CTCTGAGCAG 240  
AGGACTGTGG CATTCACTGT CCTTGAGTGT TTCACCTTCT TGGATAACAC ACGGGCCTTC 300  
TCTTCTGGAT TTCATCAGAG ATTACAGCCA GATGGGGGCT GAAGACCATC CTCTTTGACC 360  
ACAGAGGGTG TGAAGTGTGGG GAATTCCTCC CAATTTATGG TTTCCNAGGA AAATCTTAGT 420  
TCCTTTTATT TATAGGAATG CATGNCNTTT TGGTGTTAAG GAAACCCAAG GGGNANTTAA 480  
NGGGACCANT CCTANTNAAA 500

SEQ ID NO:879  
SEQUENCE LENGTH:500  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01002  
SEQUENCE DESCRIPTION:  
GATCTCCAGC CTCCAGAAG CCTGCTGTGC TTCGTCCCA CAGCTTTCTG CCCATTGTTT 60  
CTTACTAGTT TCTGAATTG TNCTTGTGGA CTTNCCCTCA GGGATACATT GGCCTGCAGG 120  
TCCCAGTTCA CATGTAGTCC CCTGCTCACC ATTGGAGAAT CAGCTCACTG CTCTCTAGAA 180  
ACGTGGCGTT GGTGAACGGA CCATGCTTCC GTAGCTCTGA CCTGGGCAGC TTGGACCTGG 240  
TCATCCTCTA CTGCCATACC TTTCCCTGGG GGCTTGAACA CAGAACAGGG AGATGGACAA 300  
CCACTTCAAA GAAAGACCCA CCGAATGCAG TTTCTGCTTG ANTGACTGGG NCTGCAGTTC 360  
CNTTNTCCTG GGAAGTAGAG GTGGNCAGAT NTANGGCCCC TTTACTCATC CANCTTNGTN 420  
TTCAACTGGN ACTNCCNAAT NANTNAAAGA GCCTNAAATT TTAAACTNGN TGTGGATNGG 480  
GNATATGGGA NTAGGGTTGN 500

SEQ ID NO:880  
SEQUENCE LENGTH:500  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01003

SEQUENCE DESCRIPTION:  
GATCGTCAGC AAGTACTGTA NCTGTAAAGG AAAATCTCTC TCTCTGGAGA ACCCACACAA 60  
ACCATTGACC TGAGTGCGCA TGACAGCCAC TGGNNATNTT TTCTATGATT GAAAATCTGC 120  
CATCGCTGAC TGTTGGCCAG TTTCAAAGGG ACCCATTGTA TACAGGGTGC AAATGTATTA 180  
TACGGATGTT TCCTTTTGTA CACTTCATTT TTACAAGTTT TGCTACTCAC AAGCTTTATG 240  
TAGTGGAGGA TAGAGGTATT TTTGGTCTTT AGAAGCTTGT CGGGGTGAGG GCTGCTAACT 300  
TACACTTCAG AGGCCTGTGT CCCAAAGGCC TGGCTGCGTT TGCCGTGCTG TGCGAGGACC 360  
TGTGTACACA GGCAGGTGTT CGCCTGCCCG AGCGCGAGTA GCTCTTTGTG TAGTNGGTGA 420  
AAATGCTTGC AGGCATCTGT TTAATTAATA ATTNCCTGCT GTTAAAGNCA GGGGTTAATA 480  
ATNTCCACAA TTTANGGAAA 500

SEQ ID NO:881  
SEQUENCE LENGTH:498  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01004

## SEQUENCE DESCRIPTION:

5 GATCAGGATT CAGANGTGA CATCTTCCCC GCAGACTNCC CTACTGAGCC ACCTAGCACT 60  
 GCCACGAACC GGTGGGGCTA GGAAAGAAGT AAAATATTTT GCAGAGTCTG ATGAAGAAGA 120  
 AGATGATGTT GATTTTGCAA TGNNTAATT AAGTGCCCAA AGAGCACAAA CATTTTTCOA 180  
 CAAATATCTT GTGTTGTCCT TTTGTCTTCT CTGTCTCAGA CTTTGTGACA TCTGGCTTAT 240  
 TTTAATGTGA TGATGTAATT GACGGTTTTT TATTATTGTG GTAGGGCCTT TTAACATTTT 300  
 GTTCTTACAC ATACAGTTTT ATGCTCTTTT TTTACTCATT GAAAATGTCA CGTACTGTCT 360  
 10 GATTGGCTT NGTAGGAATT GTTTATAGGN CTGCCCGTGC ATTAGGCACA GGATTTTAA 420  
 ATTGTCCATG GGTNNCCANC CTACCAGACC CTGCTTTTTT NGNNAATNGG AATTTTNAAC 480  
 CATTNANAAA TNGGGAAA 498

SEQ ID NO:882

SEQUENCE LENGTH:494

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01005

## SEQUENCE DESCRIPTION:

20 GATCTTACTC CACGNATACT TTTTGGTNTG TGAAGGCATC GGTAAAGGGC ACAAAGACAG 60  
 CCATGGGGAC ATTTATGTAA ATACGTCTCT AATTGCCACA CTGCAGCTGA ACAGTGTGTA 120  
 GTATTTTCCC AGTCAGCTTT GCCATACTGA CGTCAATCAT TTGAGAGAAA TTATTCAGAT 180  
 TTNATTTTGT TATCTGTGGT AACAAAACAT TAACCAAAAG ATTTTNTGTC CAGAAGCCTC 240  
 25 CCCGNCCCCC CAAGCTATTT GCTCACATTA ACANATTAAA GTGCCTGAAG CATAATTCAT 300  
 TCTTTACCTG TATACTAAAA ACCCTGTTGT ATTGGTTTTT TTTNTAATAA GCCTTTTTTAC 360  
 CTCTGTGTAA ANANATATAT ATACCAGGTG TATGATGGTN CATTTTGGGT CTTNANCTTT 420  
 TTTTAAATGG TTTCTAATNT GTNTGNCCNA ATGTTGGCNT TGNTTTTANA NTTGTNCCGG 480  
 30 GGTNNATTTT TANN 494

SEQ ID NO:883

SEQUENCE LENGTH:493

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01006

## SEQUENCE DESCRIPTION:

40 GATCTTGATG CTGTGGAAGT AGTTTGAGGA ACATCCTATG AGTTTNCCTA GAATGTATAA 60  
 AGGTTGTAGC CCATCCAAC TCAAAGAAAA AAATGACCAC ATACTTTGCA ATCAGGCTGA 120  
 AATGTGGCAT GCTTTTCTAA TTCCAACCTT ATAACTAGC AAAAAAGTGT TTGCTTATTC 180  
 CACCAGTTCT ACTGTGACAT ACTCGAGTAT AAAGACATGT AGCAATAACG GGGAGTGGGG 240  
 GGGGAGTCTC ACAGTGCCTT TGAAGGGGCC CGAACTTGCC TTAAATCTTC CTCAACCAAA 300  
 TAAGTATTTT ATTAGTGCTT GAGAGAATCT GGAATGTAGG NTGGGTTCOA CTGCACAAAN 360  
 45 GGAAAANGNT TTTTACCACT NTTTTATAT AGNTATAAAG TGNAGCAACC GCCTTAGTGC 420  
 CTGAATATGT AGTCCATGAN TATGCCTTGT NTAATTTCCA GAAATTCCAN ACCTGTACT 480  
 GTTTTTTTTC CCN 493

SEQ ID NO:884

SEQUENCE LENGTH:492

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01007

SEQUENCE DESCRIPTION:

GATCAGCACT GCCAGTGGAG ATGGGCGTCA CTA CTGCTAC CCTCATTTC CCTGCGCTGT 60  
 GGACACTGAG AACATCCGCC GTGTGTTCAA CGACTGCCGT GACATCATTC AGCGCATGCA 120  
 CCNNGTCAG TACGAGCTGN NCTAAGAAGG GAACCCCAA ATTTANTTAA AGCCTTAAGC 180  
 ACAATTAATT AAAAGTGAAA CGTAATTGTA CAAGCAGTTA ATCACCACC ATAGGGCATG 240  
 ATTAACAANG CAACCTTTCC CTTCCCCGA GTGATTTTGC GAAACCCNCT TTTTCCTTC 300  
 AGCTTGCTTA GGATGTCCA ATTTTAGGAA AGCTTAAGGC GGCCTACAGA AAAGGGANAA 360  
 ANGGGCCACA AAAGTTTCCT TTAACTTTT NAGTAAAAAT TAANTTAAAN CAGCAGCAGC 420  
 AACCANTTTA AATTGGATTT AANGGTCCN AATTGGAATT NAATTTTTTG GNTTNNNCG 480  
 GGNTTTNAAA AN 492

SEQ ID NO:885

SEQUENCE LENGTH:490

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01009

SEQUENCE DESCRIPTION:

GATCGAGTTT NATGCATCAC AGTTAACATG TCAGCTGGCC CTCCAGGCC CCGCCCCCAT 60  
 CCCGTCCACG TTGCTGTGTC GTGAGGTGCA GCGGGTCACC CTGTGGCCCG TCCTGTGACC 120  
 CATATTTAGC CGTGTGTTGGG ACTCCGTGTC TTCAATGGTT TGTTAGTTGC CATTACAACT 180  
 TTGTCTGGGT AGAGTTTTTG AGTTTTNCA GTTCAGTATC CCTCTGTCTA TTCACACTTC 240  
 GTGTTAGTGG TAACTCAGTT TGTCTTTAA TAGTTACAGA AGGGATACGT CATTTGTNAA 300  
 TGCTTTTGTG AAGTGAGTTA AACGAGCTTT CTGTATTTTA ATGCTTTAGT GTTTCAGTTT 360  
 TATAAGTGAA GATTTTATTT TAAAAACCAG TGGGAAAGAG TGGGGGGTTT CTTTTATGT 420  
 CTGGGTCATT CAGGCAGTAC ATCTGNTTTA AAGCTGAATG TAGGACANTT AATGAAATCC 480  
 ANATCTGAAA 490

SEQ ID NO:886

SEQUENCE LENGTH:487

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01010

SEQUENCE DESCRIPTION:

GATCAGCTAT ATACTATTTA TATACAAGTN ATAATACAGA TTTGTAACAT TAGTTTTAAA 60  
 AAGGGAAAGT TTTGTCCTGT ATATTTNNTT ACCTTTTACA GAATAAAAGA NITACATATG 120  
 AAAAACCTC TAANCCATGG CACTTGATGT GATGTGGCAG GAGGGCAGTG GTGGAGCTGG 180  
 ACCTGCCTGC TGCAGTCACG TGTAACAGG ATTATTATTA GTGTTTATG CATGTAATGG 240  
 ACTATGCACA CTTTAAATTT TGTCAGATTC ACACATGCCA CTATGAGCTT TCAGACTCCA 300  
 GCTGTGAAGA GACTCTGTTT GCTTGTGTTT GTTGTTTGC AGTCTCTCTC TGCCATGGCC 360  
 TTGGCAGGCT GCTGGAAGGC AGCTTGTGGN NGGCCGTTGG NTCCGNCCAC TCANTNCTTC 420  
 TGGNGCACTG GTTTNTNCTT TANAGTTANG GTNCCATGNN NCAAGGGGGG TTCCNANGNG 480  
 GAGGNCN 487

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SEQ ID NO:887

SEQUENCE LENGTH:485

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01011

SEQUENCE DESCRIPTION:

GATCGCAAAT AACTAAATG TGGAGTGTAG GAACCAAAAT GAAACCTGCT GTATGGAAAC 60  
TACTTTCACT TATGGTTCAT TGGTTTTTGT ACCAATATTT TTTATGCACT TCAGTGCAAG 120  
TNTTGTCACT TAACCTTACT TTATGAGTAA GCTAAATAAC CCAAATTACA TTTNTTTAAA 180  
CCTGTTTTAC TACTATGGCA CTTTGATAAA ATGGTCAGGA ACCAACTTTA CTGGCAAAAG 240  
GGTCCATGTA CCACCATGTG CTGGAGCATC TGTTCACAT GTGGATATCT ATGANTGGTA 300  
ATGTTTTTCT TCATGTAAGT GCCTATTCAG AGTTTCAGAA TTTTAAAATG CCAAATATTT 360  
TCATGGGTCA TTTGCATGTA GTAAGCCAGA AAATATTCAA NGGGATTTTG GAAAACCAAT 420  
TGGTATTTAA CCAGCCTCAA ATTGTGCAAC CATGGTTGTA TAATAANGGA TTTGGAACCC 480  
GGAAA 485

SEQ ID NO:888

SEQUENCE LENGTH:485

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01012

SEQUENCE DESCRIPTION:

GATCTAATGN CATATTCCAA AAGCTCAACA GCAACACCCA GGTAGTTTTG CTGTCAGCCA 60  
CAATGCCTTC TGATGTGCTT GAGGTGACCA AGAAGTTCAT GAGGGACCCC ATTCGGATTC 120  
TTGTCAAGAA GGAAGAGTTG ACCCTGGAGG GTATCCGCCA GTTCTACATC AACGTGGAAC 180  
GAGAGGAGTG GAAGCTGGAC AACTATGTN ACTTGATGA AACCCTGACC ATCACCAGG 240  
CAGTCATCTT CATCAACACC CGGAGGNAGG TGGACTGGCT CACCGAGAAG ATGCATGCTC 300  
GAGATTTTAC TGTATCCGCC ATGCATGGAG ATATGGACCA AANGGAACGA GACGTGATTN 360  
TNTGGNANTT TCGTCTNGC TCTAGCAGAG TTTTGATTTC CANTGACCTT TTGGNCAGAG 420  
GAATTNTTGT TTNNGAAGGT TTTTTTTAG TCATCANNCT NTTGTCCTTT CAACTATCAG 480  
GGGTN 485

SEQ ID NO:889

SEQUENCE LENGTH:492

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01013

SEQUENCE DESCRIPTION:

GATCGCAACG CCAAAGGTGA AGAACCANCT CAAGGAGACC ACTGAGGCAG CCTGCAGATA 60  
CGGAGCCTTT GGCCTGCCCA TNACCGTGGC CCATGTGGAT GGCCAAACCC ACATGTAATT 120  
TGGNTCTAAC CGGATGGAGC TGCTGGCGCA CCTNCTGGNA GANAAGTGA TGGNCCCTAT 180  
ACCTCCAGCC GTGAATGCNA GATTTTAAGA TTGCCCGGAG GAAGCAAACCT TTTCGTATAA 240  
AAAAAGCAGG CCATCTGCTT AACCNTTGGN TCCACCATAA GGCCTGGGA CTNGGATTTT 300  
TNTATCTGAT AGAGGTATTT NTTGTGGCCC TGGGAGCTGT CTGNTTTTCC CCTACCCCA 360

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AGGNTGCCAG GAAGACGTCC ACCATTAGCC ATGTGGNAAC CTTTACTTCT ATGCTTACAA 420  
GTGCCTTTNA GNGAGCCCCA ATTCTGGTTT TNCCACAAAA TAAACCTAAT GCNNTCAGGG 480  
AAAACNNTTA AA 492

SEQ ID NO:890  
SEQUENCE LENGTH:478  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01015  
SEQUENCE DESCRIPTION:

GATCTTGCTT CCAGGCAGCA GCTTGAATTC CCGAATCTNC CTGCAAGCNG CATACAAATG 60  
CAGCGTGAGA ATCCATACAC GTAATCCATA TTCACCTTCC CATCCATCCC GCAGAAGAGG 120  
CATGGTGACA CCCAGGCTAC TGTCCATGCT TGAGAGGACG TATTTGAAGG TTCTGTACT 180  
ACAAGTTGGG AATATTCACG GGCCATGCCT GAATACCCGG NCTGTANCTC ACACNGTGGT 240  
CTGTGTAAGG GGNTACCTN GGGGCGGCCT GGTTTAATCN TGATTAATAT CTGAAAGCNT 300  
GGGTTNNNTG GGGAATGTNA GGGTTTTCTT AATGCCATTA AATTTTTTTT TAGGCNGTAA 360  
AAATTAATAA NCATTTTTNT ATCCAGCAGG CCTCTTTTAT ACCTTTATNG GGGAATCTNC 420  
CATACTTACT TTCCGGCCAN NTTTTCAATA ATNAAATTA TTTTGAAAN TTTTAAA 478

SEQ ID NO:891  
SEQUENCE LENGTH:474  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01016  
SEQUENCE DESCRIPTION:

GATCTTACAC TCTGCTTTTG TCCAAATAAA ATGCAATAGT ATCAATATCA ATTCAGAAA 60  
AATGGACTGA ATATGCTTTT TTGGTGATGA AATCTCATGT ACGATATTTA TAGTGATGTG 120  
CTTTTATTTN CTCATGAGAT ACTAAATATT AATTGTGTG TACATTTGTN CTTAGCATAT 180  
ATTAAAGTTT TGAACCAAAT GTGTAAAGC TTACGCTTTG CCATGTAAAT TTCCCAGAAG 240  
TTGTTGAGCT CAAATGTATC CTACATCCAG CTGTAGAAAT TTGTCAGAAA TTGTTAAAT 300  
TTTGTATATA ATTGTACTGT TTAATTCTAG CCATTGCGCT GAACAGTATT TGAGTTACCA 360  
TATAATATGG CTTTACACAA NGGNAATGTG TGGCTTTTGT TTTGGTATTT TTTCCAGTAT 420  
AGGAAGTTCC CTGTGGCCTT ATTTAAAATA AAGGTTATTA GGTAAGACTG GAAA 474

SEQ ID NO:892  
SEQUENCE LENGTH:473  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01017  
SEQUENCE DESCRIPTION:

GATCACAGCT CACTGCAGGT TCAGCCTTCT GAGTTCAAGC AATCCTTCTG TCTCAGTCTC 60  
CTCAGTAGCT GGGGCTTTAG GTGGGCACTG CCACACCGTA CTAATTTTNG TATTTTTTGT 120  
AGAGACGAGG TCCCACCATG TTGCCCAGGC TGGTGTCAAA CTCCTGGGCT CAGTCAGTCC 180  
CCCCATCTCA CCCTCCCCAA GTGCTGGAAT TACAGGCGTG ANTTACTGTG CCCAGCCTTA 240  
CGGACATCCT TTTGAATTAT CTTTTTCACT CATAGAATAT GAATACATTT ATTTAGACTT 300

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TTTCTAGAAC TTTCTGTTT TCATGTCTTT GNTTCACCTG GAATTGGGTT TAACACCCTT 360  
TTATAAAGTT TGTGGTTTGN AAAATTTCCA TTGGGGCCAT CAATACGGAA ATATATTTGG 420  
TAANATTNGG GGGTTCNATT TTTTAATTAA AATGGCAAAT GANNGGCAGG AAA 473

SEQ ID NO:893

SEQUENCE LENGTH:473

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01018

SEQUENCE DESCRIPTION:

GATCGGGTTG AGGATTGGGG CTAGCTCGAT NACANTAAGG CCCCAACATC GNNGGACCTG 60  
CTGTGGCGCG GATTCTTAGG AACGCTGTTC TAGCCGGCCC CCTCTCCAGG GGTCGCCGTG 120  
GCCGGCATT TTTCTAGTT CTTCTTGTA CCCTGAGGTG CCAGCGCGGG GAGTGAGGAG 180  
GGGTCAGGGG GCTAAGGATG CAACCTCTGA CGTTCTGCGC CTCCTAGGA GAGTCTTACA 240  
TGTNTTGAGA TTTACAAGC AATGCGAGTT GTAAAATACC AGCTCTACAN GAAGCTAGGC 300  
TCTGTGACGG CATAGTTTT AGTAGCTNTA TCACAATATT CACAATGGAG AATTATATGA 360  
CATGGTAAGC AGAAATAGGC CCCTTTTAAAT GNGNTGCTTC TATTTTACCT CANATTGGTG 420  
GNTNTAGGNT AATCANTAAA AATCNATCCA NNGCNTTCA CAACACTNNN AAA 473

SEQ ID NO:894

SEQUENCE LENGTH:468

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01019

SEQUENCE DESCRIPTION:

GATCAGGGGG CCAGGCCAGC AGCTCGGGGG CCACAAGGAG ATGGATAATG TGCCTGTTTT 60  
TTAACACAAC AAAAAAGCCT ACCTCCAAAA TCCCCTTTTT GTTCTTCCTG GACCTGGGCA 120  
TTCAGCCTCC TGCTCTTAAC TGAATTGGGA GCCTCTGCCA CCTGCCCCGT GTATCCTGGC 180  
TCTCAGCTCA TGGGGAAGCC ACATAGACAT CCCTTTCTTC CTTGCACGC TCGCTAGCAG 240  
CTGGTAAGGT CTTACACCCC TGATTCTCA AGTTTCTGC TTAGTGGCAC TGACATTAAG 300  
TAGTGGGGGG ACAGTCCATG CCAGGACACC CTGGAGTAGC CTTCCCCCTT GGCCGTGGGG 360  
CAGGNCCTAA CTCAGTGTG CTTTGGAGTT GAGGGTGTCT TTTCTTNTTC TTTCTTTAGT 420  
TCCTGTATTC TAAACATTAG TAAAAATAAA TGTTTTTTAC ACAGGAAA 468

SEQ ID NO:895

SEQUENCE LENGTH:462

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01020

SEQUENCE DESCRIPTION:

GATCCTGCAG GACTACAAAT CCCTCCAGGA TATCATTGCC ATCCTGGGTA TGGATGAACT 60  
TTCTGAGGAA GACAAGTTGA CCGTGTCCCG TGCACGGAAA ATACAGCGTT TCTTGTCTCA 120  
GCCATTCCAG GTTGCTGAGG TCTTACAGG TCATATGGGG AAGCTGGTAC CCCTGAAGGA 180  
GACCATCAAA GGATTCCAGC AGATTTTGGC AGGTGAATAT GACCATCTCC CAGAACAGGC 240  
CTTCTATATG GTGGGACCCA TTGAAGAAGC TGTGGCAAAA GCTGATAAGC TGGCTGAAGA 300



GCATTCATCG TGAGGGGTCT TTGTCTCTG TACTGTCTCT CTCCTTGCCC CTAACCCAAA 360  
 AAGCTTCATT TTTCTGTGTA GGCTGCACAA GAGCCTTGAT TTGAAGATAT ATTCTTTCTG 420  
 ACCAGTATTT AAGGGTTTCC AATAAAATGT ACACCNCTCA AA 462

SEQ ID NO:896  
 SEQUENCE LENGTH:462  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01021

## SEQUENCE DESCRIPTION:

GATCTAAATC CTCATTTATC TCTNCTATGT CTAGTATTTT ACTGTCACTG GAGGCTCTGT 60  
 GGGCTGTCAT AGTTAATTGA CCATAATTAG CAATATACTT TTAAAGTGGG AAAGCTGAAT 120  
 GACACTNTTT AAGACAATGA ACATTATCAA AACAAAATGT ATAATTNCTT AATTTGAATA 180  
 ATAAATTAGG CGTTTAAATG CTATTTGTAG TCTTGATATA CAGAAATAAA ATAATTAGGG 240  
 TTGGTCTTTT TTATTTTAGG TTGTTTTATG TTGAATGTTT TATATCTTAT TAGTTAATTN 300  
 GTATATTTNA TTAGTATTTN GGGAAATAGC ATATCTGAGA CTGAAGGGGA AATTGGCCAA 360  
 TTCAC TTATT TGTGGTTTTT TTCCTCAGCT ATTCTGAGCT TATTTATTAA TTGNATGGCC 420  
 TAATGGCTAA CCATTACAT TAAAATGGTT TTTNCCCCA AA 462

SEQ ID NO:897  
 SEQUENCE LENGTH:459  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01023

## SEQUENCE DESCRIPTION:

GATCTNCTCT TTCCTCTCCT TTTCTCATT TATTCCTAAA GGAATCTGAC CATTAAAACG 60  
 NCTCTACGGC CCAAAAAAAG ACAAAAATAA AAATTCCTTT TTATTCCTGT CAACTGGATG 120  
 GAAACACAAA TTTCATGGAG CTGTGTACCA TCGAAGAAAC CTGGTGTCTG GCATGAAATT 180  
 ACTGTAAAGA ACTTCTGTA AAACACGTTT TTTAACAAAC TGAAATGAAA AGCATTGGAG 240  
 CGTCTGANTG AAAGACGTGA CCTCTGCTG GGACTCTGAT GGTCTTCAGC ATTCACCTTC 300  
 GTGTGTCTTC AGTGTCTCAT TGTATCCCT NGCTTCTGGN TTGGNCCTTA GGAGTNGTTT 360  
 GGGATATAAC CTNAAATTGT NGGATGGGTA AANGGGAAAT TTNATGNNG TTTTTTTGGT 420  
 TTTTAAAAAT NATTTTNAAT NCGGGGTCAN TTTTAAAA 459

SEQ ID NO:898  
 SEQUENCE LENGTH:457  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01024

## SEQUENCE DESCRIPTION:

GATCCACCTG AGCGACCTCC GGGAGTACAG GCGCTTTGAG AAGGAGAAGC TCAAGTCCCA 60  
 GTGGAACAAT GATAATCCCC TTTCAAGAG CGCCACCACG ACGGTCATGA ACCCCAAGTT 120  
 TGCTGAGAGT TAGGAGCACT TGGTGAAGAC AAGGCCGTCA GGACCCACCA TGTCTGCCCC 180  
 ATCACGCGGC CGAGACATGG CTTGCCACAG CTCTTGAGGA TGTCACCAAT TAACCAGAAA 240  
 TCCAGTTATT TTCCACCCTC AAAATGACAG CCATGGCCGG CCGGGTGCTT CTGGGGGGCTC 300

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GTCGGGGGGA CAGCTNCACT CTGACTGGCA CAGTCTTTGC ATGGGAGACT TGAGGAGGGG 360  
 AGGGGNTTNA GGTGGGTGAG GTTAAGGTGC GTGTTTCCTG GTGCAAGTCA AGACCATCAG 420  
 TCTTATTA AAA AGGTGGGTGC CAATTTTTTT TACNAAA 457

SEQ ID NO:899

SEQUENCE LENGTH:457

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01025

SEQUENCE DESCRIPTION:

GATCCAGTAT CTTCTCGGC TTTTAGGGA GCAGGAAAAA TCGTCTNAN AGCAACTTTT 60  
 TTTAAAAACC TGCCCTGTTG TATATAACTG TGTCTGTTTC ACCGNGTGNC CTCCAAGGG 120  
 GGTGGGA ACT TGATATAAAC GTTTAAAGGG GCCACGATTT GCCCGAGGGT TACTCCTTTG 180  
 CTCTCACCTT GTATGGATGA GGAGATGAAG CCATTCTTA TCCTGTAGAT GTGAAGCACT 240  
 TTCAGTTTTC AGCGATGTTG GAATGTAGCA TCAGAAGCTC GTTCCTTCAC ACTCAGTGGC 300  
 GTCTGTGCTT GTCCACATGC GGTGGGCGTC TTGGGACCTT GAATGCCTGC CCTGTTGTG 360  
 TGGACTCCTT TAATGCCAAT NATTTCTTCA NTTTCTCTTG GGACACCAG GGNTGCCNGT 420  
 TNGACAAAGT TTTGGNGAAC NTCCTAATTT AAAATGN 457

SEQ ID NO:900

SEQUENCE LENGTH:454

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01026

SEQUENCE DESCRIPTION:

GATCCGANGA CCACATCAAT GGGCGCGTGC TCTACTATGC CACCTGCAAG TAATGCTACA 60  
 GCTTCCAGCC CGTTGCCCCA CTCATCTGCC GCCTTTGCTT TTGGTTGGGG GCAGATTGGG 120  
 TTGGAATGCT TTCCATCTCC AGGAGACTTT CATGTAGCCT AAAGTACAGC CTGGACCACC 180  
 CCTGGTGTGT AGCTAGTAAG ATTACCCTGA GCTGCAGCTG AGCCTGAGCC AATGGGACAG 240  
 TTACACTTGA CAGACAAAGA TGGTGGAGAT TGGCATGCCA TTGAACTAA GAGCTCTCAA 300  
 GTCAAGGAAG CTGGGCTGGG CAGTATCCCC CGCCTTTAGT TCTCCACTGG GGAGGAATCC 360  
 TGGACCAAGC ACAAAAACCT AACAAAAGTG ATGTAAAANT GAAAAGCCAN ATAAAAATCT 420  
 TTGGAAAAGA GCCTTGGAGG TTCAACGGGG GAAA 454

SEQ ID NO:901

SEQUENCE LENGTH:453

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01027

SEQUENCE DESCRIPTION:

GATCTTNCTT NTTAAGTGA TAAGACAGTC CCACAGTCCA GCCTAACTAT GGGACAGCTT 60  
 TACGAGAAGG AAAAAGATGA AGATGGATTC TNATATGTGG CCTACAGCGG AGAGAACT 120  
 TTTNNAANCT GAGGGCCATT GCTGGGCTAG GTGCACCGTA ACTGCTTGTG TATCTTGTA 180  
 ATAGCCAGCC ATTTNCAGTT ATTATACCAG AACCTCTTCA CATAGACCTA TTAGTGCATT 240  
 TGTAAGTGGN TTTATTCTT AATATATTGG AAGGTTTGT TCCTTAGNCT AGTAAATTAT 300

CATACAGNGT TTTATTTTGA GGTTCCTT NNNTGTGCAT TNTCCTCATG GCCTGTAAAC 360  
 CNCCAGGAAA CCTTTCCTT CTNGGAAATC ATATTTGAAA TGATAATTCTN TATATCCGAN 420  
 GTGAGGNTAG GNNCCGGGTC CTCCCAATAA ANN 453

SEQ ID NO:902  
 SEQUENCE LENGTH:452  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01028

## SEQUENCE DESCRIPTION:

GATCTTAAGT GAAGAAGGAA GACTTGGCCT TTTGTATTGC TTGAATATTA ACTGTCTTGG 60  
 AAGGAAGTTA TGCTACAAGA AGTCATACTT TCATAAAATT ATTTGCATCT GTGTCAAATG 120  
 CAGTTTAGTC AGAACGTAAG ACATAATAGG TGTGGACATG AACTCTGGAG TGTGAAATAA 180  
 AATCCACAGT TACTTAAGCA GTCTGTTTTG ATGGAAAGTA TCTTGGGATA ATACTTCCT 240  
 CTGTGGGATT TTGTTTCTTT TAGATGGTGC ANGNAGTAT CAGTCTTTAA TTTTTTGT 300  
 GTTGTTTTAA TCANTCATTT GCTCTGATGG TATGATGCAT GGGCTTCAGG ACTCCAGCTG 360  
 CACCACTGTA TAAACTCAG TTCAGGTTT CTAGCGGTCN TTGGNTAATT TTCGGGGCNT 420  
 ANCCCGATNC CAATTNTTTT TAATGTGNTA AA 452

SEQ ID NO:903  
 SEQUENCE LENGTH:448  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01029

## SEQUENCE DESCRIPTION:

GATCAGGGAC CCTCCNGCT TTCCTGGGCC TCTNAGTTGA ACAAAGCAGC AAAACAAAGG 60  
 CAGTTTATA TGAAAGATTA GAAGCCTGGA ATAATCAGGC TTTNAAATG ATGTAATTCC 120  
 CACTGTAATA GCATAGGGAT TTTGGAAGCA GCTGCTGGTG GCTTGGGACA TCAGTGGGGC 180  
 CAAGGGTTCT CTGTCCNGG TTCAACTGTG ATTTGGCTTT CCCGTGTCTT TCCNGGTGAT 240  
 GCCTTGTTTG GGGTTCTGTG GGTGTTGGTG GGAAGGAGGG CCATCTGCCT GANTGTAACC 300  
 NGCTAGCTCT CCGANGCCCT ACGGGCCTGN CTNGTGTGAG CGTGTGGACA GTGGTGGCCG 360  
 GCGCTGTGCC TNCTCGTGT GCCTACANTG TNCNTGGCTG TTGAGGCGCT GCTTCANGCC 420  
 TGCAACNCGT CCNTNGTCTC ANTACAAA 448

SEQ ID NO:904  
 SEQUENCE LENGTH:461  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01030

## SEQUENCE DESCRIPTION:

GATCGGTTTA CAGATGAGGA AGTGGATGAG CTGTACAGAG AAGCACCTAT TGATAAAAAG 60  
 GGGAATTTCA ATTACATCGA GTTCACACGC ATCCTGAAAC ATGGAGCCAA AGACAAAGAT 120  
 GACTGAAATA ACTTCAAATT CCAGCCAAAC GTTCCTTGTG GCCACTTTGG GTATTCTGAG 180  
 ATTTCTCTT GCATGCCCTT AGCTTTACAG CTTTGCATT TCCTGTTGTA TTTATTCTCA 240  
 GCCATTTTGG GCATATGTAT CTTTATAATC AGACTGGAAG CGGGACTTTC TATTAATATC 300

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ATTTTTCAGA ATAAAAATA GGGTAATTTA ACCTACCAGC CTTTCTCCCC CAATAACTGT 360  
 GGGCCTATAC AGNGTCAATA TATTTTNC AGNGAAAGGT TTATTCGGCT CGATTTTTTT 420  
 CTGGAANTCC ATAATTTAAC CTTTATGGG TTAAANTTAA A 461

SEQ ID NO:905  
 SEQUENCE LENGTH:453  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01032  
 SEQUENCE DESCRIPTION:

GATCAGGGAC CATGAAAAGA AACTTGTGCT TCACCGAAGA AAAATATCTA AACATCGAAA 60  
 AACTTAAATA TTATGGAAAA AAAACATTGC AAAATATAAA ATAAATAAAA AAAGGAAAGG 120  
 AAACTTTGAA CTTTATGTAC CGAGCAAATG CCAGGTCTAG CAAACATAAT GCTAGTCCTA 180  
 GATTACTTAT TGATTTAAAA NCAAAAAAAC ACANAAAAAT AGTAAATAT AAANCCAAAT 240  
 TAATGTTTTA TAGACCCTGG GAAAAAGAAT TTTCAGCANN GTACAAAAAT TTANCGCATT 300  
 CCTTCTTTA ATTTTGTANT TCTTTACTGT GGAATAGCT CAGAATGTCA GTTCTGTTTT 360  
 ANGTAACAGN NTTGGATAAC TGAGCAGGGN ANCGNAATTT TGGNTTNTA AAATTCCTTG 420  
 CTTTNANTAN ANNTCCCTT NNCCCGGTGG AAA 453

SEQ ID NO:906  
 SEQUENCE LENGTH:445  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01033  
 SEQUENCE DESCRIPTION:

GATCCGATGG AGAAGGGGGG ACCCAGGCCA GCAGGAGACA GGACCCCGA AGCTGAGGCC 60  
 TTGGGATGGA GCAGAAAGCCG GAGTGGCGGG GCACGCTGCC GNCTTCCCCA TCACGGAGGG 120  
 TCCAGACTGT CCACTCGGGG GTGGAGTGAG ACTGACTGCA AGCCCCACCC TCCTTGAGAC 180  
 TGGAGCTGGC GTNTGCATAC GAGAGACTTG GTTNAACTTG GTTGGTCCTT GTNTGCACCC 240  
 TCGACAAGAC CACACTTTGG GACTTGGGAG CTGGGCTGA AGTTGNTCTG TACCCNTGAA 300  
 CTCCAGTTT GCGAATTATA GAGACAATCT ATTTTGTTAC TTGCACTTGT TATTCGACCA 360  
 CTGAGAGCGA GATNGGGAAG CATAGATATC TATATTTTA ATTCNCTAT NGAGGGCCTN 420  
 GTAAATAAAT TTCTAAAAGC CTAAG 445

SEQ ID NO:907  
 SEQUENCE LENGTH:444  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01034  
 SEQUENCE DESCRIPTION:

GATCTCAATG AAATTAATTA AATAACTATA TCTAGAAAAA CTCCCAATAT GTGAATATTA 60  
 AGCAACATAC TTATAAAAAA TTCATAGTTC ATGGATGAAA TCAAAAGAGA ATTCAAAATA 120  
 TTTCAAAATA AATTATGATG ATTATATAAN ATGTAGAAAT GTGTGGGATG CCACTACACC 180  
 AGTTCTTAGA GTGAAATGCA CAGCTTTCAA GGCTTCTGTT AAAAGAGTTG GGAATTACAA 240  
 AACAAGGAGC AGCGACTGCC AATGGGTGTG GAGTCTTTT TGGGGTGATG ATGAAAATGT 300

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TCAAAAATTG ATTTTATTGA TGGTTACACA CGTCTATAAA TATATTTNAN CGGNAGAATT 360  
ATATGGATAT ATATGTGATA TATGGAGGTA TATCCTCTGT AAAATTCCTA NGGGTTTAAAN 420  
GGAGGATTGG GTATCCACAC CAAA 444

SEQ ID NO:908  
SEQUENCE LENGTH:440  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01035

SEQUENCE DESCRIPTION:  
GATCCAGTG TTGCCTTAAC AGGGTGTCTG TCGTGCCGCA GTAGAGCACT GCTGCTTCCT 60  
CCAACCCCAA AATTTATGTT CCTAAGTAAG TCAGGTCCCT AAGCCCCGTC CCAAGAAGTG 120  
ACACAAGTGG CCAACATCCA CACTGTAGGC TTGCAGGCTA CCCGCCCTGA GATTTGGTAA 180  
AGAACTACTGC CTTGTTCCCC ATCAGTAAAC AAGGTTACCT ACCTCAGGAG GCTGCTTGTG 240  
AGAGAGCAAA TGCAGTATCT TCAGANTGAT TTATTTTTTT ANTAAATTGT AAAGACTTGT 300  
GCCATTGGCT GCTCTTTCTA GTCCCTTAAN TTTCTGTTCT AGTTTAAANT TTCTCTAGAN 360  
CTTGCAATNG TTGGGGGGTT TTTATANTGG TGTTTTNC AATGNTTGTG TCNTTANNNT 420  
AAANCCTTAA AAGTTCCAAA 440

SEQ ID NO:909  
SEQUENCE LENGTH:439  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01036

SEQUENCE DESCRIPTION:  
GATCGGCGTG GGGGTGCTGC TCATCTTCCT TGCAAGTAC GACCTTAACA ACCNGGACAA 60  
GCACGCCAAG CTGGACTTCC TCAACAACCT GGCCACGGGN CTGGTGTTCA TCATCGTGGT 120  
AGTCAACATC TTCATCACGG CCTTCGGGGT CCAGAAGCCC TTGATGGACA TGGCACCCCA 180  
GCAGTAGGAC ACCCAGGACC NTGGATGCTG CCTGCCNNTG CAACTCAGCT GCCCGACCCC 240  
AGGAGTCGCC ATACCTGTNA GGTGTCCACC TCCCTGCACA TGGCACTACC CAGANTGCCA 300  
GAGCCCAGGC TGGNCTCATC TGCACCATGT CCCCAGGACCA GCCCTTGCTC TGANTGCGGG 360  
CCAAGNACCA NGTAGGAGGN CACTNTTGTG TNTNAGCAGN TTTTCCAGG NGGGNAGTTN 420  
NNTTCTGGGA AATTGGGGN 439

SEQ ID NO:910  
SEQUENCE LENGTH:435  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01037

SEQUENCE DESCRIPTION:  
GATCCAAGGA CCCACACTTT GTCACCTCAT ATCTCTCTCT CTCTCCCACT TTCGCTTTCT 60  
CTGTCTCTTC TTAGTTCTGC TTTCTCCAC TGTGCCTTCG CTCTCAGAGA GAGCTCTCCC 120  
CTGGCAGTGA CAAGATGGCT GCAGCAGCTC CAGCAACCTC AGAGGACTCC CCCATCCAGG 180  
GTCCTTGTGA GCTCCTCATC TGTAGGATGT GCAGTAAACA CTCACGTGTC CTTTCCTGAG 240  
GAGCCCAGTG GCTGGGGTGG GGGCTGAGGG GCAGCCCCCTA TGCCCTCACA GTGCAGCAAC 300

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CTTGGTTAGC TCACCCATCA GGGCAGACTT GGGCAGAAAT CATGTCTTGG CATATTGTTT 360  
TGTAATCTGC TTTTAAATT GTCACTATAT ATTATGAGCA TTTCCCTATA ATATACAATA 420  
TTCTTCCACA TAAA 435

SEQ ID NO:911

SEQUENCE LENGTH:433

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01038

SEQUENCE DESCRIPTION:

GATCATATGA AAAAGTAACA AGCTGTTCCN TGTTTCTGAT ACATAAAATN ATTTTAAGCA 60  
TTTTATCAAT CATTAAATTT TACTGCCAGT TGTGAGTGGC TTTTAAATTA ACTTGTCTTT 120  
CATTGCACTT CACTCTGCCT GTTTTCAAGG GGAGTAAGAT TGGTAACATT TGGGGAGACT 180  
GTATCTGTCT ACTTAGCGTG GCTGTTTTGA GGGACTGTCC CATCAGTGAA CAAACTGCAT 240  
GGCCTTGGAG AGAGACTCTG GGCTCTTGGC TCAGATGTGT TCATCAAATA CTCCTTTCAG 300  
AGCTGTTGTG GGTGTAAGTG ACATGATGTG GCCAAAAAT CCAAAGTGTG CAGTTGCGNT 360  
TGTGACAACC ATGCAATGTG NCTGTAAAAA TTNANTTNCA GTTTAAATTN ANATNNTTTA 420  
TATTNNGTGG AAA 433

SEQ ID NO:912

SEQUENCE LENGTH:431

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01039

SEQUENCE DESCRIPTION:

GATCTTTCTA ATTCGAAAGC TGTGTTCTTT TTGAATACCG TGCATGGGGG TTAAGCTGAT 60  
GTTAAACAG TTTGCAATAA AAAAAATGA ATNAGCTTAA GTCATTTAAT CATTCAAGT 120  
GCATTCTGCA TCCTTAAAA ATAAGTTAA GAAATTTAAG AGAATTGTGT TTTCATTAAG 180  
TTTTGCATAT CTTTGTAT GCCATGTAAA TNCCCTTTN CGTATGATTA AAGGAAGGTT 240  
ATGATAAAAT GATTAGTTCA TTTACATTCA CTTGTAGCAA TTACATGAGA ATTTGAATTT 300  
NGTCGTGTTT GGGTTGTNC ATTCCTGTGA ATGATGGTNC AGTTAGGTGA GATTNCTGT 360  
TATGGNACCC CAACTCACCA TTTGGNCCTC TTAAATCTTT GGGGGGTTCC AATAAAAAAT 420  
GGTCACTNAA A 431

SEQ ID NO:913

SEQUENCE LENGTH:431

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01040

SEQUENCE DESCRIPTION:

GATCCAAANT TTAAGGGATA TTGCCTATTT TGGAAGAATA AACTAAAAT GTTAAACTG 60  
TTGAATTACA GAGAACAGAT GTACTCTGAG ACATAATTTT AAACAAATAT TTAAATANG 120  
GCAGGTTAAC ATTTGCGTTT AGGCACAATA AATCTGTATT AAAGGGAAGC ACATCAAGGA 180  
AATATATACA TGTGANTAA TGTAACNAA AAATATTTT TAAANCCAC TTAAATGA 240  
NAAATAATTT GATGGGTACT TTAAGCATTG TAGATAGAAA TTAATGTATA ATAGTGTCTT 300

# EP 0 679 716 A1

CCCNGTCTTT GTATGAAAAN TTA AAAANCTC TCTAGTCCTT TAATGAGCAT GANTTTTATA 360  
CTTCTACATT TTGTTGCCTA GGNAAAATTN TCCTCNGTA CCTTTGAGGT NATTCGGAT 420  
TTTATGGTTT N 431

SEQ ID NO:914  
SEQUENCE LENGTH:430  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01041  
SEQUENCE DESCRIPTION:

GATCTATAGA GAGAGATATA TACACTTTTG ATTGTTTCT AGATGTCTAC CAATAAATGC 60  
AATTTGTGAC CTGTATTAAT GATTAAAGT GGGGAACTA GATTAAAATA TTTGTTTTTT 120  
AACTAGTTTA TTAGTTTCTN TGGAATCTGC CTGTGTCCCT GGGTTTGGGT TTTGCTCTTG 180  
GCAGCAGCAG GTGCCTCTTG GGTGCTCCTC CTGCTCCTGC CTGCAGCCCT AAGAGCAGGT 240  
GGGTGCCGAG TGTCTGGCAC AGCTTGGATG CCGCCCACTG AAGACAGCAG AGGGGGGTTG 300  
TNTTGAAGCT CCCGNGACAC AGTCAAGCAT CTTCTGAGNC TTCGATGTCT TCGGNAAGTA 360  
AAAATGGGGN TTTAGTAAAA CCCTGCCCCN GTTNTCACA GGGGGTNTT TTGCAAGNNA 420  
AANTGATAAA 430

SEQ ID NO:915  
SEQUENCE LENGTH:428  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01042  
SEQUENCE DESCRIPTION:

GATCAGATTC TAATTTGACA GGCAACCAGT CAATGAAACA GACACACCTG CACAGTTGGA 60  
AATGGAGGAT GAAGATACAA TTGATGTGTT TCAGCANCAG ACAAGAAAGT TCTACTGNAA 120  
AAGGANCCTG CTTCTTTACT CTAGAACTTT GTTCTTATAG ACCAAGATTA CATTCTCAAT 180  
TAGAAAACCTG CAATTTGGTT CCACCACATC ATGACTATTA CTATAGTATA GTTTTCTCTA 240  
TTCTTTTATT TTTCCCTTTA CCCATTCCCT TATTTGTACA TAAAATAATG GGTGTATGTT 300  
CACAAGCATT TTGCTGGTTT TNAAATATTA ANTGGCCAAT GACATCCACT TGATGTCANT 360  
CAANACNATA TCTGTGGGGG NAAANTACCG NTTCTNGAA ATTTNCCTCC NNTTTTTCCTCA 420  
TNAGTGGN 428

SEQ ID NO:916  
SEQUENCE LENGTH:428  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01043  
SEQUENCE DESCRIPTION:

GATCGCCAGG TTCTACAAGC TGCACGAGCG GAGGTNTGAG CCCATTGCCA TGACAGTNCC 60  
TCGAAAGTCG GACCTGTTCC AGGAGGACCT GTACCCACCC ACCGCAGGGC CCGACCNNTC 120  
CCTCACGGCT GAGGAGTGGC TGGGGGGTGC GGATGCTGGG CCCCTCCTCA TCTCCCTCAA 180  
GGATGGCTAC GTACCCCAA AGAGCCGGGA GCTGAGGGTC AACCAGGGGC TGGACACCGG 240  
GCGCAGGAGG GCAGCACCAG AGGCCANTNG CACTCCCAGC TCGGATGCCG TGTNTCGGCT 300

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NNGAGGAGGA GATGCGGGAA GTTCCAGGCC ACGGTGCAGG ANCTCCAGAA GNNGTTNGGA 360  
CAAGGNTTGG AGGAGACAAG TCCAAGNNCA AGTAGNAGCC CCTGAAGGNN TTNCAATCAN 420  
GGTTTCAN 428

SEQ ID NO:917  
SEQUENCE LENGTH:424  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01044  
SEQUENCE DESCRIPTION:

GATCCAATAT TCAATTCATT TGTGTACTCC CACATGCAAA ATGCTAAATT ACAATGCAGA 60  
CATTAAAGAAA AAGTATTGAC TGGAGGGGTT GAATTCCTTG AGAATTTATT TTATAGTCTA 120  
AATCACAAAT ACTTTACTCA ATTTAGTTTT TAAAATAGTA AACTGAATAT TTTTGTTGTA 180  
AGCCTATCAG AGTCAATCCT TCGTTTGGAA TTGTTTTCCT GTTTTNCCTT ACTATAAATC 240  
ATTTAAAAAC TGAATTCATT TTCTTAGATG GCATAAGTCT GTCTCTTGAG AAATAAGTAA 300  
AATACTCCTA TTTTCAGTAT CTGTAGCACC TGAAATAGGT CTTTGTATAG CCAGAANCAA 360  
GTTATGNTTG AAGTTAGCTT TTCTTTGTCA CCAGTTTGG NCAATAAAAA TCTGAANGTT 420  
TAAA 424

SEQ ID NO:918  
SEQUENCE LENGTH:422  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01045  
SEQUENCE DESCRIPTION:

GATCAACATA ATGGACCACT CCTGAATGAG ACTTAATTTT GTCTTTCAAA TTTACTGTCT 60  
TAAATCAGTT TATTAAATCT GAATTTTAAA ACATGCTGTT TATGACACAA TGACACATTT 120  
GTNGCACCAA TTAAGTGTTG AAAAATATCT TTGCATCATA GAACAGAAAT ATATAAAANT 180  
ATATGTNGAA TGTTAACAGG TATTTTCACA GGTTTGTTC TTGATAGTTA CTCAGACACT 240  
AGGGAAAGGT AAATACANGT GANCAAAATA NGCAACTAAA TGAGNCCTAA TAATTGGCCT 300  
TCGATTTTAN ATATTNGTTC TTATAAACCT TGCAATAAAA AATAAATCTA AATCAAAAAA 360  
AANTTGGTTC CACCTNTGCA GGTTTTTATA ANTGGTGCCA ATTAAGGTT TTTGTTTTTA 420  
AA 422

SEQ ID NO:919  
SEQUENCE LENGTH:422  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01046  
SEQUENCE DESCRIPTION:

GATCCTTACT AAGTNTTTC TGGGAGACTT CCTTCATCAC ATCTTATGTT GAAATCACTT 60  
TCTGTAGTCA AAGTATACCA AAACCAATTT ATCTGAACTA AATTCTAAAG TATGGTTATA 120  
CAAACCATAT ACATCTGGTT ACCAAACATA AATGCTGAAC ATTCCATATT ATTATAGTTA 180  
ATGTCCTAAT CCAGCTTGCA AGTGAATGGA AAAAACNNNC AAGCTTCAA CTAGGTATTC 240  
TGGAATGAT GTAATGCTCT GAATTTAGTA TGATATAANG AAAACTTTTT TGTGCTAAAA 300



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ATACTTTTAA AAATCAATTT CNTTGATTGT AGGTAATTTC TATTTGCACT GGGCCTTTCA 360  
ACTCCAGAAA CATTCTGANG GTGGTACTTG GGGTTTAANT TAAAAAGGTC CACTTTGGTA 420  
AA 422

SEQ ID NO:920  
SEQUENCE LENGTH:410  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01047

SEQUENCE DESCRIPTION:  
GATCGCTGTT TCCAGAACGG GGAGGAGTAT CTCATTGTGA AACAGACTCT AGAGTGGTTC 60  
TATTTGGTCT TCAGTGTITT AGCCTCATTG GTTCATATTT GGCATGCAGC TTGTGGTGAG 120  
TACTGTTCTA GGACTGGCCA AAAATGGGCA AAATGTATCA CTCCAAACAC TACTGATTCA 180  
GCATTGTTTT CATGTCCTAA AATTGCCACC TGCACTTTGT TTCTGCACTA TTATGTAGTG 240  
CATTTTAACT TAAATTTTTT CCAGCAACAT GTTACTTATT TANGATACAT TACTGATATT 300  
TCATTATAAT TANGTTCATC TTCCCTGTGA AACAAGAGAA TTGTAAAATG TTGTGGGAAA 360  
ATGATACATA TGTGGGATGC TAATGNAAAT CATAGGTATT TTTGTGTAAA 410

SEQ ID NO:921  
SEQUENCE LENGTH:409  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01048

SEQUENCE DESCRIPTION:  
GATCACANTT GANCTGGCAG CGGGATGGCG AGGACCAAAC TCAGGACACC GAGCTTGTGG 60  
AGACCAGACC AGCAGGAGAT AGAACCTTCC AGAAGTGGGC AGCTGTGGTG GTGCCTTCTG 120  
GAGAAGAGCA GNGATACACA TGNCATGTAC AGCANGAGGG GCTGCCAAAG CCCCTCACCC 180  
TGAGATGGGA GCCATCTTCC CAATCCNCCN CCCCCATCGT GGGCATTGTT GCTGGCCTGG 240  
NTGTCCTAGC AGTTGTGGTC ATCGGAGCTG TGGTCGCTGC TGTAATGTGT AGGAGGAAGA 300  
GCTCAGGTGG AAAAGGAGGG AGCTACTCTN AGGCTGCGTG CAGCGACAGT NCCCAGGGCT 360  
CTTAATGTGT CTTNACAGN TTGAAANGCC TGAGACAGCT TGTTTTGTN 409

SEQ ID NO:922  
SEQUENCE LENGTH:407  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01049

SEQUENCE DESCRIPTION:  
GATCCAGGCT GTCATGTGAT TTATGGTGGC ATGTGTTGTG TATTTGTTGG CTACTTGTGT 60  
CTTGAAATCT AGAATTATTT CACGCAGAAT TGTCAGGAGT TGTCAGGAAG AGAAAATGGG 120  
CTAGTGGAAG CCCAGTCTTG AGTTCTTGTC TTGTTACCAT TTAATTTGA CATTTAATTT 180  
TCAAATCACT GTTGGTGCCT AATCACTNAA GTTATTAATT TATTCTGTTG TATTCTTTTT 240  
TTTNAATNG TAACATATTT ATCCGGTGGG TGGGACAGGA GTGTGTTCAA GTGGGTCATG 300  
TTTTTNCCTG GGTGACACAT GGTACAGGCT TGGAGCTTGC AGGTCCCTTT CTACTGTGGT 360  
TTTGAGCAG GNCAATTAAG GTCCACTANG AAATNCACCN CTTTAAA 407

SEQ ID NO:923

SEQUENCE LENGTH:411

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01051

SEQUENCE DESCRIPTION:

GATCCAGGTT CCTCCAGAAA TAAGATATAC AGATTACTTT GTNATTGTAA GTGGAAC TTC 60  
 TACCCGACAC TTACATGCCA TGGCCTTCTA CGTTGTGAAA ATGTACAAAC ACCTGAAATG 120  
 TAAACGTGAC CCTCATGTTA AGATAGAAGG GAAGGACACT GATGACTGGC TGTGCGTGGA 180  
 TTTTGGCAGC ATGGTGATT CTTTGATGCT TCCAGAAACC ANAGAAATCT ATGAATTAGA 240  
 GAAATTATGG ACCCTACGTT CTTATGATGA CCAGTTAGCT CAGATAGCAC CTGAGACAGT 300  
 ACCTGAAGAC TTTCATTCTT GGAATAGAAG GTGATACTTN ATCTGTNACT NCANTGGGNG 360  
 TTAATATGTG GATTAAATTN TTTTANTGCA NTGNNGTAG TCATTTTCAA A 411

SEQ ID NO:924

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01052

SEQUENCE DESCRIPTION:

GATCAGAGCN TATNTTATGA TTGTTGATAA CTAACCAAAG TAGNTGCCTG CAGAGACTTT 60  
 AAAATGTAAA ATAAAGATGT ATGCTGCCTG TCAGCTATTC TCATTTAAA 109

SEQ ID NO:925

SEQUENCE LENGTH:405

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01053

SEQUENCE DESCRIPTION:

GATCCGAGGC TGGGAAGAAG GGGTTGCCCA GATGAGTGTG GGTCAGAGAG CCAAAC TGAC 60  
 TATATCTCCA GATTATGCCT ATGGTGCCAC TGGGCACCCA GGCATCATCC CACCACATGC 120  
 CACTCTCGTN TTCGATGTGG AGCTTCTAAA ACTGGAATGA CAGGAATGGC CTCCTCCCTT 180  
 AGCTCCCTGT TCTTGGGTAA GGAAATGGAA TACTGAAGGG CCCTTCACTG CCTTTGTCTC 240  
 TCCCATGTTA TGCCAGCGT TTGATGGGTA GCAGAGAGGA CANANATCAC CACATGGCTA 300  
 TTTTCCCNC TGAATNCTGT CTNGNATTGN GTACCTNTCA AGTGTTATTA GTGNATGCTT 360  
 TNGAAATGAA AAATTTGGGC NACCTTATGG GNAGGGNGTN GGAAA 405

SEQ ID NO:926

SEQUENCE LENGTH:405

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01054

SEQUENCE DESCRIPTION:

GATCTTAAGC AGTAATCTGT CAGTGTGTTG ATTTGTATTC TCTGCAATTT TACTGTGAAA 60

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AAAAATTTGT TTTCAACAAT TGGTGTCAAT TTCTTGATGT CACTATTTGT NGGAGAGTTA 120  
AATGGTCTCT NCCCTTTGTG TATCTTACCT AGTGTTTACT CCTGGGCACC CTTAATCTTC 180  
AGAGGTGCTA AATTGTCTGC CATTACACCA GAAGGATGCC TCTGATAGGA GGACAACCAT 240  
GCAAATTGTG AAATAGTCCT GANGTTCTTG GATTACTTTA CACCTCAGTA TTGATTTGTC 300  
CCAGAATTTN CTGGCCTTNC ATGGCANTGA AANTNTTNGG GGGAAAGATT TAANGTATTT 360  
NANTTTTAAN GAGTGTGTGA TAANNATANT TGTACTGNNT NCTNN 405

SEQ ID NO:927  
SEQUENCE LENGTH:404  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01055

SEQUENCE DESCRIPTION:  
GATCTATGTT ACATTTACCA CACTGAAGTT TTTTTGTTG TTTTTGTTT GTTTTTAAAG 60  
AATCACCTC ATTGTTGAAA GTAAATGTAC TCTTAGGGTG CGAATATTAG TGTTCCTAATA 120  
AGCATGTGAT TATATTAAGG TGGTGGTAGC GGGAAAGATAA TTCTGATTCC ATTGGGAATC 180  
TTAGGTTTTT GTAAATTTAT TGGGAAAATA GTTTTCTCTG TACTGCTGAA GTTTCTTTTT 240  
GGTAAACAGT ATCTTTCTAA AAGAAAAAAG CATGAAGGGA GAAATTGAGG TGTGTATACA 300  
TTTCTCTCAA TGACCAGCAT TGTATTCGTG AATACTGTGT ATCTTGCAGT GAACAGTGTG 360  
GAAGCTGTTT ATTTTCAAT CTGAAGTAAA ATACTTTCAA GAAA 404

SEQ ID NO:928  
SEQUENCE LENGTH:399  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01057

SEQUENCE DESCRIPTION:  
GATCANGTGT AAATGTGACC TTGTACAGTT TACTAAAATT ACTGATATTT TTCCTACAT 60  
TGAGACAGTT ACTGTGAGAA TAGGACACAA ACACCAGCTA TTGCCTGCAT CTGGGAAATT 120  
GCTGAATCGC ACAGCAGTCA TGTCATAATC AGAAAATTAC TGCCAAATAA TTGTAAAATT 180  
TGTAAGTAT AAAGTATATA AAGTAGATAC TAAATACAGN CACTTCANTA TTTTGTGAA 240  
GCTATTGACT GTACANTTAG ACATTTTCAN ANGGGTGTAA TTTATTTANN GTTGTCTCAT 300  
TTTGGTAAAA TTTATGTGAA CTTTAAAGC TAANTATTAA NCCTTAATAT GCTATGTAAA 360  
TNTTTCCNT NTATACCATT TNCTGGTGGT NTTTTTTN 399

SEQ ID NO:929  
SEQUENCE LENGTH:397  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01061

SEQUENCE DESCRIPTION:  
GATCTGCAGA AGGTATCTGG TGATGCAGAG ACTCTTTCCC CGCATCCNTC ACATGAAAGA 60  
CCCCATCGGT GACAGCTTCC AAAACGACAA GCTGGTGGTC TGGGAGGCGG GCAAAGCCGG 120  
CCTGGAGGAG TGTCTGGTGA CTGAAGTACA GGTCTGTCAG AAAACTTGAG ACTGGGGTTC 180  
AGGGCTTGTT GGGGTCTGCC TCAATCTCCC TGGCCGGGCC AGGCGCCTGC ACAGACTGGC 240

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5 TGCTGGACCT GCGCACGAGC CCAGGAATGG ACATTCCTAA TGGGTGGTGG GCATGGGAGA 300  
 TGCTGTTTA ATTCGTCCG AAGCTGCCAA GGAAGAAGAC CAGAACTTG TGTGTTTATT 360  
 TCATGATAAA GTGATTTTTT TTTTTTTTNA ACCTAAA 397

10 SEQ ID NO:930  
 SEQUENCE LENGTH:402  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01062  
 SEQUENCE DESCRIPTION:  
 15 GATCCCCAAC AATGTCAAGA CAGCCGTCTG TGACATCCCA CCTCGTGGCC TCAAGATGGC 60  
 AGTCACCTTC ATTGGCAATA GCACAGCCAT CCAGGAGCTC TTCAAGCGCA TCTCGGAGCA 120  
 GTTCACTGCC ATGTTCCGCC GGAAGGCTTC CTCCACTGGT ACACAGGCGA GGGCATGGAC 180  
 GAGATGGAGT TCACCGAGGC TGAGAGCAAC ATGAACGACC TCGTCTCTGA GTATCAGCAG 240  
 TACCAGGATG CCACCGCAGA AGAGGAGGAG GATTTCCGGT AGGAGGCCGA AGAGGAGGCC 300  
 20 TAAGGCAGAG CCCCCATCAC CTCAGGCTTC TCAGTTCCCT TAGCCGTCTT ACTTCAACTG 360  
 CCCCTTTNCT NGTCCNTCAA GAATTTNGTG TTTTGCTTGC CN 402

25 SEQ ID NO:931  
 SEQUENCE LENGTH:396  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01063  
 SEQUENCE DESCRIPTION:  
 30 GATCTGCCGA CCTTGCTATA GATGCCATGT TACCAATGAT TTCCTGTGGT GGGGGCTTGC 60  
 CATNTTTAC TCTCTTATT ACCAACTTCT GGCCTAGGCA TGACAGTGGG CACCTTCCCC 120  
 CAGCCCTGGN TGGGCCCAGC GCCTNTTTC TGTGTTAGAA AGGTTTTATA TATATATAAA 180  
 ATTACATATA TATGTAGAAA TATATGTAAT NTTGGGGGCC CTGTTCCCTG CACATTTTAC 240  
 AGTTACCTCA TTTTNNCCA TGTATGTATT TGAGAAAATG CTAATATATA GNGAAAAAAA 300  
 35 TGGGTCTTA AAGCTNAAAT GTGNGGTTTT TNCCATTCCA GGGGNTCACA TTNGGTTTGN 360  
 GGCATNGACN ATACCTNGTA TGTCGNNTA TAAANN 396

40 SEQ ID NO:932  
 SEQUENCE LENGTH:394  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01064  
 SEQUENCE DESCRIPTION:  
 45 GATCCGTGGA TTTTGGTGC AATCCCCCTT TTATTCTTG TCTGAAGAAA GCCTACTGCC 60  
 TTCTGTTGGG ACCAAAGAGG CCATAGTGCC CATGGAGGTT TGGACTTAAG AGATATTCAT 120  
 TGGCAGCTCA AAGACTTCCA CCCTGGAGAC CACACTGCAC ACAGTGACTT CCTGGGGATG 180  
 TCATAGCCAA AGCCAGGCCT GACGCATTCT CGTATCCAAC CCAAGGACCT TTTGGAATGA 240  
 CTGGGGAGGN CTGCAGTCAC ATTGATGTAA GGNCTGTAAA CATCAGCAAG NCTTATAAT 300  
 50 TCCTTNTGCC TAANTTGTA AANGGGGNC TGCATTCTTG TTGGAAGNAT GNACTNTNTT 360  
 TNNGGAAAAC CACATTTTA AAANTTCCCG TAAA 394

55

SEQ ID NO:933

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01065

SEQUENCE DESCRIPTION:

GATCCACAGG CTTTTGTACT CAACGCTGAC AACAAACCCTA AGAGGTAGGT ATCATTATAT 60  
CAACCATTTT ATGAATAAGA AAACAACAGC ACAGAGAGAT GCAGTCACTT GCCCAAGGTC 120  
ACACAGGGCC AGGGGTGTTG CCAGGATTCG AAGCAGGCAG GCTGTCTCCT GGGTCTGAAC 180  
TCTCAACTAC TACACCCTAA TCAAACAATC CCTCTGGTCA AATGTGAGTG ATAATAATAG 240  
TACCCACCTC GTGGGTGTTG AGGGTGAGCC CAAGTTAGCA TTCAGCGTGG GCATGTGAAC 300  
AATTATAGTC AATATTGANT GGAGACCTAT GATGCTTTTA TGAAGGTTTC TATTTTGGGT 360  
TAAAAAATGC ATAAAATTC TCCTGACCAG AAA 393

SEQ ID NO:934

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01066

SEQUENCE DESCRIPTION:

GATCACCTTA AGTGAAATNA TTTNCCTTTA ATCTTTNATG TATTTATTCA CTTTGGGAAG 60  
CTAGGAATGA GCAACACAAA TTTTACTCTG AAGTCAGAAG AGCTCATATA TAATANTTCT 120  
AATGTCCAC CTATTTTCAC TTGTCCATTC CATGTACCAG CTTAGTTATG ATANNNGTC 180  
ACATAATTAT CTTTGATAAA GGTAGAGGCA CAAAGAGGCA AACTAAGCAA GTCAAATTCT 240  
AATGTGTGTA CTTCATAATA ATTTTTATC CATTTTCATC TTTATATTCT GTAACATGAA 300  
NCTTACCTAA TCTTCAAATG TTAGCTTCCA TTTTTCACCT TTGAAATACT TAAATCTTTC 360  
TGGANTAAAT ATAATGGGGC CTNTAAAANT AAA 393

SEQ ID NO:935

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01067

SEQUENCE DESCRIPTION:

GATCCTGTTC TTTCAGCAGG TGAAAAATAA AACGCANTCA AATTTTCATGG TTTTAATTTT 60  
NAACTCAGAA GCACTCAAAA ATGCAAAATG TGATAATGGG CACTTGTTTA AAAGANTTAG 120  
TGTATCCAGC CTTCACTCCA GCTGGTTAAA AATGTTGCAC TTATCAGCAA CCNNACCACT 180  
TTCATCTGCT GAAAGGNCAA ATGTGCTTGG TTTTACTATT ATGTAATCAC AACTTTCCTT 240  
TNTGCTTGTA GTTGCTTAAA ATTATGTATT TGGTCTNGGG CTGCAATTTG GTTTNATGCT 300  
NTATNTGATT ATTACNGCAG TAGGTTGCCT NTCCNGTATG GGAAAAATAA AGTGGAATNG 360  
CCCNAAATTAA ACCNCCTCTN TCTTAAGGTA AA 392

SEQ ID NO:936

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01068

SEQUENCE DESCRIPTION:

GATCAGGCAG CCTCCTGATG CCAGANCACC TCAGGCAGAG CCTACTCAGC TGTACCTGTN 60  
 TGCCTGGACT GTCCCCTGTC CCCGCATCTC CCCTGGGACC AGCTGGAGGG CCACATGCAC 120  
 ACACAGCCTA GCTGCCCCCA GGGAGCTCTG CTGCCCTTGC TGGCCCTGCC CTCCCACAG 180  
 GTGAGAAGGG TCCTGTCCAC CAGCACATC AGTTCTNTTC CCTGCAGTGT TTCATTTNAT 240  
 TTTAGCAAAN ATTTTGCCTG TTNNTGTTNA AACATGATAG TTGATATGAG CTGAACCCCT 300  
 GGGTTNGGNG GGAATTGGTC AGAGTGGCAA CCTGGGACTG TGAGCCCTGT TCGGNACAGN 360  
 NTATGGATAT GAAAANTCTG NCCNNNGCNA N 391

SEQ ID NO:937

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01069

SEQUENCE DESCRIPTION:

GATCTTTCCC AAGATTGTAA CTGAAACTG CTGTCTCTTG TTTTNTTCGT TTTGGGGGTG 60  
 GTGGTGCTGG CTGGGCCATG CTTGTAAAGT GATGTGTGTC TCTGATTAA CGGATTCACT 120  
 GTTTTCTCTG CTAATTGAGA GAGCGTTATT TACATTATTT ATTTGTTTTG ACACAAGTNC 180  
 TTTCACTGTT TTATCCTAGC TAATGGCTTC TTAAAGGTAA TAAAACCCTT CCAACGTAAT 240  
 TGGTCAGATA AAACTTTTTT CTTGTATGC TTAAATAAAG CAATTAGTGA AGCACTTCTA 300  
 TCCAAAATGA CTTTTTTGTC CTTTTTTAAA ACCAATTTAC TGTTACTGGA AACTTTGTAC 360  
 AATAAAGCAA ATCACGCAGA TTAANGGAAA 390

SEQ ID NO:938

SEQUENCE LENGTH:389

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01070

SEQUENCE DESCRIPTION:

GATCAGAGGG AAAGAATGAC CAACCNNGCA ATAAGTGTAC TAAACTCTAC GCTCTGGTTA 60  
 ATGTAATGTA CTCTCCTGGA CTGAATGCAG TGTATAATTN CTGTCTACAG CTAGAAGCTG 120  
 TGCCCCAGTT CCACATTGGA TTACACATGT NAGATTGCT GCTGTTGCAG TATAAACACT 180  
 AGGTATAATA GGATTTGAAA TTGCATTACA GTTCATAAAA NTNGAAAATG AGGAATTAAA 240  
 CCNGCAAGTG AACATTTGAA CGNTTATNCT NTCTACATAA GACATGGTTG GGACATCAGT 300  
 ACTNACAAGA TGGTTTANGT ATGGTACTAG NGNANTTAAG NTTTCTTCT CTCTGGTTTA 360  
 TNGATNGGGT TATTTCCATT ATGTATTNN 389

SEQ ID NO:939

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01071

## SEQUENCE DESCRIPTION:

GATCTCACGC TGCCTCTGTG GTTCCCTCCC TCATTTTTC TGGACGTGAT AGCTCTGCCT 60  
ATTNCAGGAC AATAATGGCT ATTCTAAACG CTAAGGAAAA AAAACAAACA CAGAACTGTT 120  
TCAAGTACTC AAGACTGACT TACAGACCAA CCAACCACCT TGCTGGAACC CTTGCTAGCA 180  
GGCATTCTTA TAAAAGAAAC TTTCGAGCCT CTTATATTG CTGGAAGCTC AGCTGTGCTC 240  
CAGACTAGAG CCTCCTTACC TATGCTATGG ATTTTAAATT TATTTCTCT TATTTCATGT 300  
ACACTGCTTT TTTTGGTTAC AGTGTATGAT GGATGTGTAT GAAAAAATG TATCTTGGG 360  
GAACCAATTA CAGTTTGTG AATTTGAAAA 390

SEQ ID NO:940

SEQUENCE LENGTH:543

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01072

## SEQUENCE DESCRIPTION:

GATCCACACA CGTTGGTCTT TTAACCGTGC TGAGCAGAAA ACAAACAGG TTAAGAAGAG 60  
CCGGGTGGCA GCTGACAGAG GAAGCCGCTC AAATACCTC ACAATAAATA GTGGCAATAT 120  
ATATATAGTT TAAGAAGGCT CTCCATTGG CATCGTTTAA TTTATATGTN ATGTTCTAAG 180  
CACAGCTCTC TTCTCCTATT TTCATCCTGC AAGCAACTCA AAATATTTAA AATAAAGTTT 240  
ACATTGTAGT TATTTTCAA TCTTTGCTTG ATAAGTATTA AGAAATATTG GACTTGCTGC 300  
CGTAATTTAA AGCTCTGTTG ATTTTGTTTC TGTTTGGATT TTTGGGGGAG GGGAGCACTG 360  
TNGTTTATGC TGGAAATATGA AGTCTGAGNC CTTCCGGTGC TGGGGACCAC ACANGNGTTN 420  
GTTGNAAAGT TTGACCAAGN AGNCCTGCGC ATNNNCTCTG GATGCCTNTG GTATCCATTC 480  
TTNGANGCAA TCCGCTCGGG NCCCGTGGGC CCAATAAANC NGGTATTTNT CCCAANGGGG 540  
AAA 543

SEQ ID NO:941

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01073

## SEQUENCE DESCRIPTION:

GATCTCAAGA TTTCTAAATT GTCAAGATT ACATGGCATT GTGGTGAAC TAGTTAACAC 60  
TTAGAGCTTT TGGTATGTAA TAACTATTTG CTATGGACTG ATTAAATGTT TCAAAGATT 120  
GTGTTCTTCA AA 132

SEQ ID NO:942

SEQUENCE LENGTH:387

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01074

## SEQUENCE DESCRIPTION:

GATCAGCACT AAGTCCTGCA TTCCTGTAA AGCCACTTGG GTCATAAGAA GGGAGTAAAA 60  
AATGAAGTCT GACTAGNAAC CTATTGCAGA GGCCAAGTAC ATTAGTATG GCATTGAGTT 120  
GTGATATAGT TTTACTTTGA TGTGCATTTT GAATTTTACG TACACCTAGA TAGACGTAAA 180

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ATGATAATTA AAATGCTGTA ACCAACTTAT CTAATAAAAT TGGCAACCAG CCACTATTTT 240  
 GTTGACTATG AGAAAAGTTAA AAGTTTATGT TAATTTTTNG GGTCTGATAG AATATTTTCAT 300  
 GTGTATTACA GTGGTATTCA TATGCTATGT CTCTAAACTT TATTTTCAA AGCTTANGGC 360  
 CCANATACAA NCTTCTCTGG GNNTAAA 387

SEQ ID NO:943

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01075

SEQUENCE DESCRIPTION:

GATCAGANAA AAAGTCCATA TGGACTGTGG ATACCTATCT AAAAGAAGAA AACTGATGGC 60  
 TAAGTTTGCA TGAAACTGC ACTTTATTGC AAGTNAGTGT TTCTAGCATT ATCCCATCCC 120  
 TTTGAGCCAT TCAGGGGTAC TTGTGCATT AAAACCAAC AAAAAAGAT GTAAATACTT 180  
 AACACTCAA TATTAACATT TTAGGTTTCT CTTGCAGATA TGAGAGATAG CACAGATGGA 240  
 CCAAAGGTTA TGCACAGGTG GGAGTCTTT GTATATAGTT GTAAATATTG TCTTGGTTAT 300  
 GTAAAANTGG AATTTTTTAG ACACAGTAAT TGAAGTGTAT TCCTGTTTG TATATTTAAT 360  
 AAATTTCTTG GTTTTCAATC TTAAAA 386

SEQ ID NO:944

SEQUENCE LENGTH:383

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01076

SEQUENCE DESCRIPTION:

GATCTTCTAG CTACCATNCA TTTTCTTCAC TGTCACAAA AGATGAGTGT GAAATTCAGT 60  
 GAATGCTGTT ACTAATCCTG TTACGAGATG AATCTCATTT CACCAAAATT AAATTATGTT 120  
 TTTCCGCTAA AATGATGATA CAAGTTGAAG ACACATCACT CTGAAATTGG AAGACCTCAC 180  
 CACTTAAGGC TCCACAGTGG CTTACTCAGC TGAAGTCTAG GTTACTACTC TTTACTTTGT 240  
 TCACCCATTG GGGGGTGCAG TTTTTTAAA ATGTTGGGAG ATGGCCATTC TAACTACTGT 300  
 TGAATGTCTC TGTTTGGGA AGGTATAACA NGAANTAAAA ANGNTATAT ATGANGGGAG 360  
 AGNCTGGTTA TCTCCTCCCC AAA 383

SEQ ID NO:945

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01077

SEQUENCE DESCRIPTION:

GATCTCTCCA TGTACCCTGC AGGGGGCTTG GTACTGTGAA ATNAGTAACT TAATCCTGAC 60  
 AACCCTAGTG CAAGGTATGG CCCATCTCCT GTACGCTTGG AGCGACCTTT GGCTACGTGG 120  
 CTGGCCTTGT TATTTACCA CTCTGGATAT ACTGGAATAG AAAGCAACTT ACATACAAGA 180  
 ACAATTAAGT GGAGCAAAGG GAGATATTTT TTTGTGCAGA TTCTGTAAGG GCTGGGCAGA 240  
 AATGTGTATG GTCAAAGCCA AGCAGTTCCA TTTACAGCTC TGTTTTTTAC GTAGTTACAA 300  
 CATGATGTGA TTGTAGCTTT TTAACTATG AAACCCCTGA GAGATTGTAC CTTCTAGTT 360



GAAATAAAGT ATTTATAATA AA

382

SEQ ID NO:946

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01078

SEQUENCE DESCRIPTION:

GATCCGAACA CCTCCAGATT CCGGCTTCTA CATGGNNCAG ACGGGGACGC ACAGGCCACC 60  
TTCCTTCTGG CAGGGACTCT TATTTATTCC CATTGCTCTA GGGCTTTCNN TTCCCNNTTC 120  
TTCCGGTAGG CCGCGTAGAG GCATGCACCG GGTAGGTTTC CGCGGTGACC CCGCGGCGGC 180  
CTGAGGGACG CTCCCTGCCC CATCCCGGCT GTTGGGCTGG GCCGCTTTCG CTCTGCTTCG 240  
NCCTGTGCTG TGTTCCTCCAG CTTTGTAGCA GCAGCTTGAC AAACCCAGGC GCACTGTACC 300  
AAGGCAATGT AACTTTTAT TTTCCGTCAA TTAAAGTTCT TTTTGTACC AAATATTAAT 360  
AAACCAGTTT TGGACTTAA A 381

SEQ ID NO:947

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01079

SEQUENCE DESCRIPTION:

GATCTGAGTC CAGAGTTGGC CACTTTGTGT GGGTCCTCAC AAGCAAAGAG AGCACTAAAC 60  
TTGACATTGG GGGTCCACCA CTCCAACCTT NCTTCTGAA GGTTTGGTG TACATTGAGC 120  
CCCAGAAGGA AAGGAGAGTA TCTGTGAGTG GGGGCCTCCC TTGACCCAG TACGAAGTCT 180  
ATGCCCTGAA TCCCAGAGT AGCCCTTCCT GGTGCCCAAC TGGCCTGGGG ACAANCAGCG 240  
TCCACTACAT CTAGGCTGCC GGCTAAGTGG CACACTTCTT GACCTCCTAC CAGGACTTTG 300  
GTAAAGCTA GCTTTGGGGA GGGGTGGGTT AAATATGAGA GGTGGAGGNG CCANTGGTAG 360  
AATAACATGG GTAGACTAAA 380

SEQ ID NO:948

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01080

SEQUENCE DESCRIPTION:

GATCTGCATC AGTTGTAAAG GGGAATTGGT ATATTCACAG ACTGTAGACT TTCAGCAGCA 60  
ATCTCAGAAG CTTACAAATA GATTTCCATG AAGATATTTN NNNNCAGAAT TAAACTGCC 120  
CTTAATTTTA ATATACCTTT CAATCGGCCA CTGGCCATTT TTTTCTAAGT ATTCAATTAA 180  
GTGGGAATTT TCTGGAAGAT GGTCAGCTAT GAAGTAATAG AGTTTGCTTA ATCATTGTGA 240  
ATTCAAACAT GCTATATTTT TAAAAATCAA TGTGAAAACA TAGACTTATT TTAAATTGT 300  
ACCAATCACA AGAAAATAAT GGCAATAATT ATCAAACCTT TTAAATAGN TGCTCATATT 360  
TTAAAAATA AGGTTTTAAA 380

SEQ ID NO:949

SEQUENCE LENGTH:399

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01081

SEQUENCE DESCRIPTION:

GATCAAAGCA TGCAATAAGC AATACAAAAT ACCAAGCCTT ATACTTAAAA GAAGTTTAAC 60  
 ATATTGGTTA ATATACTGGT TAATATACTG GTTAAACATA TTGAATGTAT ATAAGTGGCA 120  
 AAAGTAGATT TTTAAGGAAG TGTACATTAT AATATTGGAG CTCAGTACTG CATGANGAGA 180  
 CTTTCATTAAG ACTAAGAAAN CATTTATTTG GGGAGAAATT TTAGGCATTT AAGANCTTGT 240  
 ATTTTCTAT TTTAAAAAGT TAAATTATTC CGTAATTTGG ANGGAAGTTT CGTTGAATGT 300  
 AGGCCATAAC CGTTTGANGG GTTTTCCTTT GGANAACCTG GTGTNTTTNG GTGCCCTTAN 360  
 TATTTTGGTC CTTTAAATAA AAATGCNCCT GNATTTTCN 399

SEQ ID NO:950

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01082

SEQUENCE DESCRIPTION:

GATCAGGCC TGGGCCCCC TGCATCTTT ATAGCAGTGG GTGTCCAGTC CAGGACACTG 60  
 GTGCTTTTT ATACAAGAGA ACGAGCCAGA GTTCACTCCT TCCTCCTGGC TCTCTATATA 120  
 CCTGTGAATA TGTGAAATAG TGTAAATATG AAAGAACTTG TACCTATCAC TTCAACCCCT 180  
 GCCTTGTA TAATACTATT CCATCCACAC AGTTTCCACC CTCACCTGCC CCNTCATACG 240  
 GAGTTGGATG GGGGCCGAGT NAGGTAACCA GGTGGCATCT ACCNNATGTT TTATAAGGAA 300  
 TTTTGTACAG TCTTNGTGAA ATAAAATAAC GTGCTTCATT TGNAAAAATN NNGTTNNNTT 360  
 TNTNTTNNNT NGNGGGTTN 379

SEQ ID NO:951

SEQUENCE LENGTH:376

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01083

SEQUENCE DESCRIPTION:

GATCTAGTAG AAAGTAAGGG ATGGGAAAAA CCTTTTCATT TTTCATCTNC TTTCCAACAA 60  
 TATGAATTC TTAGTTTTCA AACTATACTC AGGAAAGCTG GGCTTTAGGA TTTAACATGT 120  
 AGTGATGAGT TCTGTGTGTA TTTTAATATT TNACTCAGGA TTCCTATTAA TTGAAAAAAA 180  
 TTTTAACTT TTTTATTATA AATCTTTTTT TCAGGGAGGN GATATCACC AATCATGATG 240  
 AACAGGCGGA CAGTCCATTT ATGGAGACAA ATTTGANGAT GAAAATTTTG ATGTGAACAT 300  
 ACTGGTCCTG GTTACTATC CATGGCCANT CAAGGCCAGG ATTACCAATA ATTCNTCATT 360  
 TTTGTTATAC CACTGN 376

SEQ ID NO:952

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01084

SEQUENCE DESCRIPTION:

5 GATCAAGCCA CCACGTGCCC TACGATGGCC TAACAGGAGT GCCCATTGGC AGATTACACA 60  
 TGTAATATG ACCTCAGACA AAAAGGAAACC AGAGGCCCAA GGGCAATAAT AAGGTGGAAT 120  
 TTNCAGGTCA GCCCAGGAAT TGGCAGAGGA AGTAGGTGTC TGATAACCCT TTGTGGAGAA 180  
 TGAGATTCCC CCCACCTGTG TGAGAAAAAT AAACAGCTCT GGAGTCTTGT NCCTGACTCC 240  
 AGAGGAACGA GAGCATTCCA GGAAAGAGAG ATTCCCTGGA AAATTGAAAA TGTGAATCCT 300  
 10 AGGGGGAAAT TGGGGATTGT NTCTTTCCT GTTGAAAATG TTTNGNTGGG AATAAATATC 360  
 TTCAGGAACC ATAAA 375

SEQ ID NO:953

SEQUENCE LENGTH:374

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01085

SEQUENCE DESCRIPTION:

20 GATCTTCTNC ACACACCCCA TCACCCAGAT AATTACAGT TCTGTTAACA GTGAGGTTGA 60  
 TAAAGTATTA CTGATAAAAA ATTATCTAAG GAAAAAACA GAAAATTATT TGGTGTGGCC 120  
 ATCTTACCTG CTTATGTCTC CTACACAAAG CTAAATATTC TAGCAGTGAT GTAATGAAAA 180  
 ATTACATCTT ACTGTTGATA TATGTATGCN CTGGTACACA GATGTCATTT TNGTTGGTCA 240  
 25 CAGCACTACA GTGAAATACA CAAAAATGA AATTCATATA ATGACTTAAA TGTATTATAT 300  
 GTTAGANTTG ACAACATAAA CTACTGTNGC TTNGAAATGA TGTATGCTTC AGTAAATCA 360  
 TATTCAAATN TAAA 374

SEQ ID NO:954

SEQUENCE LENGTH:376

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01086

SEQUENCE DESCRIPTION:

35 GATCAAGCA AAGAGCGCCT TTCCATGTAT CTCATGAAAG CTGACCTGAT GCCTTTCCTG 60  
 TATTGGAATA TNATGCTAAG GGGTTACTGG GGAGGACCAG CGTTTCTNCG CAAGTTGTTT 120  
 CATCTAGGNA TGAGTTAAGN ATGGCTCAGC ACTTGCTCAT CTTGGATGGC TTCTGGGCCA 180  
 AAAGTGCAGT CACTGAATGA CCAAGAGCAG CACGAAGGAC TTGGAACCTA TCCTTGTA 240  
 40 GAGTTCCTTG ATGGGTAATG GTGACCAAAT GCCTCCCTTT TCAGTACCTT TGAACAGCAA 300  
 CCATGTGGGC TACTCATGAT GGGCTTGATT CTTTGGGAAT ANTAAATTGA AATANTACTT 360  
 TTNTTTTCTG AATAAA 376

SEQ ID NO:955

SEQUENCE LENGTH:371

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01087

SEQUENCE DESCRIPTION:

50 GATCAGAACCC TCCAAATACT GCCATGAGAA ACTAGAGGGC AGGTCTTCAT AAAAGCCCTT 60

55

TGAACCCCT TCCTGCCCTG TGTTAGGAGA TAGGGATATT GGCCCTCAC TGCAGCTGCC 120  
 AGCACTTGGT CAGTCACTCT CAGCCATAGC ACTTTGTTCA CTGTCCTGTG TCAGAGCACT 180  
 GAGCTCCACC CTTTCTGAG AGTTATTACA GCCAGAAAGT GTGGGCTGAA GATGGTTGGT 240  
 TTCATGTTTT TGTATTATGT ATCTTTTGT ATGGTAAAGA CTATATTNG TACTTAACCA 300  
 GATATATTTT TACCCAGAT GGGGATATTC TTTGTAAAA ATGAAAATNA NAGGTTTTTT 360  
 NAANTGGNAA A 371

SEQ ID NO:956  
 SEQUENCE LENGTH:368  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01088

## SEQUENCE DESCRIPTION:

GATCTGGGGA GGGCTAGCCC AAAACCTCCC GCATCGGGCA GGCACCCCT GAAGTACTTC 60  
 CTTAGGGTT TCCCCTTTGT NAGGGTGTCTG AGTAGCCTCA CCGGCCTGTN TGGAGGAGCA 120  
 GCTGGCTCTG CTCTGAGAAA CTCTGGCAAG TGGACGCCAT TCTNTTGCCC TTAGGATTCA 180  
 CTGCTCTCTC CTACAGCCGC CAGNCCTGGG GTCCTGAAAG ACCTTGGGTG GTAAAGCTGT 240  
 ACTTGGTGGG AGTNAGGGCG TGGGGAGGAA CCATGCAAAT CGCCTCCAT GGGTTTTTAA 300  
 NTGCAGTAAA TAACATTCT GGATGAGACT NGTTTCCAAA NTAAACCNG CTATTATCTG 360  
 TTTTAAA 368

SEQ ID NO:957  
 SEQUENCE LENGTH:369  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01089

## SEQUENCE DESCRIPTION:

GATCCGAGCT CTGGAGCGTG GATACCGGAT GTCTCGCCCA GAGAACTGCC CAGAGGAGCT 60  
 CTACAACATC ATGATGCGCT GCTGGAAAA CCGTCCGGAG GAGCGGCCGA CCTTCGAATA 120  
 CATCCAGAGT GTGCTGGATG ACTTCTACAC GGCCACAGAG AGCCAGTACC AACAGCAGCC 180  
 ATGATAGGGA GGACCAGGGC AGGGCCAGGG GGTGCCCAGG TGGTGGCTGC AAGGTGGCTC 240  
 CAGCACCATN CGCCAGGGCC CACAACNCGN TTNCTACTT TCCNAGACAA CNACCNTCGG 300  
 TTTCAGGCCA CAGTTTTCTT CATCTGTCCA GTTGGGGTAG GTTTGGGACT TGGNAAAATN 360  
 TTTTTTTN 369

SEQ ID NO:958  
 SEQUENCE LENGTH:366  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01090

## SEQUENCE DESCRIPTION:

GATCGAGCCA CTGCACTCCT GGGGCAACAG AGCAAGACTT CGTCTCAAAA TAAATAAATA 60  
 AATAAAGTGG CTCTGGGGA AAAGCAATTT AATGTACCAC GATGAATAGC TAAGTGTTC 120  
 CAAGTGTTTG CTATGTGCAA CACACCGCGT GAGAGTGTTA CCTGCATTAT TACATTAGGC 180  
 TGAGAGGTAA AATAATTTGC CCGAAGACAT ACAGCTAGTG ACGAATGGAC TGATGGTTT 240

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AACTTAACGT CTATTTGACT TAAGGTCCTG CACCCTGCCA CTTGTAATTT TCAGANTCAC 300  
TGATAATCTG AAATAATGCA GCTTAAACCA TGTTTTCTTA ATTAAGTA TAATTGGATG 360  
GTGAAA 366

5

SEQ ID NO:959  
SEQUENCE LENGTH:364  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01091

10

SEQUENCE DESCRIPTION:  
GATCCTGAAG GTGAAATGAA ACCAGGAAGA AAAGGTATTT CTTTAAATCC AGAACAATGG 60  
AGCCAGCTGA AGGAACAGAT TTCTGACATT GATGATGCAG TAAGAAAACCT GTAAAATTCG 120  
AGCCATATAA ATAAACCTG TACTGNTCTA GTTGTTTTAA TCTGTCTTTT TACATTGGCT 180  
TTTGTCTTCT AAATGTTCTC CAAGCTATTG TATGTTTGA TTGCAGAAGA ATTTGTAAGA 240  
TGAATACTTN CCTTAAATGT GCATTATTA AAATATTGAG TGAAGCTAAT TGTCAACTTT 300  
ATTAAGGATT ACTTTGTCTG CCCACCACCT AGTGTAATAA AAANTCAAGT AATACANTCT 360  
TAAA 364

20

SEQ ID NO:960  
SEQUENCE LENGTH:364  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01092

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SEQUENCE DESCRIPTION:  
GATCTGGGGC CGNCCTTACG GGGCAGGGCT CAGTCCTGAC GCTTGCCACC TGCTCCTACC 60  
CGGCCAGGAT GGCTGAGGGC GGAGTCTATT TTACGCGTCG CCCAATGACA GGACCTGGAA 120  
TGTACTGGCT GGGGTAGGCC TCANTNAGTC GGCCGGTCAG GGCCCGCAGC CTCGCCCCAT 180  
CCACTCCGGT GCCTCCATT AGCTGGCCAA TCAGCCAGG AGGGGCAGGT TNCCCGGGGC 240  
CGGCGCTAGG NTTTGCATA ATGTTCTTNT CCCNGCGGGT GGGNGCGGGG AAATTCATAT 300  
CCCCTGTTTC GTNTNATGTT GTGTCNNCG NNCCCAAATT TAAAAAGGNA ATTTNAAAAAN 360  
GGTN 364

35

SEQ ID NO:961  
SEQUENCE LENGTH:362  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01093

40

SEQUENCE DESCRIPTION:  
GATCGAGGGG CGGGGGTCAG CTATGCAGCC CATCACGTGT GTTTTTCATC TGGGATGAAA 60  
AAGCTGGTT CTCTTTTGAA ATGCTTGATT GTACTTATTG AGCTAAACAA GNCTTGGTGA 120  
CTNTTGTGTA TTTGCCTCAA AAGTTTTAAG TCCTGGGTTT TCAGACTACT GTGTAGCAGC 180  
TGTGTGTTTA ACATACTGTA GCTTTTTCTC CCTTGGGGGC ACATACAAAT AGGATGTGTT 240  
GATGTGGACT CTAACTGTA ATTTTCTGT AACTATTTTG GAATGATGCA TATTTCTAAT 300  
GTTTGTATA CTTGTACAGA GTATTTGCTG TTGGTTGCTT TTTTTTTTNN TTCANNGGGA 360  
AA 362

50

55

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SEQ ID NO:962

SEQUENCE LENGTH:360

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01094

SEQUENCE DESCRIPTION:

GATCCAGGCC AAGGCACTGG CTGTNAGTGG CAGAGTTTGG CTGTAACCTT TGCCCCTAAC 60  
 ACGAGGAACT CGTTTNAAGG GGGCAGCGTA GATTGTNTNA TTTGCCACCT GGATGAAGGC 120  
 AGACATCAAC ATGGGTCAGC ACGTTNAGTT ACGGGAGTGG GAAATTACAT GAGGCCTGGN 180  
 CCTCTNCTTT CCCAAGCTGT GCGTTCTGGA CCAGCTACTG ANTTATTAAT CTCACTTAGC 240  
 GAAAGTNACG GATGAGCAGT AAGTAAGTAA GTNTGGGGNT TTAAACTTGA GGGGTTCCCT 300  
 CCTGACTAGC CTNTNTTACA GGANTTGTGG NAATATTAAN TGCAAATTTA CAACTGCAAA 360

SEQ ID NO:963

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01095

SEQUENCE DESCRIPTION:

GATCCAATTT GTAGCTTCCT GCCTGGCTTC AGAGAGCCCA GCAACCTTCT AGGCCTGCTT 60  
 TCCAGACTTC TGAGATAGCC TGGGATGAGC AATCCTGTTA TAGTACATCT GGACCTTCCC 120  
 TACCTGGGCT CTGGGGAGGC TGTGGGCCTG GAGAGGGAAA AGGAGGGAGG GGGTGTCTGC 180  
 ACCACCTGGG AAGATAGCAC AAGGCCTAAT GAGGTCACCC TGAATCCCA CCCCAGCATT 240  
 TCATTATAC CAGATAATAG CTGCATTACT GCCANCTGAC CTTATAACCC TCTGCACCTT 300  
 CAAAAAGGTT CATGGTTTTT AATTGCTGCT TTTTAATAAC ATTTTGTNA AGNTTAAA 358

SEQ ID NO:964

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01096

SEQUENCE DESCRIPTION:

GATCGGCCCT ACTAAGATGC AGAGACCCCG NCAGAGCTNG CATTGACTAC CAGATTTATT 60  
 TTTNAAACCA GAAAATNTTT TAAATTTATA ATTCCATATT TATAATGTTG GCCACAACAT 120  
 TATGATTATT CTTGTCTGT ACTTTAGTAT TTTTNACCAT TTGTGAAGAA ACATTAAAAC 180  
 AAGTTAAATG GTAAA 195

SEQ ID NO:965

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01097

SEQUENCE DESCRIPTION:

GATCCAAGAC TGGCTGACTT CATTTGAAAT GGTGAATCT GCTGTGTAAT AAAGTGGTTC 60

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AACCATGATT AGGAACTGAA ATTTAGTAGA AGAGGGAAAA GGAGTTAATG TAACAAATTA 120  
 TTTTAGCTAC AAACCCCGGT AATAGAGCAC TTGGGGGATG GGATGGGGTG GGTGGGTGAG 180  
 ACAATCAGAA TGGTAAATTG ATTAATGCT CCTAACCTG TAATTTGTG CATAGAGCAC 240  
 CCTATGCTGT GGAAATAACT GTTCTTAGAT TTCATTGTAA CTGGACTGTT CAGGTTGCCC 300  
 AGAGGGAAAG ACCATTCCCTA ATTCTAATAA AATAACCTTT TATTTGTGA TTCAA 356

SEQ ID NO:966

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01098

SEQUENCE DESCRIPTION:

GATCTCCACC ACCATCTCCC CTCTACTTCT CATTCCTTAA CTCTCTGCTG AATATGGGGT 60  
 TGGTGTCTC ATCTAATCAA TACCTACAAG TCATCATAAT TCAGCTCTTG AGAGCATNCT 120  
 GCTCTNCTTT AGATGGCTGT AAATCTATTG GCCATCTGGG CTTACAGCT TGAGTTAACC 180  
 TTGCTTTTCC GGGAAACAAA TGATGTCATG TCAGCTCCGN CCCTTGAACA TGACCGTGGC 240  
 CCCAAATTTG CTATTCCCGT GCATTTTGTG TGTTCCTTCA CTTATCCTGT TCTCTGAAGA 300  
 TGTTCCTTGA CCAGGTTTGT GNTTCTTAA AATAAAATGC AGNGACATGT TTTAAA 356

SEQ ID NO:967

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01099

SEQUENCE DESCRIPTION:

GATCTTCCAC AAAACATCTA GCCATCTAAA ATGGAGAGAT GAATCATTCT ACCTATACAA 60  
 ACAAGCTAGC TATTAGAGGG TGGTTGGGGT ATGCTACTCA TAAGATTTC GGGTGTCTTC 120  
 CAACTGAAAT CTCAATGTTT TCAGTACGAA AAACCTGAAA TCACATGCCT ATGTAAGGAA 180  
 AGTGCTATTC ACCCAGTAAA CCAAAAAAG CAAATGGATA ATGCTGGCCA TTTTGCCTTN 240  
 CTGACATTTT CTTGGGAATC TGCAAGAACC TCCCTTTTCC CTTCCCCCAN TAGGNCCATT 300  
 TAAGTGTGTG TTAAACANCT ACAGNATACT ANNTAANAAG TTTGGCCAAN NCCAAA 356

SEQ ID NO:968

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01100

SEQUENCE DESCRIPTION:

GATCAGATTT TTGGGTCATG TCTGTGTAT TTTCAGTAAT GTGATTTTCTG ATGGTCATCT 60  
 GGATTCTCCC ACTTCTCTAC TCCATTATTT CTCTACTTTT CCTTCCAGCA NACCTGANNC 120  
 GTGAGGGAGA TGGATTAATG TGAGTAACAG GAATGTGTCT TTAAAAAGCT AGAGTGGTTA 180  
 CATTTAATCA GGCAGTAAGA TAATTTGGGT TCTTGAGTTG TTTTGGNGTA ATATCCCACA 240  
 ACTGGGGTAG GAAGCTCAGG ACTTTTTNT TAAAGCTAG TCATTTCAA AGCATATTGT 300  
 ATTTTTTTGA NTGACTACAG TATGCCAAN TTCAANANCC AAANCCCNCT TTGGGN 356

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SEQ ID NO:969

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01101

SEQUENCE DESCRIPTION:

GATCCAACAA TTTTNAAGAG CTCTCTCTTA ATCTCTGACA TAATGAGTCT GAAACAAAGA 60  
 AAAGTTACCT TACCGTGTCT TTACTTCCTT TCTTCTGGGC TGTGAAGTCA AGTGCCTTGA 120  
 GGGCCAGCTA AGAGCTTTTT GGGATATTTG TCTAACTTAA TTGAAGTGT ACTGAAAGAT 180  
 AAATTAACAA AATGGTTTCA AGTTTTGGAT TAAGACCTTT GTAAGTAACT GACCGTCAGC 240  
 ACAGGAGCTT CGGTTTCCTT CTCTGTAAAA CAGGGCTCCT CATTCCAATT CCACCTATCC 300  
 TGTAGCCTTG TGGGAATAAA AGGAGGCACC ACGTGGAGGT GCTTGGCAGG NTGAAA 356

SEQ ID NO:970

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01102

SEQUENCE DESCRIPTION:

GATCATANAA NGGCCATCTG GGCCAGCTN GTGTACAGCG AGGGNGGGCA GCCCCCTCCA 60  
 CTCCACTCTG CTTCCACAAA GTCGGCTCCC GAGAGCTCGA GGCTGCTTCT TTTTATATGT 120  
 GCAGGGCCCG GCGGGTGAA GGGTCAGAGA GACGGACACA AGGAGCCGGC AGGAGNGCGG 180  
 ANCGAGGATG TCCTTTCCCG GGAGACAAGT CGGGAAAGCC TGGCTGGACT GCCTCAGCCC 240  
 CGNGTGANTC CTGGNCTNAA GGNTTCCCCG TCCTGAGCTC GGGAGATNTT CAGAGTCACA 300  
 CTGNCGNCCT GTCTTGCCAC GGAGAGGTCA ACTTGCCACC GGNAGTNCNT GGTAN 355

SEQ ID NO:971

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01103

SEQUENCE DESCRIPTION:

GATCCAAACA ATATCTTCAA GGCATTCTTT GGCGGTCCTG GCGGCTTCAN CTTTGANGCA 60  
 TCTGGTCCAG GGAATTNNTT TTTNCAATTT GGCTAATGAA GGGCAACCAC CCAGAACCCA 120  
 GAAAATNCAG ATTCACTCAG TTTAATCTTG AATGTGGAAA CAGTTCACCT CCTCCCTTCA 180  
 TCACGTCTCC GTGTGCTTAG AGCAGTTTCG TTTTCTCAGT TGGATGCCCT GTGTCTCTGT 240  
 GAGTGGGGTG GAGCAAAGGG AACCAATGCC GAAGACCGAG GGCAGGGGAG GGGAGGCGGG 300  
 GGTNGGACAG NGAGGCAGCT TGTGAATTTT TGTTTTACTG TTAACTTTA TAAAA 355

SEQ ID NO:972

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01104

SEQUENCE DESCRIPTION:



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GATCNTAGGC TGGGGCCAAC TGGAACCATT GGCAGCTGCA CGCTCATTAC TACCCTCCGC 60  
 TCCTGCGCTC TGCCACTGTC CGGAAATTCA TGGTTGGCTA CGAAATGCTT GCTCAGGCTC 120  
 AGAGGGACCT CACCCCTGAG CAGGCTGCAG AGAGACTAAG GGCACCTCCT GAGGTTTCATT 180  
 ACCACCTGGG GCAGAAGGAC AGGGAGACAG CAACCATCGC CTGACCACGC CGACCACAGG 240  
 GCCTTGAATC CTTTTTGT TTCAACAGTC TTGCTGAATT AAGCAGAAAG GGCCTTGAAT 300  
 CCTGGCCTGG AATTGGGCA GATATAGCAT TAATAAACT GTGCATCTCA AA 352

SEQ ID NO:973  
 SEQUENCE LENGTH:358  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01105

SEQUENCE DESCRIPTION:  
 GATCAAGGGG GTTGGGAGGG GGGAAAGAGA CCAGCCTTGG TCCCTAAGCC TCCACNNAAC 60  
 GTCCTCTTAA TCCNCACCTT TTCTTACTCC CAAAAAAGAA TGAACACCCC TGACTCTGGA 120  
 GTGGTGTATA CTGCCACATC AGTGTGTTGAG TCAGTCCCA GAGGAGAGGG GAACCTCCT 180  
 CCATCTTTTT TGCAACATCT CATTCTNCC TTTTGCTGTT GCTTCCNCN TCACACACTT 240  
 GGTGTTGTTT TATCCTACAT TTGAGATTC TAATTTATG TTGAACCTGC TGCTTTTNTT 300  
 TCATATTNGA AAAGATGACA TCGGCCCAA GNGCCAAAA NTAAATGGG ANTTGAAA 358

SEQ ID NO:974  
 SEQUENCE LENGTH:354  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01106

SEQUENCE DESCRIPTION:  
 GATCTTAGGC AAAATACCAG NTGATGAAGG CATCTGATGC CTTATCTGT TCAGTCATCT 60  
 CCAAAAACAG TAAAAATAAC CACTTTTTGT TGGCAATAT GAAATTNTTA AAGGAGTAGA 120  
 ATACCAAATG ATAGAAACAG ACTGCCTGAA TTGAGAATTT TGATTTCTTA AAGTGTGTTT 180  
 CTTTCTAAAT TGCTGTTCTT TAATTTGATT AATTTAATTC ATGTATTATG ATTAATCTG 240  
 AGGCAGATGA GCTTACAAGT ATTGAAATAA TTAATAATTA ATCACAATG TGAAGGTTAT 300  
 GCATGATNGT AAAAAATACA AACATTCTAA ATTAAGGCT TTTGCAACCA CAAA 354

SEQ ID NO:975  
 SEQUENCE LENGTH:351  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01107

SEQUENCE DESCRIPTION:  
 GATCAGAGCT TGAACACAGG CTTATTTTAA AAANNANAAA TATTTTAAAC ATGGGTTTCC 60  
 TTATTGAAAA ATCAGTGTAT TAGTCATAAA ACACCATCAT TAAGAATAAT TGAACAATAA 120  
 AGTTTGCTTT CAGATGCAGT TTTCAAATTA TAATCTCATT TCAATTTATA ACGTTCTCAG 180  
 TCCTTTGTAA TAATTTTCCT TTTTCATGTA AGTTTAATTA TCTGCATTTA TCTTTTTTCC 240  
 TAGTTTTTCT AATACTAATG TTATTTCTTA AAATTCAGTG AGATATAGGG NTAAATAAAT 300  
 GCTTTGAGGA GNATGTTTAA TAGGAAATTA AAATAACTTT TTCTGGCCAA A 351

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SEQ ID NO:976

SEQUENCE LENGTH:420

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01108

SEQUENCE DESCRIPTION:

GATCCAGAAC ACTTCAAGAA CTCGTCAAAC AGCTCGATAA GCCTTTTNA CTGTNTACAT 60  
CTGTACCGGG AATAACATTC CTAGGCTGAA ATTTCCACAA AGAATAGAAC CTGTACCCAG 120  
TTCTTCAGGC TGATTTCCTT GACCTCTTGG GCATTTGTAT TTGTAGTAAA GTATTGCAGA 180  
GATTCTAAG TTTTTATAG CAGCCATCAA ATTTGGACTT TGTATTGTTT ATTCATAAAA 240  
GACACTTGGT AATAGACTTC AGTGAACCTT GTATGAATGC AGTAGTGTGC GTGCAAAATC 300  
CGCTTCCTGA GCGTAGGGTG CTGAGCTGGC GCTAGGGCTC GGTGTGTGAA ATACAGCGTA 360  
GGTCAGCCCT TGCCTNAGT GTAGAAACCC ACGGTCTTTA AGGTTCGGGC CTTGGTCCAN 420

SEQ ID NO:977

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01109

SEQUENCE DESCRIPTION:

GATCCTCATG TACTCAGAGG CACTTCCCTC CTAAGTCAAA GACCATCCTC ACTGACTATG 60  
TGCCAACGCC TCGTTTCAGG CTTGTNACTC AACAAAGGGC TTTTCCATTG ATAGAAGCAG 120  
TTTGGGATTT GTAGTTGCGA CTTCTTCGAT AGTTACCTGC ACGTCCATTG CTGGCAACTG 180  
ACTTGTCAAT AAAACCTGGC TCTTTGGTTA AGGGAGCTAC GCTGTGGTTT ATTCTTAAGT 240  
TACGTGGATA AACTAACCTC TAACAGAAAT ATACTTTGGT TAATTTTGAA ATGTGTCATT 300  
TTTAAACAAT CTTAAAAGTA ATACAGAATT GTGATTTATT AATTTTAAA 349

SEQ ID NO:978

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01110

SEQUENCE DESCRIPTION:

GATCAGAGTG GGTAAAGCTG ACCAGGAACA CCCATTTAAC CCCTTTTNC TTTTGCTTTC 60  
ATTTTTATAA AGGAAAAGAG GACCTGTCAG ATAGGCAGCC CCATGCTACG TGATTCTTTA 120  
TGTTGTGTG TTTTGTGTTG TAAATTGTAT AATTTTTAAA TATCTGAGTT TAAAAAAAAG 180  
AAAAAAGTAC AAAAAATCT TGTTATGGCC TTAAGAAGGG NNTAGTGCAT CTTTCAGGGG 240  
TCACTCTGCC ATGGGGATAA AATAGCTGTT TCACAAACAG TTTTATTTAA AAAANCAANN 300  
ACCANNAAN ANTCAAAATN TCATGNAANN TNTNAACCT TCATTTTNN 349

SEQ ID NO:979

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01111

SEQUENCE DESCRIPTION:

5 GATCACGTGG GTGTCAGTAT CTTTAACGGC CTTTATTCTT GGTGTGAGCA TTTTATTTGA 60  
 TATGCCCCACT CACCTCTGAC GAATCTGCCC GCTTTGGGCT GTGGTGCCTG TGTATCTTTG 120  
 CCGGTCTGGT CTCCAGTTGG TGGAAATNACC TTTTGTGTAC TGCCACTTCT CAGCATCTTT 180  
 NAAATTTGAC ATAATGTTGC TTCATTTTCTG TTTTAAAGT TCTGTAATTT GTTGATTGTA 240  
 TTTAACTATG TNAGTTCTGT TGTNATGTTT ACTGTATTGT AAAGCACCTC ATTCATGTNA 300  
 10 TGAGTGCTCT ATAAATCAAT AAATGATGAC TTAGAGGGCT GTAAA 345

SEQ ID NO:980

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01112

SEQUENCE DESCRIPTION:

20 GATCTGCTTG GNGTTTTCTN CCCCCACCC CAAACTTCTG TCGAGGAGCA AGGCTTGCCA 60  
 GCAAGTCAGA AGGATTTGAA CCGAGCAGCC AATCTTTCCA GCCCTCCNT ACCGACCTCT 120  
 GTCTGGAGAC GCAGCAGCCT GTGTCCTCCA GGGCCTCTGG TTTGTNGTAT TATAGTATAT 180  
 TTNGCTGTGG AAAATGTCAC GTTTAGTCAC CTTGGAGCCA CTCACCTGGT CCTGTTGTTT 240  
 TANCCCATCC CTTCTNTNGN GGGCTATTGA TTTNTTCTNA GGAGAGTACA NCGTCACTAT 300  
 25 TGTAGNGTAA CCCTGTACTC AATATTACCA TAGNCGNTG NCGN 344

SEQ ID NO:981

SEQUENCE LENGTH:357

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01115

SEQUENCE DESCRIPTION:

35 GATCAGAAAC CAACCATGAA TGAACCCCTG GCTCCTTCAC CACCCACAG ATTGGTATGA 60  
 TGCTGCCGGC ACAGNTGGGA TACACACGGC TCCCCAGGC CTGAGCTGCT TCACTAGGGA 120  
 ATCCTGCCAC CACCCTGTCT TCCTCTGCAA GTGCTCAGGG AAATGGCCTT NCCGCCGGAG 180  
 NCATNCTATC TGNCTGACAG GCTGTGACTC TTCTCTCAAC CTTGGCCTTC TCCCCTCTTC 240  
 TGAGCTAGTT GGTTGAATNN NNGTTAATGC TTAAGATTTG TTTTCTCTT TTCACAGCAA 300  
 40 CATTTTCTTG AATTTTTTTC TGCACAGCTT TTCCAAAATA AAAACCTTCC AAACAAA 357

SEQ ID NO:982

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01116

SEQUENCE DESCRIPTION:

50 GATCAGAAAT AAGATTGACT TGGGTGTTAT ATTTTCTCTC TCTCCAGACT CTAGGTATAT 60  
 TTCCAACTTT ATATATCACA GTATTTAAAA AGACATGTTT GCATTGAGAA ATTAACCCTA 120  
 AAGGGTTTTT AATAGGGTGT AGACCTCCAG TACCTTTGTA ACTAAAGTCT GTCTAGTCAT 180  
 NGTAAATATT TATCTGTCAG TTTTGACAGA TTGGGGCCAG CTTGATGTTT TAAATCTTCA 240

GCCCCGGTATG AAAACTTAAA GGTATATATT CANTTTTTTA CCATTTTATG GAAAAATATTT 300  
 AAAATCTGTT TTTACAGGGT TTTTTTTTTT TTTTTTTTTN 340

5 SEQ ID NO:983  
 SEQUENCE LENGTH:340  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01117

10 SEQUENCE DESCRIPTION:  
 GATCTGGTTC GGCTGCTGTC GGATGAGGAC GTAGCGCTCA TGGTGCGGCA GGCTCGTGGC 60  
 CTCCCCCTCC AGAAGCGCCT CTTCCCCTGG AAGCTGCACA TCACGCAGAA GGACAACCTAC 120  
 AGGGTCTACA ACACGATGCC ATGAGCTGAC GGTGTCCCTG GAGCAGTGAG GGGACACCAG 180  
 15 CAAAAACCTT CAGCTCTCAG AGGAGATTGG GACCAGGAAA ACCTGGGAGG ATGGGCAGAC 240  
 TTCTGTNTT TGAGGCTAAT GGACCCGTGG GGCTTGTAAT CTGTCTCTTT CTACTATTTA 300  
 CATCTGATTT AAATAAACCA TTCCATCTGA AAGGGGCAAA 340

20 SEQ ID NO:984  
 SEQUENCE LENGTH:339  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01118

25 SEQUENCE DESCRIPTION:  
 GATCTATGTA TTATTAGAAA AATGAAGTAT TTCTGACATG GAACAAAGAA AGTGGAAACT 60  
 GGTACTIONAAT GGGGGAAGCA AAATTAGCTG GGACTIONAAC GGACATGTTT TGTTTTGTGA 120  
 ATTCTACCTA AATGTCTCTC TATCCACAGA GAACTAGTA TTACTIONAAG ATGTGAAAGT 180  
 30 TCCTGTGGTA GCCATACCTT GAAGCACAGT GTTTGTACAT AAGTAAATAT CTTGATTCTA 240  
 AATTAAATCC AGATTATCT AATATATATN ATTTNATATC TTTGTTGTAT TAAANTGGTT 300  
 TAATANTCAC TANAANTANN ACATTTTGNA TGTTGGAAA 339

35 SEQ ID NO:985  
 SEQUENCE LENGTH:339  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01119

40 SEQUENCE DESCRIPTION:  
 GATCTCAGGA ATTTTGTAG GGGATTGAAG CCAGANCTAG TTGCGTCCCA GGGACCAAGA 60  
 GAAAGAAGCA GATATCCAAA GGGTGCAGCC CCTTTGAAA GGGGTGTTTA CGAGCAGCTG 120  
 TGAGTNAGGG GACAAGGGGC AGGTCCCAGG AGCCACACAC TCCCTTCCTC ACTTTGGACT 180  
 GCTGCTTCTN TTAGCTCCTC TGCCTCTGAA AAGCTGCTCG GGGTTTTTNA TTTATAAAAC 240  
 45 CTCTCCCCAC CCNCCACCCN CCAACTTCCT GGGTTTCTC ATTGTCTTTT TGCATCAGTA 300  
 CTTTGTATTG GGATATTAAA GAGATTAAAC TTGGGTAAA 339

50 SEQ ID NO:986  
 SEQUENCE LENGTH:339  
 SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS01120

SEQUENCE DESCRIPTION:

5 GATCCTTTCC GACACACATG TCTGAAGACT TATTTTCAAA GNCAGCACAT TTTTGGAAC 60  
 TAATCTCTTT TCCGTAATAT TTCCTTTATT TCAATGATTC TCAGAAGGCC AATTCAAACA 120  
 AACCACATT TAAGGTTCTT TAGGATTATA GAATAAATTG GCTTCTGAGT GTTAGCTCAG 180  
 TGAGCTAGGA AAGCACCAAT CGATATTTGT TTCCTTTAGG GATACTTTGT TCTCACCCT 240  
 10 GTCCCTATGT CATCAAATTT GGGAGAGATT TTTTAAATA CCACAATCAT TTGAAGAAAT 300  
 GTATAAATAA ANTCTACTTT GAGGACTTTA CCAAGTAAA 339

SEQ ID NO:987

SEQUENCE LENGTH:337

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01122

SEQUENCE DESCRIPTION:

20 GATCCAAAGT GTTAAAAATG CTGAAGTCAT GTCAAGTACT GTCTGGAGGG TTTTTTAAAG 60  
 AAAAGGCATT TGGCATTAA CTGTCTCTTG TTTTATTTT AAGTTTTTGG AAACCTTTTG 120  
 ACATAAAATG CTGCCAAGTA TCTAAGAAAT GTATATACTG ACAGAAGATA TTTGAAAGTG 180  
 GAAAATTGGA AATGAAATAT GTTGCTGGGN GCGTTAATCA CCTCCGCCA GGATTTAGTC 240  
 ACTTGAGGA CCTCTTTATA GTCTAGGATG GCAGAGCAGA AGATTTTAAT ATGCTTTTAT 300  
 25 TAAGTGATGT AAAATAAATG CTTTTTGGAT TATCAAA 337

SEQ ID NO:988

SEQUENCE LENGTH:371

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01123

SEQUENCE DESCRIPTION:

35 GATCGGCCAG CCCCCACCTA CAGCAACATG GAGGAGGTGG ATTAGCAGGT CCCTGGCTGA 60  
 TGGGGGGGAC TGGGTTTGGG ACACCCACAC AGNGGGCCAG CTCCTTGCCG CTTCTCCTTC 120  
 TCTAACCCAG AGGACACTGG CTCTGTCAGT GGGAAGCTGA GGGGTATGAT TTGGGTGTGG 180  
 AGACCTCTCA GGTGGGACT TCTGTGAGC TTGGACCCCT GACCAGTGGG CTTTGGCTTC 240  
 TCCAGCCGCC TCCAGTGCTG CGTGATTGA TTCTGTTGA CTTCAATTC TTCTGACCCG 300  
 40 CATTATAAAC ATTATAATTN NATTCTAAAA ATTGTAATTT TTTTGCAAT TTTGGAAGTG 360  
 ACTGCTGCTG N 371

SEQ ID NO:989

SEQUENCE LENGTH:334

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01126

SEQUENCE DESCRIPTION:

50 GATCTTCTTT ATATTCTACT TGAGTGCTGT CTCCATGTTG ATGTATCTNA GCAGGTTGTC 60  
 CACAGGTAGT CTAGGAGGTG GGCAACTTAG AGGTGGGGAG AGAGATTCTC TTATCCAACA 120

55

EP 0 679 716 A1

5 TCAACATCTT GGCAGATTTG ACTCTCAATC TCTTCACTAA AGTTGTAAAG NTCNNCCGGT 180  
GATAAGTACT TCAATTTCAA CTGTAGNNT GGGGAAATTT AGAATTATGC AGNTTATGGA 240  
ATTGTATATG ATGACATTTG CAATAGGTCT ATTCTCTATC ATTGTAAGAA GNTGTGTGTA 300  
CTGGTATTTG NCCCAAGTAA TAANCTAACT GAAA 334

10 SEQ ID NO:990  
SEQUENCE LENGTH:333  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01127  
SEQUENCE DESCRIPTION:  
15 GATCTGNCGT GCCCACC AAC TGGTGATGGA AGGTTACAAG TGGCACTTCA ATGAGACGGT 60  
GCTCACTGTG TGGTCGGCAC CCAACNACTG CTACCGCTGT GGGCGTGTGG CAGCCATCTT 120  
GGAGCTGGAC GCGCATCTCC AGAAAGATTT CATCATCTTT NAGGCTGCTC CCCAAGAGAC 180  
ACGGGGGCATC CCCTCCAAGA AGCCCGTGGC CGACTACTTC CTGTGACCCC GCGCGGCCCC 240  
TGCCNNTTNC AACCTTCTG GCCCTCGCAC CACTGTGACT CTGNCATCTT CCTNAGACGN 300  
20 AGGNTGGGCG TGGGNGGGNN TGTNCTGGNT NTN 333

25 SEQ ID NO:991  
SEQUENCE LENGTH:329  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01128  
SEQUENCE DESCRIPTION:  
30 GATCGGACTG AACAGGAATC CTCGGGGGGT GAACAGCCAT TCCTTCGTGA CCTGTGCACG 60  
NCTTCTGCAA CCCTGGAGCT CTGCTCGGCT AGTCTGACTC GAAAAGGGCG TGACTCAAGC 120  
TGACGGGACT CCAGTAGGGA CTTTGAGAGC ACATTTTGTA AAAATATTTA TCTAGACGCA 180  
AATGCTTATC CATGAATGTC CTCTTAGACC ATTTGGGGAT GAAGCCATCT TAATAATTAG 240  
TAATAATTAA TTAGTAATAA TTAGTAAGCA TTTTCTCAAT GCTCTGATTC CATCATGTTT 300  
35 TCTTAACATG ATAACCTAAA AAATTGAAA 329

40 SEQ ID NO:992  
SEQUENCE LENGTH:332  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01129  
SEQUENCE DESCRIPTION:  
45 GATCCTCCTC AGAAACTACC GGACTTGTTT TCTGTATTGG TGTGTTTTGT ATCTTGCTTG 60  
AACTTCCTGT TCTTCTTGGT ATACTTTAAC ATTATNATNA TGTGGGATTC CAAAAGTGGA 120  
AGAAATCAGA AGAAATCAG CTAGCTGTAT TCCTAAACAA ATTGTTTCCT AAACAAATGT 180  
GAAAATGTGA ACAGTGCTGA AAGGTTTTGT GAACTTTTTG CTATGTATAA NTGAAATTAC 240  
CATTTTGAGA ACCATGGAAC CACAGGAAAG GAAATGGTGA AAAGTCATTG TTGTCTACAC 300  
50 AAAATAAATG TATATGGAGA CCAAAGACCA AA 332

55 SEQ ID NO:993

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01130

SEQUENCE DESCRIPTION:

GATCAAGAAA TCAGGATGGC CATTATTTTA ATATCCATTC ATTCATGTT AGTGGGACTA 60  
 TTAAC TTGTC ACCAAGCAGG ACTCTATTTT AAACAAAATT TAAACTGTT TGTGGCCTAT 120  
 ATGTGTTTAA TCCTGGTTAA AGATAAAGCT TCATAATGCT GTTTTATTC AACACATTAA 180  
 CCAGCTGTAA AACACAGACC TTTATCANGA GTNGGCAAAG TTTTCCAGGN TTCATATACA 240  
 GNTAGGCTAT NNGNCATGTA TTTTGAAACG CAGTGTTNCA TNATGAAAGN GCTCTCAAGT 300  
 NGCTTNAAG NTANTTTATT AAANGGGTNN 330

SEQ ID NO:994

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01131

SEQUENCE DESCRIPTION:

GATCCGGGCC TTGCGTGCAG CCTCCCAACC ATGGGCTGGG TTTNGTGCTT ACTGTATGTT 60  
 GGCGACTTGG NNAGGGCAGG AGACGCAGCG TGGAGCCTAC CTCCCGACAT TCACGCTTCG 120  
 CCCACGNTGC TCCGACTGGC TGCAGCGGAC ACTGCCCAA GCAGAGGGGA GTCTCAGTGT 180  
 CCTGCNAGCC AGCCGAACAC TTCTCTCCGG AAGNAGGCTG GTTCGACTGT NAGGTGTTGA 240  
 CTAAC TGT TCTCTGACTC GCCCANAGGT CGTGGCTAAA GGCACCTAGG CGNCTTAAAT 300  
 TTGTAAATAA AATGTTACTA CGGTTTTAAA 330

SEQ ID NO:995

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01132

SEQUENCE DESCRIPTION:

GATCTGAATG ATGATGGAAG CATGCAGACA GCCTCTCAGT CTTACTATTT AATGTTGTAG 60  
 CTGGGAAAAA ACCCAGAGAG GTTAACTGAT ATACTGGGTT GGGACTAGGA TGTGGGTTTT 120  
 GTNACTCTNA ATCCCATGTC CTCAAAC TAC GCTGCCTTCC GAAGTCTGGC ATTTGTNAGC 180  
 TCATGCTTCC TTGTAGTCCA GCTTCTTATG TGCTGTAAAT ATTCTCCAGT ANGATTGTAA 240  
 GCCCCTTAAG GGCAGGGACG TCTTTNCATC TCTAGCACTG CTATAGTGTT CTATCCTTAG 300  
 TTATGGACCT AGATAAATAA NTNGGTGGTG GCAACAAA 338

SEQ ID NO:996

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01133

SEQUENCE DESCRIPTION:

GATCTTTATA TTTNATACTC TAAANTCGTA CAAGCCAATC TNCATTTCNA CTAGTGGAAG 60

EP 0 679 716 A1

CTGTATAGCT GGTCACTTTT CCAGGACCCT TTTATCAAGA AACAATGCAG CTTCTACATT 120  
 TGTNCTGCTT CTACACCAAA ACAGCTGGAA TGTATATNGT ATGGTTCTGG ATGCTCTTGT 180  
 ATACCTNACT CTTCACTTTCT NACCTAACCC ATGTGCTATG ATTTGAATGT TTCTCCCCTG 240  
 CAAAACATCAT GTTGAAATGT AATTGCCATG NTAACAGTAT TANTAGGTGG NNTATTTNAG 300  
 NGGTGNNTAG GGTGGGATTG GTGNTGTN 328

SEQ ID NO:997

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01134

SEQUENCE DESCRIPTION:

GATCTTGTGT CTTAGAGAAG CCCCCATACC TGGTAGAGCA TGTACCATCT TACATGCTTA 60  
 AATAACTCCA CATTTATTTG TGTATATNAC TCTGTGTTAT AAATATACAT TTGTNGGTCT 120  
 CTCTCTTGGG TATTTTGTG TCTTTGTCCT GTAACCTACCA CTGAAAGGGT GCAATACAGC 180  
 TTTCTTGAAA TGTGTATTGA ACGGATGAAT GTATAAATAA AANTTAAATT TTGTAAATTT 240  
 CTGCTTATNC TTAGAAAAAG AATCTAAATN GTGACAAATC AGAATTGAAA AANGTATTCT 300  
 AATAAAGANA AACANGCTTT TATAAA 326

SEQ ID NO:998

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01135

SEQUENCE DESCRIPTION:

GATCCCCAGT GTTGGAGGTG GGACCTAAGT GGCAGGTGTT TGGGNCATGG GGATGGATTG 60  
 CTCACAAACG GCTCGGTGGC CTCCTGCAG TAACGAGTGA GTTCACACAC TATTAGCTCA 120  
 CATGAAACCT GGTATTATTA GAGTCTGGGA CCTCCCTCCA TGCTCTCTCT CTTGCTCCTT 180  
 TCTCTACCA CATCACAGT GGCTCCCCTT GCCTTCTGCC ATGAGTGAAA GCTTCCTGAG 240  
 GGCTCACCA GACACAGATG CTGGTGTCTAT GCTTTTTGTA CAGTCTGCAG AACCCCGAGT 300  
 CAAATAAACC TCTTTTCTTT ATAAA 325

SEQ ID NO:999

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01136

SEQUENCE DESCRIPTION:

GATCACTTTC AATTGAAGTC AGGGTATTGT GCATAATAGA AAGTATTGGA CTGAGATATT 60  
 TGGTTACCAT GGAGGCCAAT GCTTTTTTCA TCTTATTTAA TGTGATGTGA CTTTTNCTT 120  
 TGTACAGAAG AGTACTGTAT TTTTGAATAG CCTACTCCCA AGTAAGAGCA AATCTGTATG 180  
 ATAACATTTT TNCCNCTGGA CATAAGACAT AACAGTAACA CGATGTACAT TTACAAGCGG 240  
 CCTTATGTAC ATTTCCCAAC ANTCTTTTAA AGGCAAAATT GTGACCATAT GTGTATAATT 300  
 AAAATCGTTT TTAATCCNTA AA 322



SEQ ID NO:1000  
 SEQUENCE LENGTH:322  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01137

SEQUENCE DESCRIPTION:

GATCTTAGAA ACCTCTGCAC AGAAGCTGCT TTGCTGGCTC TGCAAGAAAA TGGACTAGAC 60  
 GCAACTACAG TNAACAAGA GCACTTTCTA AAATCACTTA AGACTGTAAA ACCGTCGTTA 120  
 AGTTGCAAGG ACTTGGCTTT ATATGAAANC TTATTTAAGA AAGANGGATT TTCTAACGTG 180  
 GAAGGTATTT AAAANTCACC TTAAACTCTT GTNCAGTTCA CATTAAATTGA AATGTGAACT 240  
 TGCTGTCTGT TTGCAACTTC ACACTTTTAG AATTTGTGTT TATATTCCT GTANGTGAAT 300  
 AAATANANCA NNNCAGNNCA AA 322

SEQ ID NO:1001  
 SEQUENCE LENGTH:353  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01138

SEQUENCE DESCRIPTION:

GATCTCAGAA CAACCTTTCT TGTTAGTAAC ATATTTTGG CAATACATAN CAACCTGGGC 60  
 CTGGTGGATA ACCAACAAGA TGGGGAAGAA AAGNATTGAG AACTTTAAGA GTGGTGTGGA 120  
 TGCAGACTCT TCTTATTNA AAATCTTTAA GACAAAACAT GACTGAAAAG AGCACCTGTA 180  
 CTTTCAAGC CACTGGAGGG AGAAATGGAA AACATGAAAA CAGCAATCTT CTTATGCTTC 240  
 TGAATAATCA AAGACTAATT TGTGATTTTA CTTTTTAATA GATATGACTT TGCTTCCAAC 300  
 ATGGAATGAA ATAAAAAATA AATAATAAAA GATTGCCATG GANTCTTGC AAA 353

SEQ ID NO:1002  
 SEQUENCE LENGTH:320  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01139

SEQUENCE DESCRIPTION:

GATCTGACCT GGTGAGATTA TTTCTGATGA CCTCATCAA AAATAAACAA TTCCAATGT 60  
 TCCAGGTGAG GGCTTTGAAA GGCCTTCCAA ACAGCTCCGT CGCCCCTAGC AACTCCACCA 120  
 TTGGGCACTG CCATGCAGAG ACGTGGCTGG CCCAGAATGG CCTGTTGCCA TAGCAACTGG 180  
 AGGCGATGGG GCAGTNAACA GANTAACAAC AGCAACAATG CCTTTCAGG CAGCCTGCTC 240  
 CCCTGAGCGC TGGGCTGGTN ATGGCCGTTG GACTCTGTNA GATGGAGAGC CAATCTNACA 300  
 TTCANGTNTT CACCAACCNN 320

SEQ ID NO:1003  
 SEQUENCE LENGTH:318  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01140

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCCTNCNA GTTAGCCTAG TACTGCTGTA CTGGCCTGTA TGTACATGGG GTCCTTCAAC 60  
 TGAGGCCTTG CAAGTNAAGC TGGCTGTGCC ATGTTTGTAG ATGGGGCAGA GNCATCTAGA 120  
 ACAATGGGAA ACTTAGCTAT TTATATTAGG TACAGCTATT AAAACAAGGT AGGAATGAGG 180  
 CTAGACCTTT AACTTCCCTA AGGCATACTT TTCTAGCTAC CTTCTGCCCT GTGTCTGGCA 240  
 CCTACATCCT TGATGATTGT CCTCTTACCC ATTCTGGAAT TTTTTTTTN GNNGATANNT 300  
 ACAGAAAGCA TTTTAAA 318

SEQ ID NO:1004  
 SEQUENCE LENGTH:320  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01141

SEQUENCE DESCRIPTION:  
 GATCTTTCTG TCTTCTGGGT TCCATTTTNN AAATGTTTAA AAATATGTTG ACATGGTAGT 60  
 TCAGTTCTTA ACCAATGACT TGGGGATGAT GCAAACAATT ACTGTCGTTG GGATTTAGAG 120  
 TGTATTAGTC ACGCATGTAT GGGGAAGTAG TCTCGGGTAT GCTGTTGTGA AATTGAAACT 180  
 GTAAAAGTAG ATGGTTGAAA GTACTGGTAT TGTGCTCTG TATGGTAAGA NCTAATTCTG 240  
 TNNCGCCATG GTNCATAATT NCCTATNCAC CTTNCCTNCC CCTTTNCAGC CCAATTAAAG 300  
 GTTGGGGTCN TAACCTCAAA 320

SEQ ID NO:1005  
 SEQUENCE LENGTH:315  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01142

SEQUENCE DESCRIPTION:  
 GATCTGGGGG CTCGAGACTG TGAAGGCAGG GACCCTCTGA CCATCGCCAT GGAAACAGCC 60  
 AACGCTGACA TCGTACCCT GCTACGACTG GCAAAGATGA GGGAGGCTGA AGCGGCCAG 120  
 GGGCAGGCAG GAGATGAGAC GTATCTTGAC ATCTTCCGCG ACTTCTCCCT CATGGCGTCA 180  
 GACGACCCGG AGAAGCTGAG CCGTCGNAGT CATGACCTCC ACACGCTGTN ACCCGAGGCC 240  
 CACGGGGCCG CGCCTGCNTC CTTTCCCCGN NACCGNGCNN TCTGCCATTA AAGCCTCCGT 300  
 GCTTCGNTCT TCAAA 315

SEQ ID NO:1006  
 SEQUENCE LENGTH:315  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01143

SEQUENCE DESCRIPTION:  
 GATCCCTTGC NTGCCCCCTCC CTGTGGCAGG GCTAACTGCC TGGCCCTCCT GGCTCGCAGC 60  
 CAGCCAGNCC CCTGGCAGCA GGTTCCTCTC AGGGCTTGGN TCTTCAACCT GTGGCGACAG 120  
 GAGGCAGGGC AGACTGTGGA GGACAGGATG CAGGTCAGGG AGAGGGAAGG CAGGGGTGGA 180  
 CCGCCATGAG CATGAAAAGC CCGAAGCAAG TTGACTCTTN AATTGCAAC TGTTATGNTC 240  
 TGAATATGAG AACGATGTAT CAANTTGATG CANTTTNGAT GTTGTACTTA CAATAANGTT 300  
 TTAATGTGTN TTAAT 315

SEQ ID NO:1007  
 SEQUENCE LENGTH:315  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01144

SEQUENCE DESCRIPTION:

GATCTGAGGN CAGGANTTAA ACCACAGAAT GTATNTGCCT GTAAAGCACA GGGGAAGAAA 60  
 CGACTCATTA GAACTACACC TGTTACATAC CATTCCGTAA ATGNTTTAAG NGGGGAATGG 120  
 TGTGACAAAC CTTCAAAAAA NATGAACACC TTAATGTTCA GGAAGTGAAGC TAACTCCCTA 180  
 TGNTTAGGCA CAGCTTGATA CGAGCGGAGA CTTGGCAGTC AATTCCANGT CTTTATACT 240  
 NATTACCTCA TCGTNACTGT NAGTGCAACT ATAGTCTGTT GTNGGAATTT GGNCATCCCT 300  
 TAGTNTCNGA TGGTN 315

SEQ ID NO:1008  
 SEQUENCE LENGTH:314  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01145

SEQUENCE DESCRIPTION:

GATCAGAAAA AACAGAAGCC AAACTCGGGG TCATCTTTGT TTTTAAAGCT GAAGTGGGAC 60  
 TGTCTGGCAC TCTGTGTATT TATGCGTTCC AGCATCTGGA ACCTCCCATC CCTGCCCTCC 120  
 TCCTGTGTAG CTGCCACCTC CCCGCTGGGC CCAGCATGGC TCACCTGTCC CGTGGGCTGT 180  
 GTTCTTGTT GTTTTCTCT TTGCAAAGAC ATAGCTAGGA AAGCGAATGA TAAGGGAAAA 240  
 GTTCTCAGGG AATTGAAGTG TTGTTGCTAT GGTGACGTCC TTTTGCTGTG AATAAAGGTG 300  
 CTCTTTGCAG CAAA 314

SEQ ID NO:1009  
 SEQUENCE LENGTH:313  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01147

SEQUENCE DESCRIPTION:

GATCCACAAT AGTGGCATGA GGCAGGCGAC TGTNTGTNAC CTCTATGTCC GCAGAGTCCA 60  
 GCACGCTAAC AGCTGGGAGA TAAAAGCAGT GGAGAGGGCT GTTGGGGGAC ATGCCATGGA 120  
 AACTACCTAG GACCTGTTCC CTGAGTTAAC ATTCTAGCCT CATCTACTTG TTTGCCCCCT 180  
 GCAGCTCATA TACANACTGG CCCACCATTT ACGNACCATC CCCTCAAGTA ATCTTAAAGG 240  
 TTCTCAGCCC ANACANATTA ACTGTTCTGA CCCCACCTNC TTAATAAACA ATCCTGGGNT 300  
 CAGCCATNTG AAA 313

SEQ ID NO:1010  
 SEQUENCE LENGTH:311  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01148

## SEQUENCE DESCRIPTION:

GATCTGGCAG TTGAAAATTG TGGGAAAGAG AATTTGTATG GGCACGTGTAT CTATGAAATA 60  
 CCTCATAACT TACGTTTACA TGTTCCTTA ACTTTTNGTA TTTTCNTNGT ATAGCCACCT 120  
 AGAGAATTCT TCATAGATTA AGAACTACAG TTTTNACCAC TTAACATAAG TAAAACAAAG 180  
 TCCTTCATAA TTNAACCATT AGCATCTTTG GCCAAACCAA AATAAAGANA AGCATCTNCT 240  
 CCTAGTTGTG TGTGGGCAAC AGANACANGT TAAGGNAACA NAAATACTTA TATATACACN 300  
 GANCANANGT N 311

SEQ ID NO:1011

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01149

## SEQUENCE DESCRIPTION:

GATCTCCCTT GGTCTTCCAT GGGATGGTTA GTGTGGAGGG GAGATATAGA TTGTCCGGCC 60  
 GNTTGTGAT TCCATGGGAT TGATTCAGTC TTCTGGATT TTTTNTCTGT ATATTTNGGG 120  
 TACTGGAGCT TTTAAAAATG CTTGGNTTCA GGTATTTTNA TTCATGTGAA GTGTATATGA 180  
 TTCTNTTGAG ATAAGGTTTT AAGCTAAAAT GTNACTCCCT GNTTNAGCNT CTGAACCCCTG 240  
 ACAGATTNAC AGGGACTTTG CTGGTGTAGG CTTTTTAAAG GGNTTANTAN TCCACTTTGA 300  
 GCCTNAAA 308

SEQ ID NO:1012

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01150

## SEQUENCE DESCRIPTION:

GATCTGGAGT TACCTGAGGC CATAGCTGCC CTATTCACCT CTAAGGGCCC TGTTTTGAGA 60  
 TTGTTTGTTC TAATTTATTT TAAGCTAGGT AAGGCTGGGG GGAGGGTGGG GCCGTGGTCC 120  
 CCTCAGCCTC CATGGGGAGG GAAGAAGGGG GAGCTCTTTT TTNACGTTGA TTTTNTTTT 180  
 TCTACTCTGT TTTCCCTTTN TCCTTCCGNT CCATTTGGGG CCCNGGGGGT TTCAGTCATC 240  
 TCCCCATNTG GNCCCCGGA CTGTCTTNGT TGATTCTAAC TNGGNNNGGA AAGAAANTAT 300  
 TATTCAAA 308

SEQ ID NO:1013

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01151

## SEQUENCE DESCRIPTION:

GATCCATGGG GCCGCAATGA AGCTTGGAGA TACATGGGTG GCTTTGCAAA GAGTGTTC 60  
 TTTTCTGATG TATTCTTTAA AGGATTCAAA TGGGGATTG CTGCATTTGT GGTAGCTGTA 120  
 GGAGCTGAAT ATTACCTGGA GTCCCTGAAT AAAGATAAGA AGCATCACTG AAGATAATAC 180  
 CTGGAAGCAT CATAGTGGTT TCTTAACTCT CCAAATAAG ATTTCTTCTC TGTAGCCTAC 240  
 TTGTCTGGTT TATCCCTTAC AGAATATTAG TAAGATTAA TCAATTAAAA TATATATATA 300

TGCCAAA

307

SEQ ID NO:1014

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01152

SEQUENCE DESCRIPTION:

5  
 10  
 15  
 GATCGGTCCA CGAAAGTTAG CCCATATGTA TATCTTGAAT AGTATAGGGG AGGGTATTCA 60  
 TAAAGTCCTT ATGTGGTTTT AACTAAGTGA AATTATGGAC AAGAGAANN NTGTAAAAT 120  
 CGTCTTAAAG GCAAATTTAA TTTTNACTCC TGTTTATGGG ACATTCGTTT TATTAAGTGT 180  
 CAGACACAAT TTCTGTTTTT ATCTGAGAGC CAGTTTTCTT TTATTTCTAC ATCTAAAATA 240  
 AGANCATATT GTACACTATT ATATAATACA GAATTGTCTT AAACTTTAAT AAATTCGCAT 300  
 TTTAAA 306

SEQ ID NO:1015

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01153

SEQUENCE DESCRIPTION:

20  
 25  
 30  
 GATCTCAGCA GTGGGGCAGG AGGGTGCCTG ATTTCCGGGA GTCCTGACCC GAGCCTGTTG 60  
 TCAGAGTTGG GAGGGGCTCT GAGCAGTGTT GGGCAGGCCG GGTCTCCCAT CCCGAGGCCA 120  
 GCGTTCCTGT GCAGAGCCCC ATCCACTGGT TCTTGCCCTG AGCCACATAT GTCTGTNCCA 180  
 TGGGCTGAGT GCCACGACAG GCCCCTGTGA CAGCTGCTGC CCACGCATNT NGAAGCTAGG 240  
 TGGGACTCAT TCCTAATTCT GCCGTTGTAA TGAGACTTGA TAAAAACACC GCCACTTTTT 300  
 TGCAAA 306

SEQ ID NO:1016

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01154

SEQUENCE DESCRIPTION:

35  
 40  
 45  
 GATCAACAAG AAATGTTATG AAATGGCCTC CCACCTTCGG CGTTCCCAGT ACTGACCTCG 60  
 TCTGTCCCTT CCCCTTCACC GCTCCCACA GCTTTGCACC CCTTTCCTCC CCATACACAC 120  
 ACAAACCATT TTATTTTTTG GGCCATTACC CCATACCCCT TATTGCTGCC AAAACCACAT 180  
 GGGCTGGGGG CCAGGGCTGG ATGGACAGAC ACCTCCCNNT ACCNATATCC CTCCCGTGTG 240  
 TGGTTGAAA ACTTTTGTTT TTTGGGGTTT TTTTTTCTG AATAAAAAAG ATTCTACTAA 300  
 CAAA 304

SEQ ID NO:1017

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01155

SEQUENCE DESCRIPTION:

5 GATCTAAAGC AGGTNGTGTT GTTTACATGT TTCTACACAT TTCATCCTTT AAAAAGTTGT 60  
 TGAGAGAGGT TGTATTTACC TTCCCAAGGT TGGAAAGCAG GGGAATTTCC CAGTGTCCCTA 120  
 GTTTTCCACC AGAGGAATAT GTGTAAGTAG CAAAGTATTT GCTGCTTACA TATAGTGTGT 180  
 ATGTATGTAT ATATGTAAAT NGTGTGTTAA AGAGCTGATA CTGATTTTCA TATGNCAATG 240  
 10 TTAAGGCAAA GGCCTCCCTG CATTTGANGA GCAGGTNTTC ATTTATATGT ATTTTNGGGA 300  
 TAAA 304

SEQ ID NO:1018

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01156

SEQUENCE DESCRIPTION:

20 GATCAGAAAT NAAGTGCAGC AATATCATGA ATTCTNAGAA GNCTTTAAGG GAGCCAGTNA 60  
 GTCATACAGT ATCCACAGTT GANTCACTTA AAGATGTCAG TATACGAACA TTATTCACAA 120  
 TCCTTGGGCA ATCTCATTTT TTTTCCCTTC TCCCTCCTC CCCTGCCCC ATACATTTNT 180  
 ATCCTTAANG TAGTTTTGGA GGGGCAGGAT GTACTTAACA TCTCANAAGC TAGATTGGGA 240  
 ACATNTCANT ATAAGACTGA GTTTAAATTT ANGGTTAAAA TGNCATCAGA ANANTTGGGN 300  
 25 GGGN 304

SEQ ID NO:1019

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01157

SEQUENCE DESCRIPTION:

35 GATCTAATAC TACTGTCAGT TTTAATGTGC ACTGTGTTTT ATACAGTATC TTTTTTGT 60  
 CACTTNGGAA ATTTTACTA AAAATTGCAA AAAATAAAGT ATTGTGCAAA GATGTAAGGN 120  
 TTTTGANAC TTGNNGTGCA TTAATAANTA GACGATTAAN TCAAGGAAA 169

SEQ ID NO:1020

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01158

SEQUENCE DESCRIPTION:

45 GATCCTCTAC CACAGACATT AATAGCTGAG CAGGAGCCAC ATGGATTGAT TGTATCCACT 60  
 CACCATTGAC GATGGCATTG AGCGTANTAG CTTATTTCCA TCACTACGTG TTTTGGAGCT 120  
 TGCTCTTACG TTTTAAGAGG TGCCAGGGGT ACATTTTGC ACTGAAATCT AAAGATGTTT 180  
 TAAAAACAC TTTTCACAAA AATAGTCCTT TGTCATTACA TTATTTACTC ATGTGTTTGT 240  
 ACATTTTGT ATGTTAATTT ATGAATGATT TTTTCAGTAA AAAATACATA TTCAAGAACC 300  
 50 AAA 303

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# EP 0 679 716 A1

SEQ ID NO:1021

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01159

SEQUENCE DESCRIPTION:

GATCCTTNGG CTCAGAATCT CGAGAACCGC CTGCTCCTAA CAATTCAGCA AGTCAGGGGC 60  
TTCCTCTCTG TTAGTCCCCA AATCCTTACT TATTTTAAAA AGACTAGACC CTCTCTAAAG 120  
ACTGTTCCAT TTTAACATGT CCTGATTCTG CATCCGTGGG TTTGTGAAA GAGAGCTAGC 180  
TGGCGGTTAG AGCCTGGAAG AAGGAGGGAA GTGGCACCTC ACTAGCATT ATCACTTTTT 240  
TCCTTCTCTT TTTAAAAATA AAACCAGACT CTGTTCTGAA AATAAAAAAC TTGAGACTTG 300  
AAA 303

SEQ ID NO:1022

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01160

SEQUENCE DESCRIPTION:

GATCTGNCTT ATCCGAGCTT GTTATTGGGG AGCCATAAGA GTCAGTTATC CAGAACACAG 60  
TTTTGCATAA GCTTGTATAT GATTCACTAA TGCAGGTGAG AGTGTCTAGC AGTTCTTGGT 120  
AAGCTACTCT GGACATCTTT AAATTATTTA TCCTAATGGA TTCCATTCTG GTTATGTAT 180  
AATCGTTTCA AGACTTTGGG AGTCTTTTAT GAACAAATGC TCATTGCACT ATATTATATG 240  
CAAATTGTNN NGCTGCTAGG TTTTCAAAT TTGAATAATA AAGCCTTTTC ATGTTCTTTT 300  
AAA 303

SEQ ID NO:1023

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01161

SEQUENCE DESCRIPTION:

GATCAAAATC CTGTACAATA CTATAAATAT ATATTNATNT TTTCACAGTC ACCAAGTGTA 60  
TTGTAATGTA TACTTGAAAA ATGTTATAAC TTATGAAGTA AAGTTTCTNA TAGTAGTCTT 120  
TAAAAGATAT AAGACTTAAT ATGTTTTATT CAGCTTCTAT AAGTGTGACC AGTTTNNATA 180  
TTTATTTATG CTAATATTTT TAACAAGTCA TTTCAAATA TGTGTATCTC AAATCCTCCC 240  
NAAAGTGTTG TGGCCTTAAC TGTTCAATAT TGCAATAAAA NATATATNTN NNTATGTGGT 300  
AAA 303

SEQ ID NO:1024

SEQUENCE LENGTH:302

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01162

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTATGGA AAACTGGGAA TGTAATGTAG GATTCTGTCA GAGCTCCTAC AGAGCACAGT 60  
 TGCCTTTAGT TTCCTTTAAA GATGTAAAAA TATTGTATAA TACAGTTTGG TCCCTACACA 120  
 ATTGTATTGG CCAAGCTTAG TGCATTATGA TACCTTTATT TATTGTGTTT GGGCAGTATT 180  
 ACTATATATA TATAANCATA CAGTTACTGT TTTATATATT CTTAGGTCAT TCAAAGCCAT 240  
 GTATGCTGTA AATGTGCTAG TCTTTAGAAT GACACATAAT AAATAACTGA CAAGATATTA 300  
 AA 302

SEQ ID NO:1025  
 SEQUENCE LENGTH:435  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01163

SEQUENCE DESCRIPTION:  
 GATCGAGCCA TTGAAAGCTC ATTACCAGTA GGACATAATT TTTGGCTCTC CCTATTACACA 60  
 ACCAGTGCAC AGTTTGACAC AGTGGCCTCA GGTTCACAGT GCACCATGTC ACTGTGCTAT 120  
 CCTACGAAAT CATTTGTTTC TAAGTTGTGT TTATTCCTGG AGTGACATGC CACCCCGAAT 180  
 GGCTCACTTT CACTGAGGAT GCTGTCTCTT GATTTAGCTG CTGCCTCCAG CCTCTGGCTT 240  
 GAGAACTTAC TAAAGGCACT TCCTTCCTGT TAAACCCCTG TTAACCTCTC ATAAATTTGG 300  
 TGATTCTCTG CTAGGCCTAA GATTTTGAGT TAACATCTCT TGAAGCCAAA CTCCACCTTC 360  
 TGTGCTTTTT TGCTTGGGGA TAATGGAGTT TTTTCTTTTA GGAAACCAGT GCCAAGGAAT 420  
 GNCAAAGGTN TTTAA 435

SEQ ID NO:1026  
 SEQUENCE LENGTH:298  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01164

SEQUENCE DESCRIPTION:  
 GATCCACATC CTCTACAGGT CGGGGACCAA AGGCTGATTC TTGGAGATTT AACACCCAC 60  
 AGGCAATGGG TTTATAGACA TTATGTGAGT TTCCTGCTAT ATTAACATCA TCTTAGACTT 120  
 TGCAAGCAGA GAGTCGTGGA ATCAAATCTG TGCTCTTTCA TTTGCTAAGT GTATGATGTC 180  
 ACACAAGCTC CTTAACCTTC CATGTCTCCA TTTNCTTCTC TGTGAAGTAG GTATAAGAAG 240  
 TCCTATCTCA TAGGGATGCT GTGAGCATT AATAAAGGTA CACATGGAAA ACACCAAA 298

SEQ ID NO:1027  
 SEQUENCE LENGTH:328  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01165

SEQUENCE DESCRIPTION:  
 GATCCACTTT GTTGGTTGTT GTTGCAGAAG ACTGAACTGT TTTGGAATAN TTAACAATTA 60  
 CAGAAACAGT CAAGTGTTTT CCAATGTGGT TGTCCGGTTT CTATGGCCTT GCTGTGTA 120  
 TTCCCTCTTT TTGACAGTAA ACTTCTGCCT ATGGCTTACA GTTTGACATT TAATTTATTA 180  
 GCGCTGCTCT GCACCCCTNC CTTGGGAGGG AGACTTCATG TGGTTTATTG CGAGTTTTTT 240  
 TGTTTACTTT TCAGGGTTNG TACCTACAAA GGTTTTAATA ATAAAAANCA AAGNTTTTTT 300



NGGCNATTNG TCTTGTCTTN GTGGGAAA

328

5 SEQ ID NO:1028  
SEQUENCE LENGTH:297  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01167  
10 SEQUENCE DESCRIPTION:  
GATCTACAGT GCTGATGAGA AGAGAGCCCT TGCATCCTTT AACCAAGAAG AGAGACGAAA 60  
GAGAGAGAAC AAGATTCTGG CCAGTTTTCG AGAAATGGTT TACAGAAAGA CCAAAGGGAA 120  
GGATGACAAA TAAAGATTTT NTGATTGTCC AGAAGACATT TTTAACAACA AAAAAGAAAG 180  
15 TCTGGGTTC ACACATACAT AGAAAAAGAT TATTATGTTC TGAGAAAGCT TTACAGTGCT 240  
ACTGTGCCTT CTATTTAATT CTTTCAGTCC TTCAATAAAA AGCTGCTTAT TGATAAA 297

20 SEQ ID NO:1029  
SEQUENCE LENGTH:297  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01168  
SEQUENCE DESCRIPTION:  
25 GATCCTGCTG AAATACATCT GCAGCTGACA ATGAGAGAAG AAACAGAAAA TGTCATGTGA 60  
TGTCTCTCCC CAAAGTCATC ATGGGTTTGG GATTGTGTTT GAATATTTT TNCTTTTTTC 120  
CTTTCCCTC CTTTATGACC TTTGGGACAT TGGGAATACC CAGCCAACTC TCCACCATCA 180  
ATGTAATCC ATGGACATTG CTGCTCTTGG TGGTGTTATC TAATTTTGT GATAGGGAAA 240  
30 CAAATTCTTT TGAATAAAAA TAAATAACAA AACAATAAAA GTTTATTGAG CCACAAA 297

35 SEQ ID NO:1030  
SEQUENCE LENGTH:296  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01169  
SEQUENCE DESCRIPTION:  
GATCCAGAAC ATGGGAAGTT AGGGAAAATG TGTGATTTTG TGTTTTGAAT TACTGTCAGA 60  
40 ATTACATACA CAATTACAAC AAACTTTTT TAAAAGACAT TTCATTGTAC TGCAAAAATC 120  
TGAATATTTA TATTCTNGT TTTTTCTTT ATATGTTTTG CATTITTANTA TGTTGAGCCA 180  
CTGGAAAATT TGTAACAGNT TANTTTGTTA TNGGCGTTTA ANTGTGTTGT CATTGNCTCC 240  
ATTGTCTTTG TCCAGAGCCT ATTATTATGG AACCAATAAA NTTAATGGG GTCAAA 296

45 SEQ ID NO:1031  
SEQUENCE LENGTH:294  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01170  
50 SEQUENCE DESCRIPTION:  
GATCCTAGTC CCCTGCCCTC TGGCACAGCT GCTTCCTGCA AGANAGCAAG TTTTGGTCT 60

55

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CCCTGAGAAG CCATGTCCCT CGTNCTGTNT CTTGCCTGTC CCACCTGTGC CCTGCCCTCC 120  
 AGCTTGTATT TAAGTCCCTG GGCTGCCCCC TTGGGGTGCC CCCNGCTCCC AGGTTCCCCT 180  
 CTGGTGTNAT GTCAGGCATT TNGCAAGGAA AAGCCACTTG GGGAAAGATG GAAAAGGACA 240  
 AAAAAAATTA ATAAATTTCC ATTGGCCCTC GGGTGAGCTG AGGGTTTTTG CAAA 294

SEQ ID NO:1032  
 SEQUENCE LENGTH:293  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01171

SEQUENCE DESCRIPTION:  
 GATCTTCAAG AAGTGAAAGA GACCGAAAAT CAGACAGGAA AGACAAAAGG CGTTAATGGA 60  
 AGAAGCCAGG CTTTCTTAGC CATTCTTTGC AGCAGAAGAT TTCTTGATAA AAAAGGATTA 120  
 CCTTTCCTTG TAAAGAGGAT GCTGCCCTAA GANTTGCATG TNGTAAAANN NCTTTTGGGA 180  
 AAATACAGAC TGTTTGTITA CCAGACATTC TNGTACTGNT NGCATAATNN GGTAAGAGTT 240  
 ATTNATCAAA ATNATGTGAG GTTCCAAAAT ATGTAAAANT GATATNATAA AAN 293

SEQ ID NO:1033  
 SEQUENCE LENGTH:293  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01172

SEQUENCE DESCRIPTION:  
 GATCAGCGGT TCTTTTGGCA GCAAAGCCTG CATCTGTGTT GACTTGCAAG ATTTTGC GTT 60  
 TATTAGGCA AAAACTGGTC AAAATGGTTA CTACATGATT TGTTCCAGA GGTTTGAAAC 120  
 ATTCAGTGAA ACTTTTAAA ACTTTGATTG CATGATGTAT TTTTTTTNA GAAAGTTATT 180  
 GTTTGAGAAT AATGTCTTTT TATACCAGGA AAATAGTTAT CCNGAATGAC GTTGAAAACT 240  
 CCCCCTCCCC TTNATTTTNN TTTAATCANT ACATGTGAAA GTNNCCANGC AAA 293

SEQ ID NO:1034  
 SEQUENCE LENGTH:308  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01173

SEQUENCE DESCRIPTION:  
 GATCCCAATT CCACATAAGC ACTTTTGGAA GAAAACAGCC AAAGTTGGCC TAAAATTGGC 60  
 GCTGGAATTT GGNCTGGGAA AAATCTTGTG GTTATTTTCT TTAAAAAGGA ACAAACCTTT 120  
 AGTATTTAAT TAGTTGATTT ATTTAATGTA ATTNCAACA ATTAAATTAT GAATAATGCA 180  
 ATGTACAGTA GAATCACGTT TTGATTTTAT TAACACTGAC CAAGTTTAAAC TCCATATGAN 240  
 GTGTAAGCTT GATATCGTTT ATGATGTCTA TCAACTGTAC CAAAAGTAAA ACATTTAAAA 300  
 NCANNAAA 308

SEQ ID NO:1035  
 SEQUENCE LENGTH:292  
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01174

SEQUENCE DESCRIPTION:

5 GATCTCAAGT GACCCGCCTG TCTCGACCTC CCAAAGTGCT ATGATTACAG GCATGAGCCA 60  
 CTGCACCCAG CCAAACATGA CTTTTCATC CAGAGTAAAT CCAACTAACA AGAATCCACC 120  
 CTTGGAGTTC ATGTAAAAAT ACATGACACA GGGTGATGAA AGTGCTTTGA AACTAGATAC 180  
 AGGCAGTGGT TCTATAGCAT GGTGAATGTA CTCAAGGCAA CTTCTTTACT TTAAAAATCGT 240  
 10 TAATTTTATG CCATGTGAAT TGCATCTCAA TAAAAATTGT TTTCATTTTA AA 292

SEQ ID NO:1036

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01175

SEQUENCE DESCRIPTION:

20 GATCGGGAAC TCCTGCTTCT CCTTGCCTCG AAATGGACCC CAACTGCTCC TGCTCGCCTG 60  
 TTGGCTCCTG TGCTGTGCC GGCTCCTGCA AATGCAAAGA GTGCAAATGC ACCTCCTGCA 120  
 AGAAGAGCTG CTGCTCCTGC TGCCCTGTGG GTGTGCAAGT GTGCCAGGG CTGCATCTGC 180  
 AAAGGGACGT CAGACAAGTG CAGCTGCTGT GCCTGATGCA GGACAGCTGT GCTCTCAGAT 240  
 GTAAATAGAG CAACCTATAT AAACCTGGAT TTTTTTTTTT TTTTTTTNN AAAANCCCTG 300  
 25 NCCNNTTGT AAAATTTTTT TTTNNNTGAA ATANGNAANG GNAATAATTN ATCNGGNNTN 360  
 TTN 363

SEQ ID NO:1037

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS01176

SEQUENCE DESCRIPTION:

35 GATCTTGGA AGCACTAGAA ACTAAACATC TTCACCAGGT GCTGAAGAAA AGTGTCTTCG 60  
 TTTTAATTGC CAAGCAGGGA TGTGGACATT TGGATGGTGA CTTTCCTGGG TGGTTCCCCA 120  
 TAGATTACCA ATTGCCTCTA ATGGTGTCTA CACCCGTCAT ACTACCAGCT GAGATGGTGG 180  
 TGGGCATAAG GAGAATTTGT GCCTATAACC CTTAGTGTGT TCTGGTTTTT TTTCTTTTAA 240  
 TTTTAAATT GTCGTAAAT ACTCATAAAA CATACTGTCT TCACCAA 288  
 40

SEQ ID NO:1038

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS01177

SEQUENCE DESCRIPTION:

50 GATCACCTTG TAGTCTTTAA ATTCTTGGTC CCTGAGGCCA AGTCCACAAC TTGCCTTCTA 60  
 GTCACCTGCC TGCCCGCAGT GGTGGTGGAT GTGTTAGCTG GTAGATTGG AATCAGTCAC 120  
 CAGTCTTTCT GTACTGTCTT GGTTAGCTCT ATATAAGTAG GGGCAGCTTA GCCCTGAGGC 180  
 CCAGAGACCT GCTGTCCTTT TTCTCCTTGA GGGAGGAAAT AAAACTGCGG AATACAATGT 240

55

CCTTCCATAG CATGGAAGA AGAAAATAAA CATCTCCTTT CCAACAAA

288

SEQ ID NO:1039

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01178

SEQUENCE DESCRIPTION:

GATCCACCCT CCTGTAAATA TGGAACAAAT ATCTGAATGA AATCCACCCT AGGAGACGGA 60  
 GCAAACTAAA CTTGTGGTTT TNCATTTAAC TTTTGACTAC AGCATGGCCC CATGGCATCC 120  
 ACACCAAGAG GGTGTTGTGA TGAGGTGCCG GTGTGCAAAG GGAACCTTAG TTTTCCACT 180  
 GGTTCCTATC TGCTAGCCTT TTACATACAT GTGTACTATA TTTGTTTATA GACTGTAGGT 240  
 GGATATATAA TTTAAAAGCT TGATTTAATA AACATTTAAC CCCNTAAA 288

SEQ ID NO:1040

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01179

SEQUENCE DESCRIPTION:

GATCTTCAAG TATTTGCNAC TTTTCGAGTAC AGCTAATTGG ATAATCTCAA ACCCTTTAGT 60  
 GAAAATATCT TAAATGCATT GAGAATATTT CCTAATTACC TGTGTATGCT ACAGTACAGA 120  
 CATTAAATCT ATAAACATGT TCATAGGTCT TCCCCCTCGC CCCGNCCGTC TTCTAAGGGC 180  
 ATTTCCCTGTT TCTNTNAGT GAGTTCATGN ATGTTTACCG GTTCTGGCGN AANGTTTCTT 240  
 GCATNCTGAG CATAAAAATA NTAAAACCNA CTGATANTTG CTTGAAA 287

SEQ ID NO:1041

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01180

SEQUENCE DESCRIPTION:

GATCTGCACA CGCATAATAA TCAGCATTGA GGGCAACAAA ATGCCATTGT GACCTTGCCT 60  
 GGAATGTGTC CCCATCTCTA CTCTAAGAAA TGCGCAATGG ACTCTTTGGA GAAAGAAGAT 120  
 ATTTTAAAC ATTTTATAGT TGTCTGTAAA TGGTTCAGCG TGTATCAGAT GTTGTCATAG 180  
 GACTCACATT TCTCTCAGTT ATATTTAAAA CCGTTGTGTA CTTTGTACAA NGGAATACTA 240  
 GTCATACTTC TATAAACTTT NCACAATAAA ATTNTCATTC TGGGTAAA 289

SEQ ID NO:1042

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01181

SEQUENCE DESCRIPTION:

GATCGACCA CTGCACTCCA GCCTGGGNAA CACAGTGAGA CCCTCTCTCA AAATAAATAC 60

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AGNCAGGCAT AGTGGCTCAT GCCTGTAATC CCNGCATTTT GGGNGGTAGA GGTGGGTGAA 120  
 TCACCTGAGG TCAGGAGTTC ANGCCCAGCC TGGCCAACAT GGCAGAACCC CATCTCTACT 180  
 AANTATACAN AANTTAGCCA GGTGTGGTGG CCTGCACCTG TAATCCCAGC TACTCAGGAG 240  
 GCTGAGGTAG CTTGANCCCN GGAGGCANAN NTTGCAGTTA NGCCAAN 287

SEQ ID NO:1043

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01182

SEQUENCE DESCRIPTION:

GATCTCTCCT GGAGTATGAA GACCTCCAAG GACTCACTTT CCCTCCCTTC TGATGCCAGA 60  
 GCAGACCAAG CTGTCACACT CCAGTCTCAT GCTGAAGTCT CCAGCTTCTC AAGCTTAGAA 120  
 GAGTTTTTNG AAGAGTCACT TTCAGCTCAT GCAGCTCTCA CAAGTGTGAA GGGAGTGGAT 180  
 TGGGGGTGTT TTCCTTGCCA TTTTCGAAAA GAAAAAATT ACCTGGTGAT TGGTGGAAAG 240  
 ATACAACGT CAAAAATGCA TGATTGAAGC AATTAGGTT GGGAAA 286

SEQ ID NO:1044

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01183

SEQUENCE DESCRIPTION:

GATCAATAAA TNATACAAA TATATGTTA CAGTATGATT TAAAGTCTGA TTCAGACCAG 60  
 GGA CTCTATT TTAAGTTCAA CTGAAATAAC ACTGGGTTTT AATTATATCA CAGGAAAAAA 120  
 AAAGTGCATT TAAGTATTGT NATCGTGGAC TTTATAAAAG CAAAGGAAAT TGAAAGTAAC 180  
 TTTNGATTCT GTATCANGAA TCATATTNC ATACAGTCAT AACTGTCTTN CTGTGACCCT 240  
 TTCACAGGGC ACTGTAGGAT GGATTAAAGG TGGCAATTGA CTGAAA 286

SEQ ID NO:1045

SEQUENCE LENGTH:439

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01184

SEQUENCE DESCRIPTION:

GATCATACCG GTAAAGCAGG AATNACAAAG CTTGCTTTTC TGGTATGTNC TAGGTGTATT 60  
 GTGACTTTAA CTGTTATATT AATTGCCAAT ATAAGTAAAT ATAGATTATA TATGTATAGT 120  
 GTTTCACAAA GCTTAGACCT TTACCTTCCA GCCACCCAC AGTGCTTGAT ATTCAGAGT 180  
 CAGTCATTGG TTATACATGT GTAGTTCCAA AGCACATAAG CTAGAAGAAG AAATATTTCT 240  
 NGGNGCACTA CCATCTGTTT TCAACATGAA ATGCCACACA CATAGANCTC CANGCAGATC 300  
 ANTTNCATTG CACAGACTGA CTGTNGTTAA TTTNGTCACA GNGTCTATGG ACTGANTCTA 360  
 ATGCTTCCNA AANTGTTGGT TTGTTTGCAN GTTTTCGANC CGTTGTTATG GCANGANGTT 420  
 NGTTTAGTTT CNGNTTGTN 439

SEQ ID NO:1046

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01186

SEQUENCE DESCRIPTION:

GATCTGGAAG CAGTTGAAAA CGAGACAATA TAGCCGGAGA CGCCTTATAT GATGATGCAG 60  
TATCGACTAC ATTAATGAAA GTAATGCCAA ATNCAACAAG AAAGCTGAAG ATTCTATGGG 120  
AATACACAGC TGAATTAACA GATTTGGAAG AGAACANCTG NTAATCCTTC AGGACTGTTA 180  
TAGAGTTNAG ATGGGTAAAT TCTCCTANAA ATCAAGTCTT TTGAATTNC AGAATCAGAN 240  
TTAGAGCCNG CTCTACTAGA TTGNATAANT GNGGTCTAAC GGAAA 285

SEQ ID NO:1047

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01187

SEQUENCE DESCRIPTION:

GATCCGGGNG GACCCCTTTG CCCTTCCCTC GGCTCCCAGC CCTACAGACT TGCTGTGTGA 60  
CCTCAGGCCA GTGTGCCGAC CTCTCTGGGC CTCAGTTTTC CCAGCTATGA AAACAGCTAT 120  
CTCACAAAGT TGTGTGAAGC AGAAGAGAAA AGCTGGAGGA AGGCCGTGGG CCAATGGGAG 180  
AGCTCTTGTT ATTATTAATA TTGTTGCCGC TGTTGTGTTG TTGTTATTAA TTAATATTCA 240  
TATTATTAT NTAATACTTA CATAAAGATT TTGTACCAGT GGAAA 285

SEQ ID NO:1048

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01188

SEQUENCE DESCRIPTION:

GATCGAAGTG ACAAAGTGTG TTTTCANTCA CAGTGGAGGC TACATCAAGC AAGGGGAGGT 60  
CCAGCCCTCT TGCAAGTGTG GTGAGAGGCT CTACTAGCAA AGACATGGGC ACCGGAGTAG 120  
GTCCCGTGTA GCATGCGGGT GCTGTAGAGA AAATTCAGTG ACGTACATGG CTCTGGTTCT 180  
GGACACAAAA TCTGTACTGG AGAGGAAATG ACTGCTGAAA TAAGGCGATT GTATGAATAT 240  
TTAAATGCC TGGAACACTA AAGTAAAGTA ATGATATTTT AAA 283

SEQ ID NO:1049

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01189

SEQUENCE DESCRIPTION:

GATCCTCGCA GCTTCCTNCG AGCGGGGTGT CGCAGTCTTG TGCACAGAGT AAACCTTNC 60  
AGCTGCCCTT TCTGTGAATA GTGAAAGTTG GTATTTAACA TTTATNCATT TTAAAAATAT 120  
TTGGAAGGTC TGANCTTGTG AAAAGAAAGT GGTGGNCTG AGGTTGGAGG NAGCTGAATG 180  
GAATCTNACG GTTGGNAGTG GTGGAAATTG GAAGGATACC AGGAGGTATT TGGGAAGGCC 240

AATGGCGTGG CTCCTTTGAG GAAATAAAAC ACTAAGCATG AAA

283

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SEQ ID NO:1050

SEQUENCE LENGTH:281

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01191

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SEQUENCE DESCRIPTION:

GATCCTTTTC ATACCTNATT TGGAATTGCT GGATTGTAAC TTTTGGNAGA AGAACAGATT 60

AAACCTGTTA ATCCTGTCTT TTGCATGCCT GAAGAAGTGC TTCAAAGAGT GAATGTTTCTAG 120

CCTGAGCTAG TGAGCTAGAT TCATTGAATT GAAAGTTGCA TAGTATAGTT TTGCCATTTT 180

15

AACATTTCTG TATTTNAAGT GCTTATCGAA TCTAAAAGTG ACTACTGTNA ATATTNNGTA 240

TATNGTGTNA AATTAATTNN ANTAAATNAT ATAATTNTAA A 281

SEQ ID NO:1051

SEQUENCE LENGTH:226

20

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01192

SEQUENCE DESCRIPTION:

25

GATCAATGAC AGAGCCTTCT GGAGGACATT CCAAGACAGT ATACAGTCCT GTGGTCTCCT 60

TGGAAATCCG TCTAGTTAAC ATTTCAAGGG CAATACCGTG TTGGTTTTGA CTGGATATTC 120

ATATAAATT TTTAAAGAGT TGAGTGATAG AGCTAACCCT TATCTGTAAG TTTTGAATTT 180

ATATTGTTTC ATCCCATGTA CAAAACCAT TTTNCCTACA AATAAA 226

30

SEQ ID NO:1052

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01193

35

SEQUENCE DESCRIPTION:

GATCACAGCA TAAAAGAATC ATAAGATAAA ACATCAAACCT ACCCAGCAAC CTGAGAAGCA 60

CAGAGTGTTA AAGCCTCCAC CGTGTGAGAA ACTAAATTAG GGTAAGTAGC TATTGAGTAT 120

ATTGAGTACC TTCAAAGCAC TCAACTGACA GGTTTTACAG ACTGGAAATT ATAATACTTA 180

40

TGACATTTCT ACCTTTTATA TAACCAATAA TCTACCATAG AATGTAGTAT TTTTANAGCT 240

ATTAGCANGC AATATATTAN NNTANTANTG NATTAAA 277

SEQ ID NO:1053

SEQUENCE LENGTH:277

45

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01194

SEQUENCE DESCRIPTION:

50

GATCCAACCC GAATAAGATT AGAAGCTTTC CATCAGTAAA AGGATGTTTT CTTTTTTCAC 60

ACAGTAAAAA TTCTTATCAT TCAAGGATAT TGGAACCACA GGACTATTTG GATAAAAAAC 120

55

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ATTATTTGCA AATTAATGCG CATAGGCCAT CTTACTTTTA TTGCAAAATG GCATGTGCTG 180  
CCATCTATTA TTCATTTTAA AATGGTCATT TCTTATTCAG TGAGTGCTTT AGTGTTTTAA 240  
ACTATATGGA TAAGAATGCA GGTAGGATAA TATTCTN 277

SEQ ID NO:1054  
SEQUENCE LENGTH:283  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01195  
SEQUENCE DESCRIPTION:

GATCCTGAGG ATTACAGCTG TGGAATTTTT GTCCATGCTT CAAATAATTT TGAAAGAAAT 60  
TTTCCCATAT NAAAAAAGGA GAGAACACTN GCATCTGTTG AAATTTGGAA NTTCTGAAAT 120  
NATAGTATTT TAAAAAATTG CACTGAAGTG TATACACATA AAGCAGGTCT TTTATCCAGT 180  
GAACAGGATG TTTTGCTTTA GCAGCAGTGA CATAAANTTC CATGTTAGAT AAGCATNTGT 240  
TNACTTACCT NGTTATTAAT TATTNTTGG AAAAGCAGTG AAA 283

SEQ ID NO:1055  
SEQUENCE LENGTH:277  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01196

SEQUENCE DESCRIPTION:  
GATCTGTGTA TGCTGTTGGG TCGGAGTGCC AGTNACTGCT TTGGAAGTCT GNGTTCTGGG 60  
GCTGCAGAAAT GACAAACGTG TCATGGGATT AAAACCAATC AACTGTGAAT TGTGAAATTG 120  
AAGCTACTCT TTCGGTTTTA TTTTCTTTAG CATATTGAGT ATAGAAATCT GAAACTTATT 180  
TAAAATTTAT ACTGCTTTTG TTGATGGCTC ATTTTGGCTG TGTATCCTCA CTTATGTACT 240  
GATTTCTGAT AAAGGCTTGA CATTATTATA ACANAAA 277

SEQ ID NO:1056  
SEQUENCE LENGTH:103  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01197

SEQUENCE DESCRIPTION:  
GATCGACCTT NCTGTTTTN TTTTGTNTN NTTTCTNTT CCTGGCCATG AGGACAAAAA 60  
TTACTGAGTG GCCCTTAAAG AGGGAAGTTT GTTTTCAGCT GTN 103

SEQ ID NO:1057  
SEQUENCE LENGTH:291  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01198

SEQUENCE DESCRIPTION:  
GATCGACCAC ATCCTGGATG CCCTGTAGCC CCTGCCCGCA TCCTCCAGGG GGCCAGGGT 60  
GCCTGCACTT TNCTGTGGCA GGCAGATTGG GTGGTAGTGG GAGGTTGTGC ATGGAGGCCA 120



# EP 0 679 716 A1

GTNAAAGCTG ACATCTGTAA AAGGCCCTCA AGGAAGAGAA ACCAGGCCCT GCGTCAGGCA 180  
GTGTGAGTTT GCCGTTTGTC CTTAACTTTC TTTTTTTTTT TTAAAAAAN GGAAANNTTT 240  
AAAAAANCTC CCTTTAAAC CAAANCATNT TTGNNTTNN NCCAAGGGAA A 291

SEQ ID NO:1058

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01199

SEQUENCE DESCRIPTION:

GATCCCGCTC TGTNTTTTCC AGGTTTGTGC TATTCTNATT ACATTATCGA CTAGTCTGAA 60  
GCAGAGCTGA TATCTCTTTA CCTGGGGAGT CAGCTTCACC AGCCACAGCT GCTGAAAGAA 120  
TAGCTTGGAG ATTTACCCA CTGCATTCT GTNGCTCAA CTTTTGACC TTTGTGCTAT 180  
TTGAGAAATC TTTGAAATGC TGAAGGTATG ATTCTCCTC AGGGGGAACA TGCTTTGGGA 240  
AAAACGCCCA CTTAATAAAA TGTATTCNT TTCAA 276

SEQ ID NO:1059

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01200

SEQUENCE DESCRIPTION:

GATCTGTATA TGGTAAACAG GGGTTTAACC ACATGTGGTT AACATGGATT AATGTGGGAN 60  
TTTGGCTTCA AGAACACAAC CTTAGGACCT TGGNCCCCAA AAGCTGGTGG TGAAATGAGA 120  
GGNGCCAATT TAAGAAGACC CTTATGGAGA CCTGAGGCTG CAGAACTGG TAGGTTTCAT 180  
CAGGTGGTTA AAGTCGTCAA AGTTGTAAGT GACTAACCAA GATTATTTCA TTTTAAACC 240  
ACAGAATAAA AATGACACCT GAGCTTCTCT NTNAAA 276

SEQ ID NO:1060

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01201

SEQUENCE DESCRIPTION:

GATCTAGTTC CCCTGGAAAA GCTGCTGTAT TTTAATTTT TAATGGAATG TAGCTTTTNN 60  
AATCCTGTCA CTGGCATCAA CAAAAGGAAT TATACCATGA GACCTTATAG CTGTACTTAA 120  
AAGCCATTCA GTTCAGCTAT TGGGAGTTCA TGATGAATTA GCATATGCCA GAAAGGTTGC 180  
TAACCTTAAC ATCTGAGAGC AGTAACACTG ATTTTATCTG CTGTATGAGA CTTTGTGCAT 240  
TTTACTTTGA AATAAAGATT TTTTCCACA CTGAAA 276

SEQ ID NO:1061

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01202

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCTGTTT CTNGCTCTGA GTNCTAGCTA GCCAGCTGTN TTCACACTGT AAACATTTCAT 60  
 CAAGCTGTAC ATTTGGTGCA CTTTTCTGTG TCATACCACA ATAAAAAAAA NCCTATCATC 120  
 TTACAAAAAC AAGACACCCA AGTCCAGGCC CAAGGAGTAA GTACAAATAT TCCTGTTTCT 180  
 GANCCATTAC TGTAATTGGC TCTNAAGNCT TGAGGTANCC TTATAGGTTA CTCATAGGGC 240  
 ATATACAAAT AAACNGTTT GTTTTCTTTT TNCAAA 276

SEQ ID NO:1062

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01203

## SEQUENCE DESCRIPTION:

GATCTTCAAC GGATACTAGA AAATGAAAA GACTTGGAAG AAGCTGAGGA ATATAAGAA 60  
 GCACGTTTAG TACTGGATTC AGTGAAGTTA GAAGCCTGAA ACTTTTCTCG TATGGGGTGG 120  
 TTTTTCATT AAATCCTGGG GTCCATTTA CAATCCATTA TTTTGACCA CTGCTATGTG 180  
 TTCAAGTAGT ATGAGAATGT GATTGTTTT ATCTGGTTAC ATATATATTT CTTTGTCTAA 240  
 TTTAATATGT CAAATAAATG AGTTCATCTA ATAAA 275

SEQ ID NO:1063

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01204

## SEQUENCE DESCRIPTION:

GATCTCACCT CTTCTCAGG ATGGGGAGCT CACTCCGAGA ACAGGAGAAA TCAACATTGC 60  
 AGTAACAAGG TAGAATGGTT TTGAAGAAGA AAAACCTGC TTTCTGACTG ATTTGCGCTT 120  
 GAAGGAAAAA AGAACCTATT TTTGTGCATC ATTTACCAAT CATGCCACAC ANGCAATTTAT 180  
 TTTTAGTACA TTTTATTTT TCATAAAATT GCTAATGCCA AAGCTTTGTA TTAAGAGAAA 240  
 TANATANTAN AATAAAAAGT CTGTGCTGTT GAAA 274

SEQ ID NO:1064

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01205

## SEQUENCE DESCRIPTION:

GATCCAAGTT CCTAGACCTC ATGGGTGTCC CCTCCCACCA GTCACCTCCA CTGCACAACT 60  
 CGGGCGGGGG TGTGACACCT CTCCCCACC NCGACTCCG TGGTTCCGT ATCGTCAACC 120  
 CTTACGCCGC CGACCCGGA GGGGTCTGGC CTACACTGGT CTTCCCTTC CCATCAACTC 180  
 TTTCTGCTTG ACAATGTAGC AACCAGGCC CCCACCCAC GGTCTCTCCC TTTTCTCT 240  
 CCCTGACAAT AAAGTCTGAA TTTGTCTGC NAAA 274

SEQ ID NO:1065

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01207

SEQUENCE DESCRIPTION:

GATCTATCCA TCCAATGTTG TCATTATATT TGACTGTGGT TCAACAGTAT TGC GTTGTCA 60  
 GACTAGGAAA GTTAAACGAA CAAAATGGTT TTAGTTTTGC TGAAGACTGG CCTTATTAAT 120  
 GGACAGCTTT CCTAACAAGA GATTATTAAC TTTTATCAGG TGTTAACATC TGTTTCAGGA 180  
 ACATGGCAGT ATGTTTACAT GTCAGAAAGTT TTGTTTAATT CTATGGTATT TCTAAATTGA 240  
 CTTGTTTAAA TAAATTCAGC AAATGGAAA 269

SEQ ID NO:1066

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01208

SEQUENCE DESCRIPTION:

GATCTGGTTG GCATTTTCTC CCTGATGATG GGAGCGTCAT TCTTTTGTCT TCATGGTTAC 60  
 TTGTGTGATA TAACATACAT CTGTNAAAGA AAATCACTTC TTTCTAGGGG AGGGAGGTAG 120  
 AAAAGTATCT TTCAAACCTG GTTTTNNAGT TTGTNTCTTG TCTTAACTTT GTGTNGGCTC 180  
 TAACTNAAAC ATGCTGATAT GTGTTTNCAN GANTTTTGGT TTAAGGANGT ATTGTATGGA 240  
 NGTCCACANA TTGGNAGGTN GTTCATCTN 269

SEQ ID NO:1067

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01209

SEQUENCE DESCRIPTION:

GATCGATTAA GGAAGGTGGT TATGGCTGGG TGGTTCAGGG GTTTTTTTGG GTTTNTTTTT 60  
 TTTTTTCTTT GTCTTTTNA CTAAGCTG TTAAAGTTGA AGCATTCTNA GATGTTTGGG 120  
 GGGAAACATC CTCTNAAAAT GGGNCCTTGT GCTTGCNTTC TGGGGAGGCG GTCCTGAGCA 180  
 GGTGANTCAT ANGGCATTTA TGCATATGTN ATATGNGGAC TGNACCCACC TTTCCCCCN 240  
 AGCCTTTGCC TCTTGGGTTG TTGTNCTGN 269

SEQ ID NO:1068

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01210

SEQUENCE DESCRIPTION:

GATCCTCTTT GTTGTNCAA AGGACCAGTT TTCCTAGGCC AAAGAAGTCT CTNCCCCATG 60  
 TAAGNCCTAT GCCTTNAAT ATCATGCACC ATGACCCACA GCCATCTGGT TATGTCTTAT 120  
 TTTTTTCTTA AAAGATAATG TTTATNNTTA AAAAGGAAGG ANGGAGCAAG TGAAGTTTCA 180  
 TTCTGCTCCA GCGGTGGGGG ANGCGCTGA ATCCACCTGN TTCTCCTTTT GCAACCGNCA 240  
 GCANGCAGCT TTTCTCCGGG CNNCAGGN 268

SEQ ID NO:1069

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01211

SEQUENCE DESCRIPTION:

GATCTAGAAG GTGAAGAATT TTTTNATGTA TATATAGACA TATCTATATA AATNGTCTGG 60  
 CTGAGGCAGG GCCTTCANCT ATCATTGGT TAATAAATAC ATTTNAGTAT TTNCATTTC 120  
 TACTGCCTGC AGAGTTTCAG GTGCTTGNG TGTGAAAGTC CTGTAGATGT GTGCAAATTT 180  
 AACGAAATGA AATTGTATGT GTAAAANTGT ACGATTTTC ACTGTGCAAC TGAAATNAT 240  
 AAATAANANA TATTTTNTCT ATTCAAA 267

SEQ ID NO:1070

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01212

SEQUENCE DESCRIPTION:

GATCCTAGTG ATTCAGCCC ATGCATTAAG CAGGAAACAA TAATAAATTT GTAGAATTCA 60  
 TATTTTCTA AAGGGAACCT AAAAAGTCT GCTACATGTT ATGTACAAAA CTGGTTTATG 120  
 CCACATGGAC AGAGAATCAC ANGTTTGGTT TTGGTACTTT NNGTTCCTCT TTGTATTCAG 180  
 TTGTATAGAC CTNCCAAATT CAGAATGAGA NGAAAGCTGT CTGTATCAAA CCATTTANGC 240  
 ANTAATTGTT ATATNTNANA GCTAAA 266

SEQ ID NO:1071

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01213

SEQUENCE DESCRIPTION:

GATCCAAGTT ATACATGAAT AGAAAAAGAT GGTGTTAAAT TTGTGTGTAG GCTGGGAATT 60  
 CTTGCTGAAG GAATTGGAGA AAACCTGTTG CTGCAAAATT TTACATGTTT CAGATGGAAA 120  
 GGGAAAGTCTA AGCNCCTTTT AAAACAATTT TTTTGTGAT TTAATTAAGC AATTNCAGTT 180  
 ATCTGGGATT TTTGGGTCAG AATTTTAAAT TCTGTTGAT TCTCCATATT CCAGTNAATA 240  
 AAATACAAAA GCATTGTNTT TTAAAA 266

SEQ ID NO:1072

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01214

SEQUENCE DESCRIPTION:

GATCTTCAAT TCCTTGAGTC TGAGCTTGTG GGTGGAATTC TAAATTTGTA TCATAATCTG 60  
 TCTTTTGTGA AACATTTTGA AAATATGTAT ATATAATATT GTATATGCAA ATTGTGTTGT 120

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TTCACTTGTA AAGGGAAAAG GCTTATTTTN CTTTATATTT CTGATAACTT GTTTTGCATA 180  
TGACCAGCAC TGACTGAAAG GCATGTGTAG CTGCAAAACAC TGTTGCTTTT TTTGTGAAAT 240  
GNAATAAAAA GTATTTAAAT ACAA 265

SEQ ID NO:1073  
SEQUENCE LENGTH:265  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01215

SEQUENCE DESCRIPTION:

GATCGTGCCA TTGCACTCCA GCCTGGGTGA CAAGAGCAAA ACTCCATCCC CCCTGCCCAA 60  
AAAAAAATN AATTTTCACA GAAAATTAAT AGCATAGGTA TTATNATCCT CATTTCACAG 120  
AGAAAGAAAC AGCCATAGAG AAAAATGACT TGCTCACAAC ACAGGCAACT TTGACTCTAG 180  
AGATANCACT TATTACAGTA AAATCCCTCT TCAGNCACAA AATACATGAT TATCTTAAAC 240  
ACATTCTTAA TAAAANTTTA NCAAA 265

SEQ ID NO:1074  
SEQUENCE LENGTH:268  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01216

SEQUENCE DESCRIPTION:

GATCAAAGAT TGTAATAATA ATTTTGTAAG TTGTAAGCAA AAAGTTATTT TTATATTATA 60  
TACAGTCTAA TTGTTTCATCC TAATTGTTCC TGTTTTTCATC TAGTCAGAGA TTCAGTAAGT 120  
NCCTTGGAAC AATATTGAAT TCTCTTAGCT TGTGTGTGTT TCTTTAATAT TTGAACTCAA 180  
GTGGGATTAG AAGACTATNA NNNTACATGT ATGTTTCAGG ATATTTGACC TGTCATTAAT 240  
AAAAACAAAC AGTTTTACAG TGCCTAAA 268

SEQ ID NO:1075  
SEQUENCE LENGTH:305  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01217

SEQUENCE DESCRIPTION:

GATCTCCATG TAGTCCATAT GAAACCTGCA GAGTGATTTT CCAGAGTGCT CGATACTGTT 60  
AATTACATCT CCATTAGGGC TGAAAAGAAT GACCTACGTT TCTGTATACA GCTGTGTTGC 120  
TTTTGATGTT GTGTTACTGT ACACAGAAGT GTGTGCACTG AGGCTCTGCG TGTGGTCCGT 180  
ATGGAAGGCC TGGTAGCCCT GCGAGTTAAG TACTGCTTCC ATTCATTGTT TACGCTGGAA 240  
TTTTTCTCCC CATGGAATGT AAGTAAACT TAAGTGTGTTG TCATCAATAA ATGGTAATTC 300  
CTAAA 305

SEQ ID NO:1076  
SEQUENCE LENGTH:263  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01218

SEQUENCE DESCRIPTION:

5 GATCCTGTAA GTTGTCACTA AAATATGATT TAGAAATATT GGCCAAGGTG TTGCTTTAAC 60  
 TGAGGAGAAA AGAAAGCACA CTGCCTAAAT GTGTAAAAGA AAAATGCAGA GGTATTATAA 120  
 ATGTAAAGAA GTAACAATCT TTGGATTTGT CTATACATAT ATATATATAT ATATNGNTTT 180  
 GCCTTAATAT ACCCCCTTTT TTGTTTGTGA CTTTCAACTG TAATCAGTTA ATAAAGTATT 240  
 TATTCTCTGC ATTCAGGTTC AAA 263

10 SEQ ID NO:1077

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS01219

SEQUENCE DESCRIPTION:

20 GATCGACAGC AAGCAATCCT TAAGGGACTT TCAGAACTGA GACAGGGCCT TCTCCAGAAG 60  
 CAAAAGGAGT TGGAAAGTAG TCTCCTGCCT TTAGCTGAAA ATCAAGAAGA GAGTTTGGT 120  
 TCTTCATTTT AAATGTAGAA AATCAAATCC TTCACATTG ATTTGTGTCT TCCAAATTAT 180  
 AAAATGTGCT CACTGGCTCA ACTGTATTTT TCAAATAGCC TAGATTTACT TATTTTTTTA 240  
 ANNGNNCATT AAAAAGTGT ATACTATGTA GTAAAATGCT GTACTTGTNC TATACAATAA 300  
 ANCAGATACT TCTTTGTAA AAGCTTAGTA GTAAAACNCC ACCNNNNNN NNTN 354

25 SEQ ID NO:1078

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS01220

SEQUENCE DESCRIPTION:

35 GATCGTGCCT GTGAATAACC ACTGCACTCC AGCCTGGGCA ACATAGTAAG TAAGACCTTG 60  
 TCTCTTAAAA AAAATACATT CTGAAGAAAG TTCTACTTAT GANTACATTT TATTATAAAC 120  
 AAAGTGGTGA AAATTTTAGA CCAAACCATG TCTTTCTGGG TTGTAGTGAT TAAAAAATGG 180  
 TTAAGAGAAT GTTCCCTATA CAAGGCATAT GTTATTAANC ATGAAATTTA GGNTTAGTTT 240  
 TCTCTTTGAA NNTCCTTTTN 260

40 SEQ ID NO:1079

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01221

SEQUENCE DESCRIPTION:

45 GATCCCGAGA CTTGTGTTCT CTTGGCTGAA NACACTNAGG TGCTCCCATC TGTNCGTGGC 60  
 CCATGANCTG GGATGGTCCT CCAGCTGCCC ACAAGGTCCG CCCCTCTNTC TCTGCACCAC 120  
 CTGTTTGCAT AAACACACTT TGCTACAATC TTGCTAGTNC GTTTTCTTAA AAGATAATCT 180  
 ATTTACTGTA AAAATAAATT GGACTTTGCA AAAGCTTTTA GAAGGAAAAG AAAGAGGATT 240  
 AAAGAGAATT GCTGGTGAAA 260

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SEQ ID NO:1080

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01222

SEQUENCE DESCRIPTION:

GATCCAAATT TCCTTTTGAT ATTATTTTAC TTCTGCCTGA AACATTTTCT TTAACATTTT 60  
 TTATAGTGTT GTTTACTGG TGATGATTTC TTTCAGGTTT TAAGTGCCTG AACAAAATCT 120  
 TTATTTTACC TACATCTTGA AAGATAGTTT CTCTGAGTCT ACAATTCCCA GCTGACAATG 180  
 TTTATCTTCC AGTACTTTAA AGATGTTGCT TCATTATCTG CTAATTTNNT TTGTTTCCAA 240  
 TAAAATGTTT GCTGGCAAA 259

SEQ ID NO:1081

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01223

SEQUENCE DESCRIPTION:

GATCTGCGGT GAAGCCAAGC CGCAAGGTTA CAAGGCATCC TCACCAGGGA TACCCGCCTG 60  
 CTGCTCCCAG GTGGCCTGCG GCATNGCTAT GCTCAAGGAC CTGGAAACCC ATGCTTCGAG 120  
 ACAACGTGAC TTTAATGGGA GGGTGGGTGG GCCGCAGACA GGCTGGCAGG GCAGGTGCTG 180  
 CGTGGGGCCC TCTCCAGCCC GTCCTACCTT GGGCTCACAT GGGGCCTGTG CCCACCCCTC 240  
 TTGAGTGTCT TGGGGACAGC TCTTTCCACC CCTGGAAGAT GGAAATAAAC CTGCGTGTGG 300  
 GTGGAGTGTT AGGAAA 316

SEQ ID NO:1082

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01224

SEQUENCE DESCRIPTION:

GATCCAAATG GATTACCAGT GTGCTACAGA CTTCTTATTA TAGAACAGCA TTCTATTCTA 60  
 CATCAAAAAT AGTTTGTA AGTTAGTTT GGTTACCATC TAAAATATTT TTAATGTTT 120  
 TTTACATAAA AATTTATGTT GTGTTTAAA ATCCTTAGGG GCTTTATCTA TTTTCTAAG 180  
 TCAGTTAACT GTACTTCTAA AAAAAGTATT TTGTATCTAC TTTTGTAAC TCGTCAGAAT 240  
 AAAATATATT GAANGCAA 259

SEQ ID NO:1083

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01225

SEQUENCE DESCRIPTION:

GATCGCTTCA CATNTATAAA AAAAATAANA ATACCCGGGC AAGCTTTCTT TGAAGNTGCT 60  
 ACAGCATTA ATATCGAGAA TTTTGGGTGG GAGAGAGCAG TTCAATTTT TTTACCAGCT 120

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GAAGTTCATT TATGATACAA AAGAGATGAA ATGGAAGTGG CAATATAAGG GGATGAGGAG 180  
GCATGCTGGC AACCCCTTCTT TTAAGATGTG CTCAATTGTG ATAANTGGTG TTTTCATGNAA 240  
TAATCATCTT GGAGGAAA 258

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SEQ ID NO:1084  
SEQUENCE LENGTH:342  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS01226

SEQUENCE DESCRIPTION:

15

GATCGCCGCC CAGGGTTTCA CGGTCGCAGC CATCTTGCTG ACGTCTGNCT GNCACTGCTA 60  
TGAAGTCTCG ACCCTAAGCC CAGGGTCTGG CCTTGAAAGC TCCGCAGAAA TGATTCCANA 120  
ACCCAGGGAG CAACCACTGG CCCTACCGTG GGACTTACTC CCTCCTCTCC TTTGAGAGGC 180  
CCATGTGTCG CTGGGGAGGA AGTGACCNTT TGTGTAAGT TAACCGAAAG TTTTTTCAAA 240  
AATCCTAGAT GCTGTTGTTT GAATGTTACA TACTTCTATT NNGGCCACAT CTCCCNCTCA 300  
CTCCCNCTGCT TAATAAACTC TAAAAATCCA CTTGTATTTA AA 342

20

SEQ ID NO:1085  
SEQUENCE LENGTH:260  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

25

CLONE:HUMGS01227

SEQUENCE DESCRIPTION:

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GATCTAAGAA GANACTAGCC TTGTGGAGTA TATAGATGCT TTTCATTATA CACACAAAAA 60  
TCCCTGAGGG ACATTTTGAG GCATGAATAT AAAACATTTT TATTTTCAGTA ACTTTTCCCC 120  
CTGTGTAAGT TACTATGGTT TGTGGTACAA CTTCACTCTA TAGAATATTA AGTGGAAGTG 180  
GGTGAATTCT ACTTTTATG TTGGAGTGGA CCAATGTCTA TCAAGAGTGA CAAATAAAGT 240  
TAATGATGAT TCCAAATAAA 260

35

SEQ ID NO:1086  
SEQUENCE LENGTH:256  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01228

40

SEQUENCE DESCRIPTION:

GATCCTTAAT GTTTTGATTN TTGTTTTCTG AAATTGGATT TTATTTTATT TTATCTTATA 60  
ATNNCAGTTC ATCTAAATTG TGTGTTCTGT ACATGTGATG TTTGACTGTA CCATTGACTG 120  
TTATGGAAGT TCAGCGTTGT ATGTCTCTCT CTACACTGTG GTGCACTTAA CTTGTGGNNT 180  
TTTTATACTA AAAATGTAGA NTAAAGACTA TTTTGAAGAT TTGANTAAAG TGNNGNNGTT 240  
TGCATTACAC CTCAAA 256

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SEQ ID NO:1087  
SEQUENCE LENGTH:254  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS01229

SEQUENCE DESCRIPTION:

GATCTTTAAA CTCTGGCTTC TTCCTCCTCA ATCTTGACAG AAAAAGGGTG CAGACGTCTG 60  
 GTTCAAAGAG TTGGATATCA ACACTGATGG TGCAGTTAAC TTCCAGGAGT TCCTCATTCT 120  
 GGTGATAAAG ATGGGCGTGG CAGCCCACAA AAAAAGCCAT GAAGAANGCC ACAAAGAGTA 180  
 GCTGAGTTAC TGGGCCCAGA GGCTGGGCCC CTGGACATGT ACCTGCAGAN TAATAAAGTC 240  
 ATCAATACCT CAAA 254

SEQ ID NO:1088

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01230

SEQUENCE DESCRIPTION:

GATCCATCCC ATTCACCCAG TGACTTCTTT TTGCCCAGGC CGGGACTTTT TGCATCAGTN 60  
 ACGTTAACCA GATGACTTTG CCTGTAACCA AACCTCATGC ATCCACGTTT GCGTCTGGGG 120  
 AGGAATAAAA AGACATCGTT CCCGCTTCTN CGTTTTGTNA TTCCTACTGC CGCCATAGGA 180  
 ATTATTTTCT TGGCTGANCG TTACCAGCAC CCCGAGANCA CATTTTGATN GANTCAGAGT 240  
 AGAGGNCATG GCTGTNTTCT NAAAANGCCN CGCCATGNAA NTGCCAATCC CCTTTN 297

SEQ ID NO:1089

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01231

SEQUENCE DESCRIPTION:

GATCGCATTT TTGTAAAAGA ACCATGTGTG TTTATATGTG TTTATATATA TACTTGTTGA 60  
 TGCAAAGGTA AAAGTCTGAA AGGATATATG CTAAGTGTTC ACAATGATAA CCCCCAGGA 120  
 ATGGGATTGG AGGGGAGGGG GCTTCTGTGT TTGTNATGTA TGCTGGGTGG GANNTTGTGC 180  
 TTTTATTTCT ATATTGTTG AATTTTTTTA CAGTATGTAT TATTTTGTGA ATAAAAATTT 240  
 TAAAAAATTC AAA 253

SEQ ID NO:1090

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01232

SEQUENCE DESCRIPTION:

GATCTGCCTT GAAATTAAAA AATCTAAATA GCTCTTAGTT GAACAGGGGA GATATAAACA 60  
 AAGTTTGCAA AATTCCTAAA ACACGATGAT AATAAACATC ATACATCAGA NTTTTGAGAT 120  
 ATAATTAAG CAGTACTTAG AAGAAAATGT ATAGCCTTAA ATATTTAACA TCAGTAAAN 180  
 TGANAGGNTG AAAATTGGGA TTAAATTCC CAACTCAAAG AGCTAGAAAN NGANTTACAA 240  
 AGCAAGNNGA AA 252

SEQ ID NO:1091

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01233

SEQUENCE DESCRIPTION:

GATCTCATGG GCTTTCCTGG AGGAAAGTTT TTTTGTTCG TTTTTTTTA AGACTTGAAA 60  
 CTTGTAAC TG AGATGCTGTA GTTTTTTGCC ATCTGTAGTG ATGTAAAGAT TTAAACCTGA 120  
 GAGACTTTN CTTTGTTAGA TTATGAGAAG NACTAGATGC TTTAGGTTTC ATTTCCCTT 180  
 AATTGCNATT CTTGTGCGCT NGTTGGGNGG GAACTGTTAT TTTCCNCAAT AAAAAGTAAG 240  
 TCTTATCGAA A 251

SEQ ID NO:1092

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01235

SEQUENCE DESCRIPTION:

GATCATTAAA ATCAACGTTA TCTAAGACAG CTGTATCACA TTTTGGGAT ACATCATGGT 60  
 ACAGTCAGAA GCATATAAAA TTATGGTTCT GCTTGTGAGN CNCATACAGA ATCCAATACA 120  
 TTTTGACAAA CTGCCCATTG CTGCAAGTTA ATGCCCTTTT TGAAGCTTCA TTTCTCTTG 180  
 TAAAGTACAG ATAGGAATCA TTATTTTGTG GAGTTGCTGT AAAGATTAAN TAAAGGTGAA 240  
 TGAATAATAA 250

SEQ ID NO:1093

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01236

SEQUENCE DESCRIPTION:

GATCCCAACA AAGATACAAG TGAAAACGCA GAAGGTCAAA GNGATGAGAA CAAGGACGAC 60  
 TATACAATCC CAGATGAGTA TAGAATTGGA CCATATCAGC CCAATGTTCC TGTTGGTATA 120  
 GACTATGTGA TACCTAAAAC AGGGTTTTAC TGTAAGCTGT GTTCACTCTT TTATACANNN 180  
 CNAAGAAGTT GCAAAGANTA CTCATTGCAG CAGCCTTCCT CATTATCAGA AATTAAAGAA 240  
 ATTTCTGN 248

SEQ ID NO:1094

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01237

SEQUENCE DESCRIPTION:

GATCACTGNC AAAGTGGGAG CACTAAGGGG TGGGTGGGGA AGTGAAATGT TAGGCGATGA 60  
 ATTCTTGAGC ACCTTGTTTT TNTNCCAAGG TTCGTAGCTC CTCTNTGCC TTCCAAGCCT 120  
 GTAACCTCGG AGGACTATCT TTTGTCTTN ATCCTTTGTN TTGTTTGAGT GGGNCAGCCC 180  
 CAGAGGAACT GATAAGCAAA TGGCAAGTTT TTAAAGGAAG AGTGGAAAGN NCTGCAANTA 240

AAANNCCN

248

5 SEQ ID NO:1095  
 SEQUENCE LENGTH:246  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01238  
 10 SEQUENCE DESCRIPTION:  
 GATCTCCATG CGGTCCCTGG AAGTACCCAT TGAAACATGC GTATTTGTGT ATAGCAGAAC 60  
 TCTGAAATAA TATTCTGACA GCAGTTATCT CTGAGGAATT GGGTTATAGG TGATTTTCCC 120  
 TTTCCGCATG ATAAATTTAT GTAATATTTG ACTGACTTGA CCGTAAGTAT GTTACTTGTA 180  
 15 TAATAAAAGG AAAAAAGGTA CTTCTATTTT GAAAAATAA AAATAAAAGC CTTTGGGTTC 240  
 TTGAAA 246

20 SEQ ID NO:1096  
 SEQUENCE LENGTH:315  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01239  
 SEQUENCE DESCRIPTION:  
 25 GATCCTGTCA GGGNGTCCCC CATGCCTGGA AGAGGAGCTG GTGGCTGCCA GCCCTNGGGC 60  
 CCGGCACAGG CCTGGNCCTT CCCCTTCCCT CAAGCCAGGG CTCCTCCTCC TGTCGTGGGC 120  
 TCATTGTGAC CACTGGCCTC TCTACAGCAC GGCCTGTGGC CTGTCAAGG CAGAACCACG 180  
 ACCCTTGACT CCCGGGTNNN NNNGTGGCCA AGGATGCTGG AGCTGAATCA GACGCTGACA 240  
 GTTCTTCAGG CATTCTATT TCACAATCGA ATTGAACACA TTGGNCAAAT AAAGTTGAAA 300  
 30 TTTTACCACN TGAAA 315

35 SEQ ID NO:1097  
 SEQUENCE LENGTH:245  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01240  
 SEQUENCE DESCRIPTION:  
 40 GATCCCGGGA GCCTTGCCGC ACTGCCTTGT GGGTGGCTTG GCGCTCGTAA TTGCTTCCTG 60  
 TGAACGCCTC CCAAGGACGA GCCCAGTGTA GTTGTGTGGC GTGAACTCTG CCCGTGTGTT 120  
 CTCAAATTCC CCAGCTTGGG AAATAGCCCT TGGTGTGGGT TTTATCTCTG GTTTGTGTTT 180  
 TCCGTGGTGG AATTGACCGA AAGCTCTATG TTTTCGTTAA TAAAGGGCAA CTTAGCCAAG 240  
 TTAAA 245

45 SEQ ID NO:1098  
 SEQUENCE LENGTH:245  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 50 CLONE:HUMGS01241  
 SEQUENCE DESCRIPTION:

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GATCTGCAGC AGCCGAAAAT GCGTTNTGGT AAACCTGGCC TCAAATTCAT ACTACCATAA 60  
CTGTTTTTAT ATATTGCCAC TAATTTTGAC TGGATTTAAT AGCACTTTAT TGTACANCTA 120  
CAAAAAAAAA TATATNCCTA GAATNGTNNC CAGTGTAATT CCTCTAATGT CCTGGTGCCT 180  
TTTCATATAT TTCCAGNATT TTNATACTAT ATNGGTATTT CCTTTGTATA AATNGATNGA 240  
TNAAN 245

SEQ ID NO:1099

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01242

SEQUENCE DESCRIPTION:

GATCTTAGGC TTTTCACTTT TTTTGTITTTG TTTTGTITTTT GAAAGAAAGA AAAAAATACA 60  
ATTAACAAGC CTCTTTTGTA AATGGGTTTC CTTTCTATGT ATAAAATCGT GGTGGTCCCT 120  
TGTTTTTACA TGTCATGCT GTGTAATTTT GAGATGTTAC TGAGATATGT TCTGAACATA 180  
ATGTGCATTT TTNCTGTAC AGATGAAATG GGAGANTTTA ATAAAGAGTT TGCAGGTTTT 240  
TNCTTGTTAA A 251

SEQ ID NO:1100

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01243

SEQUENCE DESCRIPTION:

GATCCAGCCC TGAGCATCAC CCAAGTGCCT GATGCCTCAG GTGACAGAAG GCAGGACGTT 60  
CCATGCCGAG GCTGCCCCCT CACCCAGAAG TCTGAGCCCA GCCTCAGGAG GGGCCAAGAA 120  
CCAGGGGGCC ATCAAAAGCA TCGGGATTG GCATTGGTTC CAGATGAGCT TTAAAGCAA 180  
ACATAGCAGT TGTTTGCCAT TTCTGCACT CAGACCTGTG TAATATATGC TCCTGGAAAC 240  
CATCAAA 247

SEQ ID NO:1101

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01244

SEQUENCE DESCRIPTION:

GATCTTCCCT AAAGAGCAGN GGACCANATA NGAAGAGGAA AATTTCTACC TTGAACCGTA 60  
TCTGAAAGAG GTTATTCGGG AAAGAAAAGA AAGAGAAGAA TGGGCAAAGA AGTAATCATG 120  
TAGTTGAAGT CTGTGGATGC AGCTGTTATG AAGATGGTTA AACTTGAANC AAACAATTTT 180  
AAGANTTATT TNGTCTGAAN GATGTTTTAC TTAAATAAA TGTCTCNTTG NAATGGCTGG 240  
AGGTTTTTGG GNGCCAAACC NTTAAA 266

SEQ ID NO:1102

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01245

SEQUENCE DESCRIPTION:

5 GATCCCAGGT CCCAAGGAGT GACAGGGGCT TCCTCCCACC TTCTGTCCTT GTCCAGTNAT 60  
 GTAAATAATG TGCTTTTCCT CTCCCCGAGT CTTTTTTTTT AAAACCTACC GTGGTTCCTN 120  
 AGCTAACTGC ATTCCCTACC CAGGCAGAGA CTGTCCTATG CCTCGNGCTT CCAAACGAGA 180  
 CTCAGACCGC GACANAGCCA CCGTATTTAT GGATTGCCAA ANTAANTAAN GCCCAAANCC 240  
 10 ATCGGTCTCT GTGAAA 256

SEQ ID NO:1103

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01246

SEQUENCE DESCRIPTION:

20 GATCCTGGTG CTGGACAACG CTGCCATTGT CTGCAACTTT GGCAGTGAGC TCAGCCTGGT 60  
 GTATGTGCCC TCTGTGCTGG AGAAGCTGGA CTGAGCGCAG GGCCTCCTTG CCCAGGCAGG 120  
 AGGCTGGGGT GCTGTGTGGG GGCCAATGCA CTGAACCTGG ACTTGGGGGA AAGAGCCGAG 180  
 TATCTTCAG CCGCTGCCTC CTGACTGTAA TAATATTAAT CTTTTTTAAA AAACCATAAA 240

SEQ ID NO:1104

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01247

SEQUENCE DESCRIPTION:

30 GATCTGGGCA GTNAGATAGT GCTCTATGCC TAAGGTGAAG CCACACTAGG NTGAAGCCTC 60  
 ACTTCCCTGT TTAAGCAATG CAGTGCCTGC TGCCCGTGTG CANGAAGGTA CAGCCATTCA 120  
 GATAAGTGGA ACTATTGAGT TACATAAAGA AAGTAGATTT GCANTNNTCN GGCAGACGTT 180  
 35 TATACANCAC CACGGTGCTT TTATACATTG TNCTNATTTT AATAAACTG ANGTCTATG 240  
 TGAAA 245

SEQ ID NO:1105

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01248

SEQUENCE DESCRIPTION:

45 GATCTGGCTT CCATTTGGCC CCCTCATTTT CCAAATGTTT AAATGTATTG GATTGGATT 60  
 CTCAATGTAT AAGTTGCCTT ATCTGTTAAT GTCTATCTTC TGTCTCTTTA ATTTGTATA 120  
 TCTGCTGTTT TGCTTTTGGA TACATTTTCT AATTAGAAGT CACATGATAA ATATAATCAG 180  
 TATAGTAATA ATACCATAAT GTGCACATAC TCAATAAATA AATGACTGCA TTGTTGTAAT 240

SEQ ID NO:1106

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01249

SEQUENCE DESCRIPTION:

GATCCATTTN TCCNTGTAAC TNGGAGAAAAG GCCAGTCCCT GTAACGGGGC AGCCCTCTCT 60  
TTCCCTCGGT CAGCTCGTGT NAATCCTGGN ACCTCTTCG GTCGGCTCTG CCCGCTGTTC 120  
TGGGGTCGAC TGCCACGACT TTNNATTCAA GAAGCTTCCT CCAGGCGGNA GCGGCTATTT 180  
TCCCTAAATN AGAATTGTTA CATTGCAAAT NGTTGAATAA AATATTNGC GGTCTTAAA 240

SEQ ID NO:1107

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01250

SEQUENCE DESCRIPTION:

GATCTGAAGA AATGATGGAA TGGGGAGTGT AGAGAAATGA GAGTCTGTAT GATTCTGGAA 60  
CAGAGACATC AGAAGAAAAG ACTGGTGAAG AGATGTATCT TTGTATATTA ATAGCTGTAA 120  
TGTAAGTTCC TGATGCTTGA CTAATTGAGG TGTTAATTCT GACTTGAGAA TCTTTTTCAT 180  
GAATGATTTT AAAGAAAAAT TTGGATTTTA AAGGTATTAA AATATTTTNG TTTTGTAAA 239

SEQ ID NO:1108

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01251

SEQUENCE DESCRIPTION:

GATCCGCAGT CGAAAAAGAA CAAGCCACAG AAACGGGCTC GTCGTGCCAG GACACAGCAG 60  
TGTCTTTCAA AAAATCAAAA CCAGAAGNTT TATCANCAGC AGGAAGNATG TGGGCTCTGT 120  
CAAGTTCACC GTCACCATCA AGCCACTGCT GTGGAAGAGT TTGNCAACAG GNCAGTGTCA 180  
CAGCACANCT TCAGANGCAG CATCCGNGTG TCGTCCAACA GANGNCCTNG TCCGGTCAN 239

SEQ ID NO:1109

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01252

SEQUENCE DESCRIPTION:

GATCTATGTC CGGTGTGGGT TTTTGTCTC TCGAGTTTTG TCTCTAATAA AGGCCTTTTT 60  
TGTTTCAAAT TACATACGCT TTTTACTGCA CAATTTTTGT ATTGACCTTA TTTCAACTGA 120  
AGCGATTATT TCCAGCAGGT TTAATTTCGA CAATAAGATA TATTTNAATA GTTTTACCTT 180  
TCGCTAGAAT TTTGTATTGT TAAAAACAGT AAATGAATAA NTTTGCTGAT GATTCAAA 238

SEQ ID NO:1110

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01253

SEQUENCE DESCRIPTION:

GATCAATGAA ATGCACATAA ATNAACTGGT TCCATCAAGA CTGTGCACCC AGGCCTTACA 60  
GTCCAACCTT TTTCTGTGTC TGGCTAATAT TTAAACTAG AAAAATATT CCTAATCAAC 120  
ATGGAGTGGA GAGTTTATTC ACTGTCTTAT CTGCAGAAAT TTGCTGTCAA TATATAACCC 180  
GCCTGCAGTG GAAAGTGTAT AGTGTTTTGT AATAAATGGC CTGATGCTAA TGTGTAAA 238

SEQ ID NO:1111

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01254

SEQUENCE DESCRIPTION:

GATCTACCGG GGGCTATTAG TTTCAATGTA GTGATGAACA CAAACTATAT TTTGAGTTCT 60  
CTGCAGCAAG TGGAATGTGG TATGAAAATA TCTGATATTT ACAAAGATGA TACTGCTAAG 120  
TCAGAGTCAC GTTTATTGCT AATATGATGG TGGAGTGTG TCTTCATTCA TAATGAAGGG 180  
AAATGTTATT TTAAATAGNG GTTAGTGAAA TAAAANTAAN CCTATTTTCT AANCAAA 237

SEQ ID NO:1112

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01256

SEQUENCE DESCRIPTION:

GATCTGGAGC ATTTGAGCAA GTTTATAGAA GAACATGCCA CAAACTGAG CAGGACCAAG 60  
GAAGAGCTTT GAAGGCCTGA GGTCTGCGNA AGGTGGGAGG AGGCAGACGC CCTGCGTGGC 120  
CCATGGTCGG GCGCTCCACG CCGAGGCCGG CAACAAACGA CAGTATCTCG GATTCCTNTT 180  
TTTTTTTTTT AAATTTTNA AACTNNGGGG TTNCACTNCA NGNTCTGAAT ACTGANTANC 240  
CATGAATNCC TGAATAGTTT AGNCCAGN 268

SEQ ID NO:1113

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01257

SEQUENCE DESCRIPTION:

GATCAGCGCT GAGGACGGNC TCAAGCATGA GTATTTCCGC NAGACCCGNN NCCCCATCGA 60  
CCCCTCCATG TTCCCACGT GGCCCGCCAA GAGCGAGCAG CAGCGTGTGA AGCGGGGCAC 120  
CANCCCGAGG CCCCTGAGGG AGGCCTGGGC TACAGCCAGC TGGGTGACGA CGACCTGAAG 180  
NAGACGGGCT TCCACCTTAC CACCACGAAC CAGGGGCCCTC TNCNGCGGGN CCNGGN 236

SEQ ID NO:1114

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01258

SEQUENCE DESCRIPTION:

GATCTGTTGA CTTCCCTGGG TAGGACACTG CCACCTCTGG GCTCAGGTCC TNATGCCTCC 60  
AAATGGCATC TAGAGTTTGA GCAGCCTTCT TGGCTGCAAG GCAGGCCTAG CCTGTGGCAG 120  
CGGGCTAGGG CCCGCAGAGC ATTTGGTGCC CCTCCATGTT GCAATGCAAA CACCTTCACC 180  
ACTGGGGCAG TGGGGAGAGA TGGCTATATT AATAAAATAA CGTGTGTCTT TCAAA 235

SEQ ID NO:1115

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01259

SEQUENCE DESCRIPTION:

GATCATNATT TTTNCTGCGT AGTTGACAGA CTTAGCATAT TAGTTTTTNN TACTCCTACA 60  
AGTGTA AATT GAAAAATCTT TATATTAAAA AAGTAACTG TTATGAAGCT GCTATGTACT 120  
AATAACTT TGCTTGCCAA AGTGTTTGGN NTTTNTGTN GTTTGTTTGT TTGTTTGT 180  
TTGTTTCATG AACAACAGTN TCTAGAAACC CATTTTGAAA GNGGAAANTT ATTAN 235

SEQ ID NO:1116

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01260

SEQUENCE DESCRIPTION:

GATCACAATT NGCTTCATGA ATCAAGGTGT GGAAATGGTT ATATATGGAT TGATTTAGAN 60  
AATGGTTACC AGTACAGTCA AAAAAGAGAA AATGAAAAAA ATACAACTAA AAGGAAGAAA 120  
CACAACTCA AAGATTTTTC AGTGATGAGA ATCCACATTT GTATTTCAAG ATAATGTAGT 180  
TTAAAAAAA AAAANGGNA AAACNTTGTT GNAANTNCCN CCTTTNCCTC NGGN 234

SEQ ID NO:1117

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01261

SEQUENCE DESCRIPTION:

GATCCCCCGN TCAGCNCNA AAGTGCTGGG ATACAGGCAT GAGCACCACG TCCGNCTAGA 60  
CTTTACCTTT CTAAAGAAAT TGTTTACTGG ATTTATAAGA AGTTAATTTT TGA AAATNAC 120  
ATATTTTGT NTGATAGAAA GAATGGAGCA AGTNGTGCCT ATTTCTCCA AGTCAGATAA 180  
GGTTTCTAAA ATAAATAAAT TTCTAGCATA TAAAGGGTAG AGATAAACTC NNNN 234

SEQ ID NO:1118

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



CLONE:HUMGS01262

SEQUENCE DESCRIPTION:

5 GATCACAGGT CTTCCCTGTG AACTTTGGTT TCTTCTATA AATGTGTGTG GTTTTCAGCG 60  
CTCAACTCCT GTCTTCAAAT GGTAGTAAGT NCTACTTCTA CTTCTGTCAT TCAGAACATT 120  
TTATGTCAAA TGATGTAATG CAGAAATNCT TGTGCATATT TGTAAGTAA GGAAGCTTTT 180  
TAGATTTATT TNNGTTTTTA ATAAAATTCA GATTCCTATT CTAACTGGT AAA 233

10 SEQ ID NO:1119

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS01263

SEQUENCE DESCRIPTION:

20 GATCTNCTAT GCAGTTCTGC CATGCNTCCT GTTGGTCTCT CTGTGTTCTT TGTTACTTGG 60  
GTGCAATAGC AACTTCCCTA CCCCGTGCAT TCCATCTTN ATGTTGTGTA AAGTTCTTCA 120  
CTTTTTNNTC TGAGGGCTGG GGGTTGGGGG AGTCAGCATG ATTATATTTN AATGTAGAAA 180  
ATGTGACATC TGGATATAAA ATGAAAATAA ATGTTAAATT AAATGGAAAA 230

25 SEQ ID NO:1120

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01264

SEQUENCE DESCRIPTION:

30 GATCTAAGTT AGTCCAAAAG CTAAATGATT TAAAGTCAAG TTGTAATGCT AGGCATAAGC 60  
ACTCTATAAT ACATTAAATT ATAGGCCGAG CAATTAGGGA ATGTTTCTGA AACATTAAAC 120  
TTGTATNTAT GTCATAAAN TTCTAACACA AACTTAAAAA ATGTGTCTCA TACATATGCT 180  
GTACTAGGCT TCATCATGCA TTNGTAAATT TGTGTATGAT TTGCNNNTNT GNNNGNN 237

35 SEQ ID NO:1121

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01265

40 SEQUENCE DESCRIPTION:

45 GATCTGGCCA GTTGTACTTT TAGCTCCCAG AGGGAGAGTT GGTGGTATTA TGAGTTGAGT 60  
AAAAACCATC CAGGGGAACT TGAGGGAGCA GTCTGTTGCC AGTAATGTTT CTTGTGTGCC 120  
ATTAAACCAC CTCCAGATGA GTGGAGGAAC ATCACTTTTT AATTTTTTAA TTGTATTGG 180  
AATTGTTGCC GTGTACTAAG AACTTGACCT AAATAAAATC CCACAAAGTA TAAA 234

50 SEQ ID NO:1122

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01266

## SEQUENCE DESCRIPTION:

5 GATCCTCAGG ACGCAGGTCA CATTACCTG TGGGCAGAGG GACAGGTCAG ACACCCAGGC 60  
CCACCCCAGA GACCCTCCAT GAACTGTGCT CCCAGCCTTC CCGGCAGGTC TGGGAGTAGG 120  
GAAGGGCTGA AGCCTTGTTT CCCTTGACAG GGGGCCAGCC ATTGTCTCCC ACTTGGGGAG 180  
TTTCTCCTG GCATCATGCC TTCTGAATAA ATGCCGATTT TATCCATGGA AA 232

SEQ ID NO:1123

10

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01267

15

## SEQUENCE DESCRIPTION:

20 GATCAGGAGG CATCATTGAG GCCAGGAGCT CTGCCCGTAA CCTGTATCCC ACGTACTCTA 60  
TCTTCCATTG CTCGCCCTGC CCCCAGAGGC CAGGAGCTCT GCCCTTGACC TGTATTCCAC 120  
TTACTCCACC TTCCATTCTT CGCCCTGTCC CCACAGCCGA GTCCTGCATC AGCCCTTTAT 180  
CCTCACACGC TTTTCTACAA TGGCATTCAA TAAAGTGTAT ATGTTTCTGG TGA AAA 235

SEQ ID NO:1124

25

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01268

## SEQUENCE DESCRIPTION:

30 GATCGATGCC ACGTTCGTAA GGTCTAAGT CCTTCTTGGC TCCTNATGTG GTCCTCTCC 60  
TCGGAAGAAC TGCCAGCCA CGGGTTTTNA ACCCACCTGT TGCTCCTNAG GTCGTACTA 120  
TATCAACAGT CACAAACCCA ATGGCAATAA AGGCACTGAC GATAGCTGGC GCGCGCNACG 180  
CCACACACCA TTTTNAGATG CCGTTGCAAT TAAATCTTGC CACTGTCC TCCTGAAA 238

SEQ ID NO:1125

35

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01269

## SEQUENCE DESCRIPTION:

40 GATCCCTGGC TGGAATGTCA TACCATTGAC CCATTGAAG AGTTAAAGCT GGATTGACT 60  
GCTCTATTCT ACCAGGAATA TTGTTAGGGT AGCCTTTTAC CAGTTTCTAA ACANTNGTAA 120  
TCATTTATTG ACTCAGCAAT TCCTCAGATA ACAGGTCAAA AGATGTACAG ATACATTCNN 180  
NAGTTTTCTT GCTATTAAAG GCACAAGAGT TTCCTTGAT TTTGACTGAA A 231

45

SEQ ID NO:1126

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50

CLONE:HUMGS01270

## SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

GATCTACAGT CATGCTTTAG CATGGCTATG GAGCTAATTA TCAAGCTTAA AGGGTAACTT 60  
 TGGGAGGACT CCTCCCTTCA CTCCTAGTCT CCCTTGGAAG AGCAGTCCAG GCTCAGGGAA 120  
 GGGAAATGGAT AGGATGACAC AGTAAGTACA GAAACTGAAG CTGTCAATAG TGAAGGAAAA 180  
 AGGGGAATTC TTCGTTGCTT TGGCATTNAC ACATAAGTAC TTTGATTAAA 230

SEQ ID NO:1127  
 SEQUENCE LENGTH:229  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01272

SEQUENCE DESCRIPTION:  
 GATCCAAAAT TTATAGCATT CTTCTACCAC CACAGGGGCT CATATGACAT TAACAGACAA 60  
 GACACTTTTC AGAAAGACAG GTTGTCTTTT TGGGCCACAT CTAAGAAATC TTTGTCTAGC 120  
 CAAAAGCCAC AAATAATTTT TCATTTTTTG GCTTCTGGAA GATGTACAGT TAAATGTTAT 180  
 ATTTGGGACT GTTATCTAAT TTGATTAAAT TGCACCTAC AATATGAAA 229

SEQ ID NO:1128  
 SEQUENCE LENGTH:229  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01273

SEQUENCE DESCRIPTION:  
 GATCAGGGCT GAGGGTAAGG AAAAGAAGAG ACTAGGAAAG CTGGGCCCAA AACTGGAGAC 60  
 TGTGTGNTT TCCTGGAGAT GCAGAACTGG GCCCGTGGAG CAGCAGTTTC AGCATCAGGG 120  
 CGGAAGCTTA AAGCAGCAGC GGGTGTGCC AGGCACCCAG ATGATTCTTA TGGCACCAGC 180  
 CAGGAAAAAT GGCAGCTCTT AAAGGAGAAA ATGTTTNAGC CCAGTCAA 229

SEQ ID NO:1129  
 SEQUENCE LENGTH:227  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01274

SEQUENCE DESCRIPTION:  
 GATCCTTACT ACTGGAATTA CCGGGTTAAA AGGAAATGCT TACCACTAAG ATGTCAGTAT 60  
 TCTCCTCATG GATATTTTCA ATCTCAATGT TGCCAGTCTA ATAGTATAGT ATGTGGTTGC 120  
 TTTACTGCTG TTCTCCCCAC CCCCCTGGAG TTGTGTCATT ATTTAATGA ATGTGAGCTC 180  
 TTGACTTACT CTAGAATTCT AATACAGATA CTTTCTGCAC TAGTAAA 227

SEQ ID NO:1130  
 SEQUENCE LENGTH:227  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01276

SEQUENCE DESCRIPTION:  
 GATCCGCTTG GTGACGGGCG TCTTCCAGA TGCTGGCGTC ACCGCTAGAC CAAGGAGCCC 60

TCTGGTGGCC CTGTCCAGGC ATAACAGAAG GCTCGCACTC CTGTCTTCTG GTCACCTTCTC 120  
 ACTATGTCCC CTCAGCTCCT ATCTCTGTAT GGCCTGGTTT TTCCTAGGCT ATGATTATTG 180  
 AGTGAGGATT ATCATAATAT TGGGAATAAA AGTAATTGCT ACCCAAA 227

SEQ ID NO:1131

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01277

SEQUENCE DESCRIPTION:

GATCAGGATT GTCCTACAGT TGTAAATAAG ANTAGGTCCT GTTTATTTTG ACATCTNNTT 60  
 ACAAATGCAT TGTATTAGGG TGTGAATATT CTGAACCATC CTCTTGTTTA AAGTTTGGAA 120  
 ATTTTATTG TTAAATGTAA CATTTTAATG GTTGAATAA TTATTGTAT AGATATGAAT 180  
 ATAGTATTTN ATTTAAGANA ATAACTTTG CATTTTGGCA TNGTAAA 227

SEQ ID NO:1132

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01278

SEQUENCE DESCRIPTION:

GATCTGAAAT TTGTGTATNC TAAAGTAATT TNGTTTTATG TATTGGAAGT TCACTTAAAA 60  
 ACTGGAAATA TTTTCTAGAA GGGTACCACA CAAAAGGAAT CATCTTTAAG CTGTTTAATT 120  
 AACCTAATAA AATAATNTGA TGGGGAAGGC ATTCTAATTG TTTCTGATTT TNNGAGTGGT 180  
 TCCTGCTAAN TCATCANTAT CANTACAGCT TGATTTGATT TAAGAAA 227

SEQ ID NO:1133

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01279

SEQUENCE DESCRIPTION:

GATCTTAAAT GTTATATTGA TAACCATGCT CAGCAATGAG CTATTAGATT CATTTTGGGA 60  
 AATCTCCATA ATTTCAATTT GTAAACTTTG TTAAGACCTG TCTACATTGT TATATGTGTG 120  
 TGACTTGAGT AATGTTATCA ACGTTTTTGT AAATATTTAC TATGTTTTTC TATTAGCTAA 180  
 ATTCCAACAA TTTTGTACTT TAATAAAATG TTCTAAACAT TGCAAA 226

SEQ ID NO:1134

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01280

SEQUENCE DESCRIPTION:

GATCTTTACC AAATTCCTGA CTCAGAGTTC CTCCCATTTN CTTCTGACTC TCATTTTATT 60  
 CTTACCTCTC ATTTTATTCT TATGATGTTT ACCATTTCTN TTCTCCTCAG TGTCCCTCTC 120

TGAGTGGTAA GAGTATGTTA ATAAGCCAGT NCTGAGACCG GAGCACGAGG CAACTGCTCA 180  
 ATGTTGGTCA TTGTCAGTGT TATTAAATGT AACTTAAGGG NNAAG 225

5 SEQ ID NO:1135  
 SEQUENCE LENGTH:224  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01281  
 10 SEQUENCE DESCRIPTION:  
 GATCTGACTT AAAAACCAC CAGCATGCTC AATCCCTTGT NATCCTTATG GAATCTGTAT 60  
 GTTAACTCTC TGGGTGTTCA GGCTTCTATT TGAAGCTGT TGTNACCCTG TTTGCAAAAT 120  
 GAATATGACA CTCTGTGGAT TATTNCTCT GTAAGGCACA AGTNCTTCTN ATGATTANTT 180  
 15 TGACGTTTCA NGAGCAAAAG CAAATTNANA CTCTCTTCAG CAAA 224

SEQ ID NO:1136  
 SEQUENCE LENGTH:223  
 SEQUENCE TYPE:nucleic acid  
 20 TOPOLOGY:linear  
 CLONE:HUMGS01282  
 SEQUENCE DESCRIPTION:  
 GATCCAATAG GAGACACCAG TTCCTTGACT GANCCATGCC CCCACCTAAG TNACAAAATG 60  
 25 AGGGAAGTGG GGAGTTAGAT TTCAGAGTCC AGGCCCCTAG GTTGGGACCC ACTCCAAATA 120  
 ATCTCCTCGG TGTGGGTNGT GGTTCATAG AGGNATANAT GAATAATAAA CATTGTATAA 180  
 NTATACGATA ATGNATAAG TAATCCTTTC ATCANNTGTG AAA 223

30 SEQ ID NO:1137  
 SEQUENCE LENGTH:222  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01283  
 35 SEQUENCE DESCRIPTION:  
 GATCCATCCG ATGGCCTACC AGCTGCAGCT CCAAGCCGCC AGCAACTTCA AGAGCCCAGT 60  
 CAAGACGATT CGCTGATTCC CTCCCCACC TGTCTGCAG TCTTTGACTT TTCCTTCTT 120  
 TTTTGCCACC CTTTCAGGAA CCCTGTATGG TTTNAGTTT AAATTAAAGG AGTCGTTATC 180  
 40 GTGGTGGGAA TATGAAATAA AGTAGAAGAA AAGGCCATGA AA 222

SEQ ID NO:1138  
 SEQUENCE LENGTH:432  
 SEQUENCE TYPE:nucleic acid  
 45 TOPOLOGY:linear  
 CLONE:HUMGS01284  
 SEQUENCE DESCRIPTION:  
 GATCGCACAT CCCTGCGCCC CCATGCCCCC ATGCCCTCT GAGTCACACA GGACAGAGGA 60  
 GGCAGAGCTT CTGCCACTG TTATCTTCAC TTTCTTTGTC CAGTCTTTTG TTTTAAATAA 120  
 50 GCAGTGACCC TCCCTACTCT TCTTTTAAAT GATTTTNGTA GTTGATTGT CTGAAGTGTG 180

55

GCNACTGTGC ATTCCTTGAA TAATCACTTG TAAAAATTGT CAGTGCTTGA NGCTGTTTCC 240  
TTTACTCACA TTGAAGGGAC TTCGTTGGTT TTTNGGAGTC TTGGTTGTGA CNNCAAGAGC 300  
AGAGTGAGGA AGACCCCAA GCATAGACTC GGGTACTGTG ATGATGGCTG CAGTCCAGTT 360  
TTTATGATTC TGCTTTTAT GTGTCCCTTG ATACCAGTGG NCTTANCAAT TATACATTNC 420  
CTCATANTTA AA 432

SEQ ID NO:1139

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01285

SEQUENCE DESCRIPTION:

GATCAGACCC AGAGAAAAGT AGTTGTCACT CATAGCACAC ATCGGACATT TGGAAAACAG 60  
CAGTGGCAAC AACTGTATGA CACACTTAAT GCCTGGAAC AAAATCTGAA CAAAGTGAAA 120  
AACAGCCTTT TGAGTCTTTC TGATACCTGA GTTTTATGC TTATAATTTT TGTTCCTTGA 180  
AAAAAAGCC CTAAATCATA GTAAACATT ATANNCTAAA 220

SEQ ID NO:1140

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01286

SEQUENCE DESCRIPTION:

GATCTTGGGG CCTGTTTTCC CATGGGATTC AAGAGGGACA GCCCCAGCTT TTTTGTTTT 60  
TAAGCTTAGG AATCGCCTTT ATGGAAAGGG CTATGTGGGA GANTCAGCTA TCTTGINTGG 120  
TTTTTTGAG ACCTCAGATG TGTNTTCAGC AGGNCTGAAA NCTTTNTNC TTTAATAATG 180  
AGAAATGTAT ATTTTACTAA TAAATTATTN ACCGAGAAA 219

SEQ ID NO:1141

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01287

SEQUENCE DESCRIPTION:

GATCTAGAGA CAAAGGATAC TCAATGAGGA GCTTTTTTCC CCTCTTGGAA CAGGTAAAAT 60  
GCTTTTCCTT ATTAATATAA TTATAAACA GTATTTTATG TAACAGCTAT TCCCATATTC 120  
TAGGAGTGGC CTAAGAAATG CGTGTTCAG TGAAGTATG ATAAATATNC TCTATTGTGA 180  
ATAGTTGAAT AAAACAGCTG TTTTTTCTG CTTCTAAA 219

SEQ ID NO:1142

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01288

SEQUENCE DESCRIPTION:

GATCTGTGAA ATGCTATCTC TCCTGANGCA ATACTGTTGA CCAGAAAGGA CACTCCATAT 60  
TGTGAAACCG GCCTAATTTT TCTGACTGAT ATGGAAACGA TTGCCAACAC ATACTTCTAC 120  
TTTTAAATAA ACAACTTTGA TGATGTAAC TACCTTCCA GAGTTATGGA AATTTTGTCC 180  
CCATGTAATG AATAAATTGT ATGTATTTTT CTCTATAAA 219

SEQ ID NO:1143

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01289

SEQUENCE DESCRIPTION:

GATCCCCTGGA CACTTACGTA CAATGCTTCG TNCTGCCTGA TGACAGCCGG GCCAGCCGCC 60  
AGCNTACAAG GNTTGTNCGA CGCAGCCTCA GCCCTGTNTT CAATCACACC ATGGTGTACG 120  
ATGGCTTTGG GCCTGCTGAC CTGCGCCAGG CTTGTNCCGA GCTCTCCCTC TGGGACCATG 180  
GGGCCCTGGG CAACCGNCAG NTNGGGAGGC ACACGCNTN 219

SEQ ID NO:1144

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01290

SEQUENCE DESCRIPTION:

GATCTCGGTG CTTCTTCCTG TGCTGTGGTT TACCCCAAAC CTTTAGGTTG TTTATTCATT 60  
CAGATTAGAT AGACTGGAGC CATAAAGTTA ATTTGCACCT AGCTTTTGG AGAATAGCCA 120  
TGATTAAC TGCTATTCGTGG TGGGGGTGGG GGGGAACCCT ATGATTTACT ATGCAGATGA 180  
AGAGGGTAGG AACTAAATAA AGGACTTTGT AAGCCAAA 218

SEQ ID NO:1145

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01291

SEQUENCE DESCRIPTION:

GATCAAGAGG GAGTTCATGC AACACCTGAG AATCTGATTA ATGCACTGAA TAAGTCTGGA 60  
TTAAGTGACC TTGCAGAAAG TCTAACTAAT GACAATGAGA CAAATAGTTA GCTTCTTTTT 120  
TTTTTCTTTT TATTAAANCT GNGATAGATT TTNTTACCAA GCAGCATTTG ATAAGAGGTC 180  
CACTGGTTTT GGTAANCAAT AANCATTTTT ATACCAA 218

SEQ ID NO:1146

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01292

SEQUENCE DESCRIPTION:

GATCCCCAGC TGTTATGCA TAGATAATCT CTCCATTCCC GTGGAACGTT TTTCTGTTC 60

TTAAGACGTG ATTTTGCTGT AGAAGATGGC ACTTATAACC AAAGCCCCAA GTGGTATAGA 120  
AATGCTGGTT TTTCAGTTT CAGGAGTGGG TTGATTCAG CACCTACAGT GTACAGTCTT 180  
GTATTAAGTT GTTAATAAAA GTACATGTTA AACTTAAA 218

SEQ ID NO:1147

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01293

SEQUENCE DESCRIPTION:

GATCCTATCC AGTTGAGGAA TGCTTGCAAT GCTCATTGAA GGGATTGCT TTGGGACTTT 60  
GTCATCTTCC AGAAAGGAAA CATATTGTAT ATTTGGCCCA GTGTGATTGA TTGCTTTATC 120  
TTTGGTAACT TTTACTTGAA TGGGATTGTC TGAATTAATG ACTATTGAAT TAAAACTAA 180  
TTATGAGTTG ACAAATAAAT AAAAGGTAGT GTTTAAA 217

SEQ ID NO:1148

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01294

SEQUENCE DESCRIPTION:

GATCATAGTC AGAAAGTACT GCAGTTAACA GGAACCTTCT TGTCAGGCT GTCATAGCCA 60  
CAGTTGCAAA AAGTGCAGTA TTGATTAATG CAATNAGTGC AATNAGTGAC ATCCTGAGTC 120  
TTTTATCTGT TNAGCTTGCT NTNCTNTTCT NTCATACATC AGGATATTGC CTGTAATGTG 180  
GAGTGGACAG GATAAAAATA AGNATTTTAC TTTCAA 217

SEQ ID NO:1149

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01295

SEQUENCE DESCRIPTION:

GATCTGAAGA AAGCTTTTGG TGCTTGTCTT CACAACCACC TCAGTCCTCC CTCCTGTCC 60  
TCCCCTGTCT CCTTCTCTCC TCCTGGGTTT ATGTTGTAAT AAAAGAAGAT TGTGGGTGTG 120  
TAAA 124

SEQ ID NO:1150

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01296

SEQUENCE DESCRIPTION:

GATCATAGCT TGTTTTATT TGTGCTATAA AATTAACAGT ATTAAATGAC TTATATTCTT 60  
AGAATACATC GAGTGTCTTT TCTTAACAGA TTAGTGCCTT TTNATTTTGG TATTCCGTTT 120  
TACGTTACTG GTCCCAGCAT CAAAACCTT GTTTCATGG CCTGTTTGTG TATTGTCTCA 180



ATAAACTTG CATCAGCCGG TGGTGGCGGC AGAAA

215

SEQ ID NO:1151

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01297

SEQUENCE DESCRIPTION:

GATCATAGTG TTTTGTAATC ATTTAATGTC TGCAGCCAAA TTTTAAAGGG TAATTTAGAC 60  
 CTAATACTGC TCTTGCTGTG TCTTATTAAG TTAAAATTAA TGAATGANTN CTGGTAAAAA 120  
 TTCANNNGG CACTCTGTGA GTAGAGAGTA TCATTTAAGC TTATTNAGT CACATGTAGT 180  
 ATATATCTCC TTAAAGCTGT CACTCTCACT TTNCTTACCA TTCTCTTGAT TTNNTCAGAA 240  
 NCCATCTAGT CATCATCTTT ATACTCTACC TGCTTCTGCA ATTGTATATC ANATNGNGN 299

SEQ ID NO:1152

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01298

SEQUENCE DESCRIPTION:

GATCAAAGTT TAATTGCTTC ATTTTTGTTT AAAAAGGGAT ACTGATGTCA GAAAATCTGT 60  
 AATATGTTTT ATTCAAAAGA TGTAAATAAT GTATACAGAC TTGTATGTGA TGGGATGGGA 120  
 AATATTTAAA TNCTAGGTGT TTTTTTTTTT TTNAANGNGG AACCNCAATG TTTATAGGAA 180  
 AAAANTGATT AANTNGTTC GTTTGGCCNT GAAA 214

SEQ ID NO:1153

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01299

SEQUENCE DESCRIPTION:

GATCCCTCTC CTCGCCTGCC TTCTGGAAGA CTTCAGAAGA TTGAGCCTCA CTGGTGCCAG 60  
 GAAGCCAAAG CTTACTTTGT AGAACTGACA CTAAACTACC CGAAGACTTA GGTGCTTTGT 120  
 GTACTTAACC CCAGGACCTN CTTACTTTTT AATATAAAGA GTGATGTTGT ATTTCTGTGT 180  
 CTGCACTTTT TAATATAAAG AGTGATGTTG TAAA 214

SEQ ID NO:1154

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01300

SEQUENCE DESCRIPTION:

GATCCCAAAG CCACGCTCAT CCAATCCTGG NGAATCATTT ATTTTGAATA TAGACCATTG 60  
 AATAGGTGAA AAATGGAAAA GTCACTTTTT GTACATTTGC ATTCCTTCAA TAATGATTAC 120  
 CATTTGTNCA CATATTTGTT GACCATTGGA ATTGATTTTA GCACAGTGCC TAAAATATAG 180

TAGGTGCTCA ATAAATATTT GTTAATTGAA TAAA

214

SEQ ID NO:1155

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01301

SEQUENCE DESCRIPTION:

GATCCAACT AATAAGAATA AGCTGTACAG GAACTAGTGC TCAATATACA TTGTATAAAT 60  
 TTGTGGAAAT CTCTTGGATG TNAATTGTGA CTCAAGTGG CTTTATTAA GATTNCTCA 120  
 GACTTACTTG GAGGTAAAG CAAACCCAAA TGTGTATTAT TTTGTTACAG AGCTCTGCTT 180  
 TATAATTTTG TAATAAGTT TCAATACAGA CAAA 214

SEQ ID NO:1156

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01302

SEQUENCE DESCRIPTION:

GATCGCAGTG GAAGAAGATT AGTGCATCAT TGAGAGAGGA GAAGTGGAGT GTGGGGTGAG 60  
 CAAAAGCCAA AATACTAATC ACTAGTACAC CAGAGATGCT CCACAAGGTA TGCTCCCCAC 120  
 GGTTCCTTCT CAATTTCAAA GGTNAAGATG TTTTTTTGTG GTGATATAAA ATTTATTGTG 180  
 AATACTTGGT CCATNAAATT GGTACTTGCT AAA 213

SEQ ID NO:1157

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01303

SEQUENCE DESCRIPTION:

GATCTTGTTG AGGCATTTAG CTGCCATGCA CCTGTCCCC TTTAATACTG GGCATTTTAA 60  
 AGCCATCTCA AGAGGCATCT TCTACATGTT TTGTACGCAT TAAAATAATT TCAAAGATAT 120  
 CTGAGAAAAG CCGATATTTG CCATTCTTCC TATATCCTGG AATATATCTT GCATCCTGAG 180  
 TTTATAATAA TAAATAATAT TCTACCTTGG AAA 213

SEQ ID NO:1158

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01304

SEQUENCE DESCRIPTION:

GATCTCATTT CAATTCCTTT ATTAGAGGGC CTTATTGATG TGTTCTAAGT CTTTCCAGAA 60  
 AAAAAGACTC CAGTGATTGA TATCCTGATT TCAACCAGTC ACTTAGCTGA TAATCACAGT 120  
 AAGAAGACTT CTGGTATTAT CTCTCTATCA GATAAGATTT TGTTAATGTA CTATTTTACT 180  
 CTTCAATAAA TAAAACAGTT TATTATCTCA AA 212

SEQ ID NO:1159

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01305

SEQUENCE DESCRIPTION:

GATCTGGTCT GTTCCTGCGT CTGCGGANGG CCCTTGCTCT CCAGCTATCT ATAACCTTAG 60  
CTAGAGTGTC GCCTTGTTGG TTCCTGTTGC TGAGACTTCC TGGATGGAGC CGCCTCACCG 120  
CCGGGCCCCGT GGCCTGCNCG GANTGTGTCC AATAAAGTTC TTGGATGTGA AAACCTTAACA 180  
ATTTTGTGTA ATAAAAATGG AGAAGCTCTA AA 212

SEQ ID NO:1160

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01306

SEQUENCE DESCRIPTION:

GATCCTTGGT GTGTAGTTCA GTCTTGCAGT ATACAAGCTT TTGTGTATAA ATGTTTTATG 60  
ATATGATTCC CTGTATTTTG CAGGGGTTTT TTTCTCTTT NCTTTTGA TAAATATGTA 120  
TATCAATATT TTAAATNCAT CTTTGCTTTT TTTAGAGGAG TTTGTAATCA CCTTATAACA 180  
TGAAAATAAA CATTTCCTTT TTAACATCAA A 211

SEQ ID NO:1161

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01307

SEQUENCE DESCRIPTION:

GATCCTGTAT ATGTGTGTTT TGGGGGAGCT ATGATAAGTT TTATGGCAAA CGGTTGGTAT 60  
TGTTAACTTT TTATTGTCAT CAAAAGTTCA TAAAAGTCCT ATTAATCCCC ATATTCTNNN 120  
NCTGCCCTTA ACTCTGGTAT ACACCAAAAA GAAATCTTTA CTTTCCTTGT TTTATCATT 180  
TAAAAATAAA GTATTTTGCT AGTATGGAAA 210

SEQ ID NO:1162

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01308

SEQUENCE DESCRIPTION:

GATCCGCCCA TGTNAGCCTC CCAAAGTGCT AGGGTTACAG GCATGAGCTA CCATGCCTGG 60  
CAACAGCTTT CATATTTGTA AGTTTTTTTT CCTAGGTAAC CCAAGGTCTA TTGAAATTNC 120  
ATATAGCTTT CTTTNCATT ACATATTTAA ATAGATTTNN CCTGATTNA GAAAAGCTGT 180  
AGATTTTAT ATGTNAATCT TGTNTCCNTN 210

SEQ ID NO:1163

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS01309

SEQUENCE DESCRIPTION:

10 GATCTNGGAC TCTNCCTCTC ACGACTGCGC CTTAGTCACT CAGACATACG GCGCANTGCA 60  
GGAAAAGCCT ACACAGACGA CCTGGGTGCT GTGGGTGGCG CCTGCNTGGA GGACGAGCCA 120  
GCNTCCTGCN CTGGATGAGG ACAGCGAGCA CCCGCCATNA TTCTNCGGAC TGA CTGAACT 180  
TNACCTGTGA CCTCTTACCN GTGGAGCAN 209

SEQ ID NO:1164

15 SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01310

SEQUENCE DESCRIPTION:

20 GATCACTNCA GGCCAGGNGT CCAAGACCAG CACGNCCAAC ATGGCAAAAC CCAGTCTGTA 60  
CTAAAAATAG AAAAATTAGC TGGGCGTGGT GGCGTGTGCC TGCAATACCA GCTACTCAGA 120  
AGGCTGNAGC AGGNTAATTG CTTGANCCTG GTAGGTGGAG GTTNCAGTGA GCTGANATCA 180  
TGCCACTGNA CTCCAGCCTG GGTNACAGN 209

SEQ ID NO:1165

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS01311

SEQUENCE DESCRIPTION:

GATCCTTACC GTCCTAGAGA GCAGACGCTT TCTGAAACT ACTTGCTCCA AAAGACCCTC 60  
TGAGTTAACG TTTGAGCTGT ATCATTAGAC TTGTATTTAG AGCGTGTAC TTCCTCTGAA 120  
35 CTGTTACTGC CTGAATGGAG TCCTGGACGA CATGGGGTTT TTCCTCTAGG AGAATACAAG 180  
CCTTAATAAA CAATACTATT TAGCAAA 207

SEQ ID NO:1166

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01312

SEQUENCE DESCRIPTION:

45 GATCTGAACA AAGTCTGCAT TTNGTTAATA GTGTGGTACC AATGTTGGTT TCATAGTTTT 60  
GGCCATTGTG CTGTGTATTT ATAAGATGCT AACATTAGGG ATAGCTGAAT GTGGTATATA 120  
TAGGAACTCT GTGCTGAGTT TATAACTCCT CTGTATGTCT AAAACTATTT CAAAATAAAA 180  
NGTTTAAAGG TAAAANAAAA GATTAAA 207

SEQ ID NO:1167

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01313

SEQUENCE DESCRIPTION:

GATCCAGCCA CCACTCTGAA ACTCATCACA TCTTCATTGA CAGGGAGGGA GCCCAGGACA 60  
TATGTGTGGC TCATTGACCA GAAGGCTTTC TTAGTCCCAA CAGCCATGAA CCATGCACTT 120  
ATGGATACCC AGCCTTTTGT GGCTACGTGA AATGCATCCT TGTANCATCA TTGTATTCTT 180  
TCAATAAATA GCCTTCTGAG TTGAAA 206

SEQ ID NO:1168

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01314

SEQUENCE DESCRIPTION:

GATCTGCGCTG CCTATNAGAG CTTTGAGAAG CTCCGCCACA TGCTACTGTT GGCTATCCAG 60  
GAGTGTCTCTG AAGGCTTTGG GCTGGCCTAA TAAGGCCCTG CCCAACTCCG TGGGGTTTTT 120  
TTAACCATTG TTGGACCTGG GGAGGGGGGA GTTAAAAAAA GAACCAGAAA GAAATTGTCA 180  
AAAACCAATA AATGAAATCC ACCAACTCAC AAA 213

SEQ ID NO:1169

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01315

SEQUENCE DESCRIPTION:

GATCTAAAGT GACCTTGATG GACAGTGGAA GAAATCACAA CATGGAATTC CTCGAATAAC 60  
AATTTATTGA CTTTAAATAA TTTTGCTCTA TGCTACATAT ACACAATTAA AAAACCTTTA 120  
CACTATTTCT AGAAAGTCAG CATGTATTTT TGGCTCGNNG TTCNCCNCG TGTTTTCTGT 180  
GGAAGGAATA AAAATTTGAG TTTCAGTTGT GTAAA 215

SEQ ID NO:1170

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01316

SEQUENCE DESCRIPTION:

GATCTGTGAC AGCAGCAGCT TCATGTTGTA TTTTTTTTAC TGAAATTGTA AAATATCCAT 60  
CTTAAAGACA TCAACTATTC TAAAAATTGT TTACAGGATA TTCCTTTAGT GGTGGAATTA 120  
AAATNTACGA NTACTTGCTT TTTCAAAAAA ATGTATTTN TGTTAAAAGT TTAAAGATTT 180  
TTGCTATATA TTATGGAAGA AAAATGTAAT CGTAAATATT AATTTTNTAC CTATATTGTG 240  
CAATACTTGA AAAAAACGGT ATNGAAAGTA TTTTGAGTCA GTGTCTTACA TGTTAAGAGG 300  
GACTGAAATA GTTTATATTA AGTTTGATT AAANTTCTTT AAAATTAAA 349

SEQ ID NO:1171

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01317

SEQUENCE DESCRIPTION:

GATCCAAGCT GTATATACCA TATATAAACA TTTTACATGA ATCATTAGT TTTTAATTC 60  
 ATTTACTAAT GCTATAAAAT TTCCTATATT ACCCCAGTAA TTTGCATCAG CTGGTTTATA 120  
 TACTAAAGCA ACATGTTTTG ATGAGTTTCT TACATCCTTA TCGAGGAATT GGGTTAGGAA 180  
 AAAATACATA ATTGTAAAC TGAAA 205

SEQ ID NO:1172

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01318

SEQUENCE DESCRIPTION:

GATCTTCAGG NTTCTACAAA TAGGGTAATT GTAAATTTAA AGCATTAGCA TTTATTGGTG 60  
 AATAATGTAT ATATCCCAT TCCAAGAAAT ATAAGTNAGT NANGTTGAAA TAAATCTTT 120  
 AAAATTTACT ATATTGCCAG TGGTTTCACA NCAGTTCTCT TGTATTTATT TATCAATTAA 180  
 ATCAAATAAA AATGATTATG TCAAA 205

SEQ ID NO:1173

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01319

SEQUENCE DESCRIPTION:

GATCCCTGA CCTGCATTAC CTTGGTAACC ATTCATTTT TTAATTTAAT TTCATTTTTT 60  
 AATTTTGGTG TACAAGCTGT AACATTTTCT CTTCAAAGT GTAACACGCT GATTTCCTCA 120  
 AATAGAGATA CCCCTTTGAG TGATAAATTT GCAAAATGCT GTCTTCATT TCTGTATTAA 180  
 AATTCATTTT AGTTTAAAA TAAA 204

SEQ ID NO:1174

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01320

SEQUENCE DESCRIPTION:

GATCAGAGCT GCTGAGTTCA GGATGCCTGN GNGTGGTTAG GGTAGCTTCT TACATGGATG 60  
 TCAGGAGAGC TGCTGCCCTT GGCGTGAGTG CGTATTCAGG TGTTTGCTG CTTGGCAGA 120  
 GAGTGGTTGA GTGTNGAATC GTTCAGCTCT NAGGTTCTGT NCCCTGTGGT GGAGAGGACG 180  
 CAGCAGCNAN NTCTGGGNTC TNAN 204

SEQ ID NO:1175

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01321

SEQUENCE DESCRIPTION:

GATCAGTGCT CTCTATTGAT GTTCTTGCTG GTCTCCAGNC ACATTCCTGT TGCATTAAGN 60  
 CTTGAAAGAC TTGTAGATGT GTGATGTTCA GGCACAGGAT GCTGNAAGTA TGTTACTATT 120  
 CTNAGTTTGT AAATTGTCCT TTTGATACCA TCATCTNGTT TTCTTTTGT AGGTATAAAT 180  
 AAAANCACTG TTGNCANTAA GGAAA 205

SEQ ID NO:1176

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01322

SEQUENCE DESCRIPTION:

GATCTCAGCC ATAAAGTGCC AGTTTGCTTA GTTCTCACTG TCTCCTGGTC TGTGCTGCCC 60  
 TGCTCTGGGG ATGCACGGCG GCAGGGTGGG GGAGGGAGGT TCCTCGCAGG TCTCAGCCCG 120  
 GGACAGGGTC TTGCAAGCAG CCTCCTGGGC AGTCGTAAGG GTTGCGGCGT GATGTCTTCA 180  
 ATAAATTAAG TTTTATTTGG AAA 203

SEQ ID NO:1177

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01323

SEQUENCE DESCRIPTION:

GATCAAAATG AAACAAATAT ACCTTATCCT AAAGAGCTCA TAACAAATAA GTTACCTCCA 60  
 CTCTATAAAC TCAGACCTAC TTTTGAAGA TAACTGCTTT TAACCTCTCC TTACAAGATT 120  
 TTTGTTGTTG ATGTATTAA TTTTAGCCCA TGTCTCAATT CTCATTTTCA AAGAATCAAT 180  
 ATATTAATAT ACCTTTGGTC AAA 203

SEQ ID NO:1178

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01324

SEQUENCE DESCRIPTION:

GATCGCTCTT GTGTTTTTGC ACTATTAATT AACTTCAAGT GCAATTTTGG CAGGCAGGCC 60  
 AAGGGTCTCA ACAGGCTATT TGGAATGAGT TCTCTTTTAA GGCCTTCAAC GTAGTNNGAC 120  
 ATTTTCAAAT CAAAAAGTAC AGCAGGAGCC AGCCTTTATT TTGTCTGTGT ACACAATAAA 180  
 ATATTCCGCT TCTATAGGCA AA 202

SEQ ID NO:1179

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01325

SEQUENCE DESCRIPTION:

GATCAGCTGA AGGTTTCATGG GTTTTAAAGTG CTTGTGGCTC ACTGAAGCTT AAGTTAGGAT 60  
 TTCNTTGCAA TGAGTAGAAT TTCCCTTCTT TCCCTTGTCA CAGGTTTAAA AACCTCACAG 120  
 CTTGTATAAT GTAACCATTT GGGGTCCGCT TTAACTTGG ACTAGTGTA CTCCTTCATG 180  
 CAATAAACTG AAAAGAGCCA TGCTGTCTAA A 211

SEQ ID NO:1180

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01326

SEQUENCE DESCRIPTION:

GATCCCAGGG TGCAAAGTGG CATTGAGACA GCAGCAACAG CTCAAGAGAT ATCTCCTGCC 60  
 TACTTGCCCC TCCTTCCAGG CCGGCTCTAA GAGAAAGGCC CATCTACTCA GGAAGAGGGC 120  
 CAGGNCCTTG GGTCTG GGGG ATTGCCCCCT GAGAGGGCTA GTCCTGTGGC TGAAAATAAA 180  
 GCATGTCCCG CCCNNTAAA 199

SEQ ID NO:1181

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01327

SEQUENCE DESCRIPTION:

GATCTTTTT TGGATATTTA TACTTTTAGA TATATAGTAC CTTTAAGTAG CAGTATGGGA 60  
 CAAGGCTTGT AAATGTTTGT TCTAATGTTT TATTGTCACC TTTTATGCAT TTATCACTTC 120  
 CAAATCTAAC TTTGCACAAG TAACCCATGT AAAAAAAAAAT GTACATTTTT CAAAAGTTGT 180  
 AAATAAAAAT AACCTTAAA 199

SEQ ID NO:1182

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01328

SEQUENCE DESCRIPTION:

GATCTGGACA GCTGTCCCTC CACTACAGAA ACCTCACAGA ACACAGCAA GNATAAGTGC 60  
 ANGAAGGCTG CTTCCAGCTC CAAAGCACCT ANGAATGGAG GTAAAGCGAA GGATTCAGCA 120  
 ANGACAGCAG AGGAACTTC CANGCCAAAA GNTGACTAAA GNAGTACAGG TTANGGTATC 180  
 TGGTATCTGC ATGTAGANTC TTCAGCTGGT GGATGGTGAC TTTGAAGTA CNAAAGGCTT 240  
 TGGCAACNGN AN 252

SEQ ID NO:1183

SEQUENCE LENGTH:197



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01329

SEQUENCE DESCRIPTION:

GATCTAGGGA GTTACCTAGC AGACCTTCCG GACTGACGTG ATGCTACAGG GGTCCCATCT 60  
TTCCTTGTCA TTGAGCTATT TTACAGTTCT GTGAATTGTA AAGAACTGAG GGTAATGCGA 120  
ATNACTCTTG TTCATAGAGG CAAATGAATT TTGTCCCATG GAGATTTAAT TGATATTACT 180  
CTGTGGATGT TGACAAA 197

SEQ ID NO:1184

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01330

SEQUENCE DESCRIPTION:

GATCATAGCT ACTACTTCAT TGCAACCTTT ATTAAGTAC CACATCAGAC ATCATGCTAA 60  
ATACCTGAAT GCATGAAAAA ACTCCAAATA AGAGAATCTC TTCAGGATTA TAAAAGTTGT 120  
AAAATGCAAC TGTATTGCTG AGCAAA 146

SEQ ID NO:1185

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01331

SEQUENCE DESCRIPTION:

GATCCGGCTG CACACCAGGT GCGGAGGCTG AGCCATCCCT GCTGGACTCC CTACCGCAGA 60  
CGGAGTCANG NACGCAGCCG CAGCCNCNTT CCTTCACACC CCCTCACAGA CTCCTTGTGT 120  
CCAACGGGAA TAGGAAGAAT TAGTTACTGA CTTACCTGA GAAAAAATA AATNCTCTAT 180  
GGTGGTTTCA CAGGAAA 197

SEQ ID NO:1186

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01332

SEQUENCE DESCRIPTION:

GATCTCTTTG TGAAGTCTGT GTTCTCTATA TTAGATTGCT GTTTATATGT AAGAATTTTA 60  
TTGCTTATGT GGCATACAAT ATTTATAACT ATAAACTTTA TAGAAGTACA GTATTAAAGT 120  
CAGTGGTACA CAGACATTCT GTACATATCC TGTGAAACGT GCTGTCATAT GAAATAAATA 180  
TATCTGTCTT TACAAA 196

SEQ ID NO:1187

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01333

SEQUENCE DESCRIPTION:

5 GATCTTCCCC ATTGTCCACT CAAGTCGTGG CCTGGGGAAC ACAGACGGAG CTGTCCCCAG 60  
 TGTCCTCCGT CCCTCAGCCC CTGGCCTGGC TGAGTTTGGC AGGGCCTGGG CCATCCCTGG 120  
 GACAAAGGTG CGTCCCTTCA GCTCTTCTCC GTGGAGCTCG GGGCTTTCTG TATTTATGTA 180  
 TTTGTACGAA TGTAAG 196

10 SEQ ID NO:1188  
 SEQUENCE LENGTH:196  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01334

SEQUENCE DESCRIPTION:

15 GATCTTCGGC CTCATTCTGA ATACCTNTTC TTTGGACAGT NTTTTTCCTT TGGTGCTCTC 60  
 TTGCCTTTAG CTACCTTCTC TAATATGTAT GCTACCATCA CTAATAAAGT GATGGGAATG 120  
 20 GGTGAGAG TCGTAATTTA TATTAAAAAG TTGTTGGAAT TTTAAATACA TTTTNNCAA 180  
 TAAAAAATTA AGCAAA 196

25 SEQ ID NO:1189  
 SEQUENCE LENGTH:193  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01335

SEQUENCE DESCRIPTION:

30 GATCATGTGT GCACAATACT TGTGGCCAC AAAATTTAC AATGACTGCT GAGGAATCAT 60  
 TCTTTTGGC TGTAATAAT AACAAAGGGC ATCATTAAGT AGACCAGGTA ATTACTGCTT 120  
 GTNTCTCAAG GCTGCTGTCT TTATCAGCAC TAACTAAATA AATTTGTTGG TTCAGTTGTA 180  
 CTTGTCCTGC AAA 193

35 SEQ ID NO:1190  
 SEQUENCE LENGTH:192  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS01336

SEQUENCE DESCRIPTION:

40 GATCCTGTGT CCTAAATTAA TATACACCAG TGGTTCCTCC TCCCTGGTAA AGACTAATGC 60  
 TCAGATGCTG TTTACGGATA TTTATATTCT AGTCTCACTC TCTTGTTCCA CCCTTCTTCT 120  
 CTTCCCCATT CCAACTCCA GCTAAAAATAT GGGAAGGGAG AACCCCAAT AAAACTGCCA 180  
 45 TGGNCTTTTA AA 192

50 SEQ ID NO:1191  
 SEQUENCE LENGTH:189  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01337

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## SEQUENCE DESCRIPTION:

GATCAGTGCC TTGATGCCAA CTAAGGAAAT TTGTTTAGCA TTGAATCTCT GAAGGCTCTA 60  
 TGAAAGGAAT AGCATGATGT GCTGTTAGAA TCAGATGTTA CTGCTAAAAT TTACATGTTG 120  
 TGATGTAAAT TGTGTAGAAA ACCATTAAAT CATTCAAAAT AATAAACTAT TTTTATTAGA 180  
 GAATGTAAA 189

SEQ ID NO:1192

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01338

## SEQUENCE DESCRIPTION:

GATCAAAATTT TTGTAAAATT TTTTAAGAAG AGATGGCTTA TTAACAGGGA AGAAGCTTGT 60  
 NATATTCCAG TTGTAAGAAT AGCCTTAGTG TTTAGATTTT TTNATGATAG GNNAGATGCG 120  
 GNCATCACTG GGATATTTC AAATCCCAAG GNCATCAGAG TGAAGTGTC GTTGTTCAGAT 180  
 GATTNNAN 189

SEQ ID NO:1193

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01339

## SEQUENCE DESCRIPTION:

GATCCCAGCC AGGCCCTGGA GGTCTGACAG CCCCTCCCTC CCAGAGCTGG TTCCTCCCTG 60  
 GGAGGGCAAC TTCAGGGCTG GCCACCCCC GTGTTCCCCA TCCTCAGTTG AAGTTTGATG 120  
 AATTNANGTC GGGCCTCTAT GCCAACTGGT TCCTTTTGTT CTCAATAAAT GTTGGGTTG 180  
 GTAATAAA 188

SEQ ID NO:1194

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01340

## SEQUENCE DESCRIPTION:

GATCTGAATG ATACTGTCTG CTGTGTCTTT TTTCCATGAG AAATCACTGT TGCAAAATTGC 60  
 CTATAAATTG ACTCTACTAA AATAACAATG TTTCAGTCTG AAAATTTGAA TTGAAAAAAA 120  
 TGTATAATAT AAAATTGTAA TACACTCAA TGATTATAAA AGTAAAAGTT GGTAATTTAG 180  
 GCAGAAA 187

SEQ ID NO:1195

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01341

## SEQUENCE DESCRIPTION:

5 GATCAGGGGG GAAATGGAAT GAGTGAGGCG GGCCAGGGAG CCGCTCAGCT CCAATCTTTG 60  
TCACTGTGTG AAATGTGGAC TTGGTATGAC CTGACTGTCC AATTTTCAAG ATGAACCAGA 120  
AATCCAGACC NTTATATAAA ATCTCCTGGA TTTTAAATG TTGGCAATTA ATCAGAATGT 180  
TTTTAAA 187

SEQ ID NO:1196

SEQUENCE LENGTH:186

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01342

SEQUENCE DESCRIPTION:

15 GATCACTTAA TTCCTTTCTT ATCTTCCCCC TCACTTCCCT TTCTCCCACC CTCTTTTCCA 60  
AGCTGTTTCG TTTGAATATA TTAAGTGAAT GAGTTGCAGG NAATGCAGCA NACTTGTTTC 120  
NCCTAGATTG GAGTCAAACCT CCTGNTCAAA GAATCGGTNG GGCATANAAG AAATNTTCTT 180  
NTTAAA 186

20 SEQ ID NO:1197

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS01343

SEQUENCE DESCRIPTION:

30 GATCTTTTAA ATGACAGTAC AGACTGAGAT TTGAAGGAAA CATGCACAAA TCTGTAAAAC 60  
ATAGACCTTC GCTTTATTTT TGTAAGTATC ACCTGCCACC ATGTTTTGTA ATTTGAGGGT 120  
CTTGATTTC AATTGTCGG TGAAGAAAAT TTTCAATAAA TATGTATTAC CCGTCTGAAG 180  
CTTAAA 186

SEQ ID NO:1198

SEQUENCE LENGTH:186

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01344

SEQUENCE DESCRIPTION:

40 GATCTTCAGG TATTTTAAAT TTAGTTACA TCAATTAATG TAAATNAATC CAAATGCTAA 60  
TTTTTGTGGT GCAAGAAGTT TCTTATGTAA ATNCAGGGTA TGGATAAGCT AATTAAGATA 120  
TCCATCTTTG GTGGCTCTAA GTGTATTATT TGTNTTTAAA TAAAGTGTAC AAATATAGAT 180  
AACAAA 186

45 SEQ ID NO:1199

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS01345

SEQUENCE DESCRIPTION:

GATCTAAACA CGAGGAAACA TTATTCATTG GAAAAGTGCA TGGTGTGTAT TTNAGGGATT 60

# EP 0 679 716 A1

ATNAGCTTCT TTCAAGGGCT AAGGCTGCAG AGATATTTCC TCCAGGAATC GTGTTTCAAT 120  
TGTAACCAAG AAATTTCCAT TTGTNCTTCA TGAAAAAAAAA CTTCTGGTTT TTTTCATGTG 180  
GAAA 184

5

SEQ ID NO:1200  
SEQUENCE LENGTH:183  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS01346

SEQUENCE DESCRIPTION:

GATCGCCCGC CCCAGCCCGG GGCCGCTCAG GTCTGCTTGG AGGATGCCTC CCCAGGAGG 60  
GCAGTGAGGG ATGCCGCAAC CTCGACTTCT CAGCCTCCTG GGGTTCCGCC GGCCAACACT 120  
GTCTGTNTCA AATACTGTGC TGTGAGTTGT TTCAATAAAG GGGCCCCAAG GGCTGGGCTG 180  
AAA 183

15

SEQ ID NO:1201  
SEQUENCE LENGTH:184  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01347

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SEQUENCE DESCRIPTION:

GATCTCTGCT CAGCTTCCCT TGCCTTTTAA GGCCTGCCCT AGCCAGGGTT CCCTCCTGCT 60  
TCCAGTACCC TCTCATGGCA TAGGNTGCAA CCCAGCAGAG GGCAGCTAGA TGGACATTTC 120  
CCCTGCTCGG AAGGGTTNGC CTGCCTGGCT GGGGNGGTCA GTAAACTTTG AATAGTAAGC 180  
CAAA 184

25

SEQ ID NO:1202  
SEQUENCE LENGTH:183  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS01348

SEQUENCE DESCRIPTION:

GATCCCCTTT GGTTTTACTA CCCAAATCTA AATAGATACT TTTGATAATA GATAACTGCT 60  
CTTTTACTAA GACATAGTCT CTACCTATAG AAATGTATTT TGAAAACACT TATTTTACAC 120  
AGCAATTTTG TATCCATTTA AACTAACCTT TTATCAATAA AGCACTATTG TTTAGATATT 180  
AAA 183

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SEQ ID NO:1203  
SEQUENCE LENGTH:183  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

45

CLONE:HUMGS01349

SEQUENCE DESCRIPTION:

GATCTCATTC TCCCTTTTAA TCCTGAGTTA CCATCAGTGC TAATGTTTCT CTTTGGGTA 60  
TAGTTCTCCA GGAGAACTTG TCCTATATTT NTTTGTGTGT GTTTTTTCC TTCCAGCTTA 120

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AACAAATTAA AACTAAATAT CTAAACCTTG TATACAGACA TTAAAATTAG TGAGAGAAAC 180  
AAA 183

5 SEQ ID NO:1204  
SEQUENCE LENGTH:183  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01350  
10 SEQUENCE DESCRIPTION:  
GATCTGCTTT TNCTATTTCT CCCAACCAAA TCCTCTTAAA GACCCTTTGC TATGTAGTCT 60  
CATGGTCTAG CATGCATCTT GTAGAAACAA GGCATNCTGG CAGATTGCAG GGTGAGATG 120  
TGTTTATCT GTTTATATT TTAAAGATT CTGCCAGAAA ATAAACCAG ACCTTGTCT 180  
15 AAA 183

SEQ ID NO:1205  
SEQUENCE LENGTH:183  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS01351  
SEQUENCE DESCRIPTION:  
GATCTGAATA GAGAAATGCT TACAGATAAT CATTAGCCCA CATACCAGTA ACTTATACTT 60  
25 AAAGATGGGA TGGAGTTGTA AAGTGCTTTT ATAATACAAT ATAATTGTTA AAGGCAAGGG 120  
TTGACTCTTT GTTTATTTT GACATGGCAT GTCCTGAAAT AAATATTGAT TCAATATGGC 180  
AAA 183

30 SEQ ID NO:1206  
SEQUENCE LENGTH:182  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01352  
35 SEQUENCE DESCRIPTION:  
GATCCTTGGG GGCCAGGGTG AAGGGTATTT TACGGGAACT CTATAAGCA GGAAGAAGCA 60  
AGTTTATTCT TTAGACCAGT AGCTCTCAAC CATGATGTGG TCGTATATTT ATGGGTCAAC 120  
ATGTGTTGTG GGGATATCCC AAGTAACTTG TTATTAATAA AAGTTAAGTT GCAAAATTTA 180  
40 AA 182

SEQ ID NO:1207  
SEQUENCE LENGTH:182  
SEQUENCE TYPE:nucleic acid  
45 TOPOLOGY:linear  
CLONE:HUMGS01353  
SEQUENCE DESCRIPTION:  
GATCAAAATT GAAGACACAT TCAGAGGTTT GATTGGTTGA GATTAAGTGG TGTGGTGGTT 60  
50 GGTGTATGTA TGTTTNAATTT TNATGTCTTT GTATGTAGTT CTACATAATG CAAATTGTGC 120  
TTTCTGATGG ACAAGACCTC ATAAGTGTGA TTAATATCAA TAAAAGGGG ATGTTGTGGA 180

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AA

182

SEQ ID NO:1208

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01354

SEQUENCE DESCRIPTION:

GATCCGTCAA TCTTGGGTGG AATNATTGTN CGCATTGGCG AGAAATATGT TGACATGTCT 60  
GTCAAGACCA AGATTCAGAA GCTGGGCAGG GCTATGCGGG AGATTGTCTA AAAGTGTGG 120  
TTTCTGCCA TCAGTGAAAA TTCTTAACT TGGAGCAACA ATAAANAGCT TCCAGAACAG 180  
AAA 183

SEQ ID NO:1209

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01355

SEQUENCE DESCRIPTION:

GATCATGTTA TATTCTATAT CAGACAACT ATTTTNTTTT GACCTTTCTT CCCCTCCATC 60  
CAGTATTTTC GTTGATTCA TTTTCTCCCC TCTCTCCCC TTCCACGAAC TGCAATACCA 120  
GTAACCTTGG TATATATTTT TTGATACTGT ACACATGGAT GTNTTGTTTC TATGTGCAAA 180

SEQ ID NO:1210

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01356

SEQUENCE DESCRIPTION:

GATCAAAGAT TCTCCCCATC TCACAGACAA GGAAACTNAG GCCAGAGGGA GGAGAGAATT 60  
GCTCATGGCT CCANAAGTGG TGGCAAGTTT CTCTGGACTC TTAGGTTTAT TTTNAATATG 120  
AAATATAAAA NCAGTTTCAA ATATCTNATT GAGGGAGANG TAAACCTTA TTTAANCAAA 180

SEQ ID NO:1211

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01357

SEQUENCE DESCRIPTION:

GATCTATAAA ATGGAAGGTG ACCAATGTCA CTGCTTCTAA AATACTGTCC TAAACAACCC 60  
AGAAGATTTT ATTCAGCTC ATGAATAGCT GTTCTAAATC TGTGTATGT TAGACATACT 120  
ATGAAGTACC TCTTCACTTA TTATGGGGAA GTTTCCTTAA TAAAAGTGTG ACGATTAAA 179

SEQ ID NO:1212

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01358

SEQUENCE DESCRIPTION:

GATCCAAGAC CAGGGNGGTT GGGACGGCCT CCTNTCCTAC TTTGGGACGC CCACGTGGCA 60  
GACCGTGACC ATCTTTTGG CGGGAGTNCT CACCGCCTCA TTCACCATCT GGAAGAAGAT 120  
GGGCTGAGGC CCCCAGCTGC NTTGGACTGT TTTTNCNC CATAAATNAN GGCATTTN 179

SEQ ID NO:1213

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01359

SEQUENCE DESCRIPTION:

GATCTGAGAT GTTCCTTAAC ATGTAGCCAT GTAATTAGAA CTCACAAGGG GCATTGAAAT 60  
NTTTCCCTT TTCANATAGT CTGGGGCTAT TACTTATTT NAAGTAAGCC AAGTCTACCA 120  
TTTGA AAAAT GGTGCTTTAT TTCCATATCT GANGCCTGAN GTTATTTNNN AGTTTGTN 178

SEQ ID NO:1214

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01360

SEQUENCE DESCRIPTION:

GATCTGGCAT CCNAGGCTG CAGCTTTATT AGCTTATAAC TTACTCATCT CTATCTTTAC 60  
CAGCAGGCTC TGTATTGTTG ATATTGCAA CTNGNITTGC TTTCCCATG GTGGAATTGA 120  
ATAAATTAGT TTTNAATNAC ATAAGANGCC TGTTTGCTAT TNGNGGAAG ATAGATGN 178

SEQ ID NO:1215

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01361

SEQUENCE DESCRIPTION:

GATCAAAGAG GTTATCTCTG CCAGTCACAA GTGTGGCTGG TGTCATTCTG GGTCTGACTG 60  
GAGCCCTCCT GGACTGTTTC TTAAATTCA AAAGCCCTGC AGACATAGTA CCTGGTCAGA 120  
ACTATGCCTC GGTATTATTA TCATTTTGAA ATAAATCAA AATTCAACC TGTA AA 176

SEQ ID NO:1216

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01362

SEQUENCE DESCRIPTION:

GATCAAAACA ATTACCTAAT TGCAAAAGAG AAAGTGAAT GGAACATAGT CTCANATTCT 60



NCTAATGTGT ATCTCACAAT GTCATGTAAT GTAAAGNAAA CCCTTTTGGG ATTAGAATTC 120  
TTGTNCTGAA TGCTGAAC TA TTTGGTAATA AAGTGCTTAT NTGCAGATAA CAGAAA 176

5  
SEQ ID NO:1217  
SEQUENCE LENGTH:175  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10  
CLONE:HUMGS01363

SEQUENCE DESCRIPTION:

15  
GATCTGTGCT GGGGAACAAA GCTTTTGCAG TACCTTATAT TGTAAGTAAA ATTTTATTTA 60  
ACATATCCTT CAGTGAGCTC ATTTACACT GTAGCCTCTT CCTTAAATTT TGTGGTGCTC 120  
CTGTAACAGT AAGANCTAAT TCTGAAATAA AAGACATCTC CTAATGCTGT GCAAA 175

20  
SEQ ID NO:1218  
SEQUENCE LENGTH:174  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01364

SEQUENCE DESCRIPTION:

25  
GATCAGGATA ATAATCTGCT TAGTAAGAGA AACAAATTGA ATTTTAGAAG GAAATTGCCT 60  
TACCATTTCG AAATTAAGGT AATTAATAA CAGTGAATTT CAAAATGCCT TTTTAATGAC 120  
AATGTGTGAA CTTAATTTGT TTTAATAAAC CAAAATTGTT GTTATTGTGT TAAA 174

30  
SEQ ID NO:1219  
SEQUENCE LENGTH:174  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01365

SEQUENCE DESCRIPTION:

35  
GATCTGAGCA GGCAAAGCTC AAAAGAGAGT TTGGAGGTTA AAAATAATTT ATTTTGCAG 60  
TAGTGTGCTT TGAAATGTGT AAATCTTATT TCTAATGTAT ACAACCACAT TTCACATAAA 120  
AATATGCAAT TTATATGCCA GATAAAAATA AAACAAGTGA ATTTGCAAGT GAAA 174

40  
SEQ ID NO:1220  
SEQUENCE LENGTH:173  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01366

45  
SEQUENCE DESCRIPTION:

GATCAACATG ATGGTGACTG GGAAAAAATT ACTTCAAGTA ACATGCTTAG CTTTCCCTCC 60  
TTAATGTGAA AAATCAAGGG CTTACTGACA TAGGAACAAC AGAAATGCTC CTGGAAGTTC 120  
AAGTTGCTGA ATTATAAGTT TATTTTNNAT CAATAAATAT NNNNATACTN AAA 173

50  
SEQ ID NO:1221  
SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01367

SEQUENCE DESCRIPTION:

GATCCATATT TAGTTTTATT AAGCTTTTCC CTGTTTTTAG TTTGTTTTG GGTTTTTTGG 60  
CTCATGAATT TNATTTCTGT TTGTCGATAA GAAATGTAAG AGTGGAATGT TAATAAATTT 120  
CAGTTTAGTT CTGTAATGTC AAGAATTTAA GATTTAAAAA NCGGATTGGT TAAAAANTGC 180  
TTCATATTTG AAAAAGCTGG GAATTGCTGT CTAAAA 216

SEQ ID NO:1222

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01368

SEQUENCE DESCRIPTION:

GATCGNCTCT GAACCATCCC NTTTCTGCTG CCCGGAGCTG GGAAGCTCG CTGTGGAGCG 60  
TCTGCACGT GGCAGGCAGG CAGAGAACTT GCTGCACCTT CTAGGAAAT GCAATCGATT 120  
TGTAATGCAC TTTGCTAAT TGGGAGTTCA AAATTAACT TTAATAAAGC AAA 173

SEQ ID NO:1223

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01369

SEQUENCE DESCRIPTION:

GATCTTAAGA GCAGACTTAA AGTAGCTTTG TACGCCTTAA TGTTCATTTT GATTTATTTT 60  
AAATCTTTAC ATTCAGAAAT NAGATACTGT ATTATCAGAC CAGGAGGCAT TGCTGTGAAA 120  
GATAATNTCC TATTCTAAAA TATCAAATTT AAAATAAAGA TAATGAAAGA AAACATAAA 179

SEQ ID NO:1224

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01370

SEQUENCE DESCRIPTION:

GATCCAAAAA TGGTAGCCAC TCACCCTTCA CAACTGAAG TCCATGGACC ACGGAAGTCG 60  
AGAATTAATG TACACCTGTA TCATGTGTAG GAAACCAGAA ATGTGTTTCT TATTNTTGT 120  
TCCCAAACAG GATTAATGT GAAGACTAAT TTATAAATGT GAACCTAAGA AA 172

SEQ ID NO:1225

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01371

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCAGCATG AGGACAGAAG GCAGGAGACT TTGGTCAGTT ACCTGGGAAT TCTGGGCTGC 60  
CAGGAAACGA TTTGGGCCTC TGTCAGTTTC TTTTCCATGT ATGAGGAGGG GGAAATTTGT 120  
ATATTAGAAA CTTATTCATC CCACTCAGGA CAATAAAAC GAATGTACAA AAAGCCAAA 179

SEQ ID NO:1226  
SEQUENCE LENGTH:175  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01372

SEQUENCE DESCRIPTION:  
GATCACAGTG GCCACGNCCA GGCCACAGTC ATGGTGGCCA CGTCCACAGC CACTAATCAG 60  
NAGNCCAGGC CACCCTGCCT CTACCCAACC AGGGCCCCGN GGCCTGTTAT GTCAAACNT 120  
CTTGGCTGTG GGNCTAGGGA CTGGGGCCAA ATAAAGTCTC TTCCTCCAAG TNAAG 175

SEQ ID NO:1227  
SEQUENCE LENGTH:318  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01373

SEQUENCE DESCRIPTION:  
GATCTTTAAT CTCATGAAGT ACGACAGCTA CAGCCGCTTC TTAAAGTCTG ACTTGTTTTT 60  
AAAACACAAG CGAACCGAGG AAGAGGAAGA AGATTTCCTT GATGCTCAAA CTGCAGCTAA 120  
AAGAGCTTCC AGAATTATA ACACATGAGC CCCCCAAAAG CCGGGACTGG CAGCTTTAAG 180  
AAGCAAAGGA ATTTCTCTC AGGACCGTGC CGGGTTTATC ATTGCTTGT TATTTGTAAG 240  
GACTGAAATG TACAAAACCC TTCAATGGGA TGTGTGTTTT ATTAAGTCTC TCACCAGTAA 300  
ATTTTGCATG ATGGGCTN 318

SEQ ID NO:1228  
SEQUENCE LENGTH:171  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01374

SEQUENCE DESCRIPTION:  
GATCTGGAAG AGGCTTGTA CCTGAACTTC TGTGTGGTGG CAGTACTGTG GCCCACCAGT 60  
GTAATCTCCC TGGATTAAGG CATTCTNAAA ANCTTAGGCT TGGCCTCTTT CACAAATNAG 120  
GCCACGGCCT AAATAGGAAT NCCCTGGATT GTGGGNANGT GGGCGNAAGT N 171

SEQ ID NO:1229  
SEQUENCE LENGTH:170  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01375

SEQUENCE DESCRIPTION:  
GATCTGATGG TTTTAAAAAG AGGAGTTTCC CTGCTCAAGC TCTCTCTCTT TGCCTGCTGC 60  
CATCCATGTA AGATGTGACT TGCTCCTCCT TGCCATCTGC CATGATGTGA GGCTTCCCCA 120

GCCACGTGGA ACTGTAAGTC CAATTAAACC TCTTTTCTTT GTAAATTAAA 170

SEQ ID NO:1230

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01377

SEQUENCE DESCRIPTION:

GATCCATGGT GTTAGAAGCC AGGGGAACAG TTAACAGGGG AGGGATACTG GGGAGGGGCA 60  
TCCTGGAGTG CTGGTCTACC TCATCTGGGT GTTGATTCA TGAGTATTGT CAGTTTGTTC 120  
CCAGACTCCC TGTGGAGAT GTGGAAATAA AAACCACCTA ANCANGNAAA 170

SEQ ID NO:1231

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01378

SEQUENCE DESCRIPTION:

GATCCATCAC AAAGCGAAGT CATGGGAGAG CCACACTTGA TGGTGAATA TAAACTTGGT 60  
TTACTGTAAT AGTGTGCTGT TCATGGAAAC CGAGGGCTGC ATCTTGTTTA TAGTCATCTT 120  
TGTACTGTAA TTTGATGTAC ACAACATTAA AAGTACTGAC ACCTGAGAAA 170

SEQ ID NO:1232

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01379

SEQUENCE DESCRIPTION:

GATCTGGGAT GGAATATGGT TTTCTTGATT CCCTTTCAGC CTTCAATTCT CTCTCTCAGG 60  
ACTACTACTT TTTAATTACT TTTCACTTAA TTTCCCAATA CTGATGAAAT AAAGAAAAAT 120  
GAGGGTTATT TATATACATT TCAATAAAAT CCAATTTGAT TTTTCAAA 168

SEQ ID NO:1233

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01380

SEQUENCE DESCRIPTION:

GATCTAGAGA ACATAACAAA TGAAACTCTA GAAATTTGAA AGAAAAAAAA ACACTTAGCT 60  
GTAAGTGCTT TGACCTATTT TTTTAAAAA AAAAAAAACC TGTNTTAATT CTGTGACTGN 120  
ATTGNACCCT TCACCAGCAC TANGNGAAGT NGGANTGGAN GAAATTN 167

SEQ ID NO:1234

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01381

SEQUENCE DESCRIPTION:

5 GATCAAGCCA TCGGAGCTGC TAGAGTTCTG TCTGGACTTT CCAGAGACCA GTATTCCCTT 60  
TTGCTGCCTC TAAAGGCCT GTCCCTGCAG ACATGAGAGA CAGCAGGTCT CATGGGGGTG 120  
ACAAGCTTTT TTTTTTTT TAAANGATT TCNAAANNNA ANTCCN 167

SEQ ID NO:1235

10

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01382

15

SEQUENCE DESCRIPTION:

GATCTTTTGT CTCCAGTCT TCTCTTAGTG TCCTGCTCCT AGGTTTCCT CTCTTCTGGT 60  
TCTTCTCCA GGTATTCTCT TCCCAGGCCT CTCTGGCCAC TGCTTTGTAT CAGGGTTTTT 120  
CACGCTTTTG TAGAACTGAG GTTCAATAA ACAGTTTCAG TTGCAA 167

20

SEQ ID NO:1236

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25

CLONE:HUMGS01383

SEQUENCE DESCRIPTION:

GATCCTCCAG CCCACCACCA CATAGTAATC ACTGACACTG TGGGGTGTCT CAGCTGGGGT 60  
TCTGCTGTGT GTGTGTGTAT TTNACAAAAT ATGTATGGTT TCTGTTGAGC TCTTTTCAGT 120  
TAACAGATGA ACTGNNNNTA TCATTAAATA TTTTGAAAA CATGAA 167

30

SEQ ID NO:1237

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35

CLONE:HUMGS01384

SEQUENCE DESCRIPTION:

GATCCATCAG TAATGTAGCT AGCTGTAGAG CTTGCAACTT AATAGCAGCA GCTGCCCAAT 60  
GCCATGTNAA GTAACAACT GGTTTTGGT TTTTTTTTC CCCTTCAGTT TAAATGTNAT 120  
GTGNAATGTA TTAAACCCT TATTAAATA AANCTTGTT TCAGAAATAA A 171

40

SEQ ID NO:1238

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45

CLONE:HUMGS01385

SEQUENCE DESCRIPTION:

GATCTGGGGT TGGGTCATGA CACCAGCTAC CAATTTNAGA ATATTATTCC TNGGTTTCTT 60  
TATGAAAAAT GGGTGCTAGT GGTAATTCCT TNGTGGCTTA GTAACTACT CTNTGGATGA 120

50

55

TTTCCAAACA TTCAAAGCCA ATAGCCTNGT NATNAACAAG ANATTN 166

SEQ ID NO:1239

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01386

SEQUENCE DESCRIPTION:

GATCAAAACC CAGCAGAGTG CAAGCAGCAG TGAAGCAGGA TGGTCTACCT TCTGCTTCCC 60  
TGGAAAGGAT GAATTTACAT CATTTGACAA GCCTATTTTC AAGTTATTTG TTGTTTGTTC 120  
GCTTGTTTTT GTTTTTGCAG CTAATAATAA AATTTCAAAT ACAA 165

SEQ ID NO:1240

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01387

SEQUENCE DESCRIPTION:

GATCTGTCTG TGTGTTATA TATTCTTTTA TGCATACTTA AAGTTAAAGG GTTTTATCCA 60  
CTGTCAATTC AATTGGATAA CATTTTGTCA AGTTTTTTTT TCCTGATTAT TTGATGTAGC 120  
TGGATTCAAG AATGGATTGC CTNATCAATA AAGAATATTT AGAAA 165

SEQ ID NO:1241

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01388

SEQUENCE DESCRIPTION:

GATCCTATTT TGGGCCTGGG GTGGGTATAC CTGNGGCTGG TCTTAGGAGG GTGCTAGGCT 60  
GCAGACTGCC TTGTACTCCC TGGACACCCT CAAATGGGGT TTTCTGTGTT ATTTCATAAA 120  
ATTCTTTGAA GTCCAATAAA GCATGTAGGA GATTTTAACC ACTAAA 166

SEQ ID NO:1242

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01389

SEQUENCE DESCRIPTION:

GATCAAAGGN CAAAAGACCA AAAATCAGCG GGCTGAGGAT GGAGCACAGC CATGAACCTG 60  
CTCAGACAA GACGCACCCA TGCTTCTCAG GGTCAAGGCT TTATGTTAAA GCTTCCTGTC 120  
GGGGCTGCTA GGTCAGCATT AAAGTAAGGC AACCAACAGT NAAA 164

SEQ ID NO:1243

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01390

SEQUENCE DESCRIPTION:

5 GATCTGCTCA GTAATATAAT TTGCCATTTT TATTAGAAAT TTAATTTCTT CATGTGATGT 60  
 CATGAACTG TACATACTGC AGTGTGAATT TTTTGTGTTT GTTTTAAAT CTTTATAGTGT 120  
 TTACTTCCTG CAGTGAATTT GAATAAATGA GAAAAAATGC AAA 163

SEQ ID NO:1244

10 SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01391

15 SEQUENCE DESCRIPTION:

GATCTGGATT TGCTTTACCT TGTTAATATT ATCTAGGGGA AAAAGTGCAA ATTGCTCCAT 60  
 GTTCTTCTCT CCCTTATGTA ACATCTCCTG AGGGTGTTTA GTTGCATGGC TGTTCAAGAA 120  
 GGTATTAAGG GCTTAGGCCA AATCTTACTT TGAGTATGTT AAA 163

20 SEQ ID NO:1245

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS01392

SEQUENCE DESCRIPTION:

GATCGTCAAA AAGAGAACCA AGAAATTCAT CCGGCACCAG TCAGACCGAT ATGTCAAAAT 60  
 CAAGCGTAAC TGGTGGAAAC CCAGAGGCAT TGACAACAGG GTTCATAGAA GGTTCAGGG 120  
 CCAGGTCTTG ATATGATGCC CAGCATTGGT TATAGNGCA AA 162

30 SEQ ID NO:1246

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS01393

SEQUENCE DESCRIPTION:

40 GATCTGGAAG TGAACACAGT TTATGTACAG GGAAAAGGAT TTTATTATCC TTAGGAATGT 60  
 CATCCAAGAC GTAGAGCTTG AATGTGACGT TATTTAAAAA CAACAACAAA GAAGGCAGAG 120  
 CCAGGATATA ACTAGAAAAA GGATGTCTTT TTTTTTTTTT TNNCNCNCCC TANTAANCNCT 180  
 GNTGCTGCCT NANTTTN 197

SEQ ID NO:1247

45 SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01394

SEQUENCE DESCRIPTION:

50 GATCTCAATG CCAATCCTCC ATTCTTCCTC TCCAGATATT TTTGGGAGTG ACAAACATTC 60

55

TCTCATCCTA CTTAGCCTAC CTAGATTTCT CATGACGAGT TAATGCATGT CCGTGGTTGG 120  
GTGCACCTGT AGTTCTGTTT ATTGGTCAGT GGAAATGAAA 160

5

SEQ ID NO:1248  
SEQUENCE LENGTH:160  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS01395

SEQUENCE DESCRIPTION:

15

GATCTGAAAA TCGACCTCAA CTCAAGGGTG GTCAGCTCAA TGCTACACAG AGCACGGACT 60  
TTTGATTCT TTGCAGTACT TTGAATTTAT TTTTCTACCT ATATATGTTT TATATGCTGC 120  
TGGTGCTCCA TTAAAGTTTT ACTCTGTGTT GCACTATAAA 160

20

SEQ ID NO:1249  
SEQUENCE LENGTH:159  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

25

CLONE:HUMGS01396

SEQUENCE DESCRIPTION:

GATCTGCATG ACCTATAATC TTTGAACCAC TTTCGTACCT CATGTTTTTA TCCAGCACTC 60  
TTATTGTAAT ATGTACTAGT CTGTGAACAA TGTCAAATAA AAGAGAACGA ACAGGTAGTT 120  
TGGTGGAGCT GAGCTAGTGT ACAATACACT AGTTGTAAA 159

30

SEQ ID NO:1250  
SEQUENCE LENGTH:159  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

35

CLONE:HUMGS01397

SEQUENCE DESCRIPTION:

GATCTTGAA TTCTTGNTG GATTNCACA GTTTTAAAA TTAATCATGT CAGCCCAATG 60  
CAGCTGTGTC ATTGCCACCT AGTGGTAAAA CTAACATTAC TGTTAAGCTG TGTGATTTA 120  
AACTTGAATC CCCAGTAAAN GGTCACTGT TCTGTGAAA 159

40

SEQ ID NO:1251  
SEQUENCE LENGTH:159  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

45

CLONE:HUMGS01398

SEQUENCE DESCRIPTION:

GATCCCTCTG AGAGTTGATG AGGATGTGTA ACAAGTATTT NCTTCTATNG TGCCTGCCAG 60  
GGCTGAAGCT GCCTGGTATC CAGGAGGGGA ATGCTGGTAT CCCCATATGN CTGTNTTGT 120  
TTGAGATTTT TAATAATAAA TAATAAATTT TTGAAGAAA 159

50

SEQ ID NO:1252  
SEQUENCE LENGTH:158

55



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01400

SEQUENCE DESCRIPTION:

GATCCTATTC TTGTAAAAAT ATTTGTATGT ATGCACAGAA ATCTGCAAAG ATGTACACTT 60  
AGTGAAGTGG TTACCAACGA ATGGTGGGAC TAACTAAAAAT GGTCTTTTTA CTTATATGTG 120  
CATTTCTTTT TATAATAAAA ATGGGTATATA TGCCTAAA 158

SEQ ID NO:1253

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01401

SEQUENCE DESCRIPTION:

GATCTGCCCT GTGTTATCCA GTTATGAGAT AAAAAATGAA TATAAGAGTG CTTGTCATTA 60  
TAAAAGTTTC CTTTTTTATT CTCTCAAGCC ACCAGCTGCC AGCCACCAGC AGCCAGCTGC 120  
CAGCCTAGCT TTTNCCNTT TTTTTTTTTT NNNCNNTN 158

SEQ ID NO:1254

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01402

SEQUENCE DESCRIPTION:

GATCTCAATC TTCGGGGTGT GATGAATAGC GAATCATCTC AAATCCTTGA GCACTCAGTC 60  
TAGTGAAGAT GTTGTCAATTA TGTACAATAC ATAAC TAGTT TAATTAACTA TGTGATGTTA 120  
ACTATTATTA ATAAATTTTA ACATTTTCCA AAATAAA 157

SEQ ID NO:1255

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01403

SEQUENCE DESCRIPTION:

GATCCGGATG NGGGGAGCTC TGTACAGAGG GCTGGTGATT GTAAAAATTT CTTTGTAAA 60  
GTAGAAGTTG GGGGTGGGGT GGGTGCTGGC TGCAAAAATT TCTGGCTTCT CTTACCCCTA 120  
TTGCCCCCGG CAATAAATTG TTTCTATATG CCAGAAA 157

SEQ ID NO:1256

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01404

SEQUENCE DESCRIPTION:

GATCTTATTT GGAATTGACA TTCTCTATTG TAATTTTNTT CCTGTTTATT TTAAATTTN 60

EP 0 679 716 A1

CTTTTGTGTT CACTGGAAAG GAAAGATGAT GCTCAGTTTT AACGTAAA AGTGACAAG 120  
TTGCTTTGTT ACAATAAAC TAAATGTGTA CACAAAGAAA 160

5 SEQ ID NO:1257  
SEQUENCE LENGTH:156  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01405

10 SEQUENCE DESCRIPTION:  
GATCTTTGTN CTTGACCTCT AGACCCAAG ATGTGAACAG TGCACGTTTT AATGTCATCT 60  
TTNCTCATGT GTTATAAGCC CCAAGTTGCT GTATATTNC ACAAGTATGT CTACACACTG 120  
GTCATGATTT TNATAATAA TAACGATAAA TCGAAA 156

15 SEQ ID NO:1258  
SEQUENCE LENGTH:155  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01406

20 SEQUENCE DESCRIPTION:  
GATCTTGCTC TGATTATAAT GCCAGTGAAT GTTGCTGAAC TCTTTGTATA TGCAAATTGC 60  
AAGATTAAA CCATTCTGAT GCAAGGATAA ACCTTTACTT TGACTIONAG CCTGTGTTTT 120  
25 TGTCTTAAA TCTCTTAATT TCATTCTCT GCAA 155

SEQ ID NO:1259  
SEQUENCE LENGTH:155  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01407

30 SEQUENCE DESCRIPTION:  
GATCTGCACT CCCACTCCCC CCACACTTCC CAAAGTGCTG GGATTACAGG CATAAGCCAC 60  
35 AAGCCACCTC ACCCAGCCAA CATGTTACAT CTTAATTCTT GGATTTCTT CACTGCAGGG 120  
CTTTGGGTGG AGAAATAAAA CTCTTCAAAT GCAA 155

40 SEQ ID NO:1260  
SEQUENCE LENGTH:155  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01408

45 SEQUENCE DESCRIPTION:  
GATCTGGGAG TGCTGGACGT CATCTCCAC CNCACCCAGC CGTGGGTCTT CTCCTCGGGG 60  
GCAGACGGGA CTGTCCGCCT TTACCTAG CTGTTCTGCC TGCCTGGGGC TGGGGTGGTC 120  
GTGCTGAAGT CAACAGAGCC TTTACCCTGT GCAA 155

50 SEQ ID NO:1261  
SEQUENCE LENGTH:158

55

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01409

SEQUENCE DESCRIPTION:

GATCTTGGAG GCCAGCCAGC TGAAGGAGAC ACTGCAGGCG GTGCCCAAGC CAGGGGCCTT 60  
TGACCTGGAG CAGGTGAAGC GTTCCACCTA CTTNTTCAGC TGACACCCCG TGAGCCTTGT 120  
CAGTGTGTAA ATAAAGCTCT TTTGCCACCC CCAGGAAA 158

SEQ ID NO:1262

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01410

SEQUENCE DESCRIPTION:

GATCCATCAT NGATGTAAAA GTTCACAATC ATGGTTCAAA TGTAACAGTG CAGAATTGAA 60  
TATGGAGGCA TGCATAACCT TCCTCTTAGA AAATGGCAGG TGTTGTAATT TCAAATTTT 120  
GTGCAATTAG ATTAAATCAT AATGCAACAA A 151

SEQ ID NO:1263

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01411

SEQUENCE DESCRIPTION:

GATCTGATGG GTTTATCAGG GGTTCCTACT TTTGTTTCTT CATTTTCTCT TGCCACCAGC 60  
ATGTAAGAAG TGCCTTTGGT CTCCTACCAT GATTCTGAGG CCTCCCTAGC CATGTGGAAC 120  
TGTAAGGCCA ATTAAACCTC TTTTCTTCC CAAA 154

SEQ ID NO:1264

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01412

SEQUENCE DESCRIPTION:

GATCAGCACC TTGTATAGGA ATTCCCATGA ATTATGACTT CTCATTCTGT TTTATCAGAG 60  
TGCATATATG TCCTACTTCA GGAAAAGTAA AACAGTCATT TACGAAAGAA AGTCAATCTG 120  
TATCCTAAGC ATTTTAATAA AAAGTAAAA CAAA 154

SEQ ID NO:1265

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01413

SEQUENCE DESCRIPTION:

GATCCTGGCC TGAGAATTGA GGGGAGGTGG CCAGCCCGCA GAGGTGGGGT GCTGGGGCTG 60

CATGATTTTN GCCCTGCGTC CCTTCTCTTT GGGGCTCCTT TCCCCTCTCA TACATAAAAT 120  
CGCTTTTCAAA TTAATAATCGC TGTTTTCTGG AAA 153

5 SEQ ID NO:1266  
SEQUENCE LENGTH:163  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01414

10 SEQUENCE DESCRIPTION:  
GATCCGAGTG AAGCCCCAGG TCTCANAGAG CAAGCTGTAG CCAGATGGTA CCAGCTTCGC 60  
CTGGGGCTTC AAGAACCTCC CATCTATCCC CATTCTGAN ACAGGGAGTT ACAGTCCCTT 120  
TTTGCCCTC ACATNCAATA AANGTGACTG ATANCACTGG AAA 163

15 SEQ ID NO:1267  
SEQUENCE LENGTH:153  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01415

20 SEQUENCE DESCRIPTION:  
GATCTGGCAA CACGTTTTNN TTGGAATATT TGTGTTTCT TGAGGAGGTA TAATTACTGT 60  
ATCCTAGGTG TGAATTTTG AGTGCAGATG CACATTTAA AGAAATNATG ATTAANCTGA 120  
25 TAATGTTTTT NGGCTGAAAA TATAAANNA AAN 153

SEQ ID NO:1268  
SEQUENCE LENGTH:152  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS01416

SEQUENCE DESCRIPTION:  
GATCATAAT CAAGGAATGC TGACAGCCAC TAAAGCTGGA GAAGGCCAAG GACAGATATT 60  
35 CAATCCTCCC GTAGAAGTAC AGCCCTGCTA ATGCATTGAT TTTGGACTTC TGGCCTCAGA 120  
ACTGTAAGAG AATAAATTC TATTGTTTTA AA 152

SEQ ID NO:1269  
SEQUENCE LENGTH:152  
40 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01417

SEQUENCE DESCRIPTION:  
45 GATCAGACCA ACAGTGCTGT TTCCGGGAG GAACACTTTT TNATTNTTAC CCTTTGCAGC 60  
TCCCACCTTT AATCTGTTTT ATACCTTGCT TATTAAATNN GCGCTTAAAT NATTGAAATA 120  
ATGCTGNCTT AGTAGCAACT AAAATGTGNC TN 152

50 SEQ ID NO:1270  
SEQUENCE LENGTH:156

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01418

SEQUENCE DESCRIPTION:

GATCCCCCT ACCCACCCCA GTCCCAAATC CAGTCCTCTG GCCCTTGCT AGCCCTGAAT 60  
TGCTTCTCTA AGCTGGTGTT CCCATGCACA GGGCCATTCA GGAAGGGCTG GGGGAGTGTG 120  
TGTGGCAATA AAGCTTGAAG GCACCGTGGG AGCAAA 156

SEQ ID NO:1271

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01419

SEQUENCE DESCRIPTION:

GATCCTCTTC TCTCCAAATG TTAGCCATCC TGAAGTAGCC GAACAGTAGA AACTTTGGTG 60  
GGGATTAACC GGGAGCTTGA AAATTTGTNT TTGGTAACCT GATACTGGAC AGCTGAACTG 120  
AATGGCTGCA AAATAAATAC CTCACATGAA A 151

SEQ ID NO:1272

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01420

SEQUENCE DESCRIPTION:

GATCCTGGAG GACCCTGGGC CCCAGGCCAG CTCCCATCGC TGGGGGACGG TGAACGGCCA 60  
TGTGTTAATG TTACGATGTT TTAAAAGAC AAA 93

SEQ ID NO:1273

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01421

SEQUENCE DESCRIPTION:

GATCCCTTT GTCAGTGGGG AAACCAAGGC AGAGCTGAGG GGACAGGGAG GAGCAGAAGC 60  
CATCAAGATG GTCAAAGGGC CTGCAGAGGG AGATGTGGCC CTCCTCCCC CTCATTGAGG 120  
ACTTAATAAA TTGGATTNAT GACACCAA 149

SEQ ID NO:1274

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01422

SEQUENCE DESCRIPTION:

GATCTCAACG TGCTGATATG GAAAGTGCTT CAGAATGTAT TAAGGACATA AATTAAGTGT 60  
ACAATAATGT GTGTGTGTGT ATATATGTAT ATGCTTACGT GTGTATGGAA AGTATCTCAG 120

CAGATACAAT AAAAAGTTAA TTGTGATTAA A

151

SEQ ID NO:1275

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01423

SEQUENCE DESCRIPTION:

GATCCTCCCT CTATTTTGCA AACAGTCTGT AAGTAACTNA TAAAACTTTA AAATATGCAA 60  
 ATTTTAAAAT TATATAGTTT GATTACTCA TCAAATTATC ATGTATGCTG TTATTTAAGT 120  
 ATGAATAAAG GCTTTTTTAA ATNGGAAA 149

SEQ ID NO:1276

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01424

SEQUENCE DESCRIPTION:

GATCCTACTC CTTTGGAGTA AAAC TAGTGC TTACCAGTTT CCAATTGTAT TTAGCTTCTG 60  
 GTTGGAATTT GAAAAAAAAA GAAAAAAGA AAAAGAAAAC CTAAATAAAA TAGGTGAAAG 120  
 TTCCCTGACT ATTCAGGTGA ATACACAAAG TTTGAAGTGT TAACTTTTTC TTTCCATTTC 180  
 ACTGATGTTA CTGGTCACCT TAGAGAATTA TTTCATAGTC TGTGGCTAAA TAGTAAATTC 240  
 AGANGAAAAA TAAA 254

SEQ ID NO:1277

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01426

SEQUENCE DESCRIPTION:

GATCCTACTG TTGAGTTAGG AAAATATGGT TAGACAGACT CACATTACTT TTTTTCAGAG 60  
 GTAAACTCTA GATTACTGTG TCAACCCAAT ACTATTTGGC CATAGATGTA AAAACTACCA 120  
 AATAAAAGTG GATTTTGTGG TCTACAAA 148

SEQ ID NO:1278

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01427

SEQUENCE DESCRIPTION:

GATCCACAGT GGAGTCTCAG TAATTATATC TCCTTGATTT CTTCAATTTNC TCTTCTGCTA 60  
 TAAAAGTAGA GATAATGTGT AGTCACTNCT CATTTAGTGA ACCAATTGTN ATANTTCTGG 120  
 AAATCTNITT TCTTTAAGTG TAAATANN 148

SEQ ID NO:1279

EP 0 679 716 A1

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01428

SEQUENCE DESCRIPTION:

GATCCCAATC AGATTCCCGC TAATGGAAGA AGTTTAGAAT CTTTCAGGTG GAATAAAGTC 60

ACATGAAAAC AAAACACAAC TATATATATT TCCAGTTTTT TTGCCTTATT GATTTTTTNC 120

CAAA 124

SEQ ID NO:1280

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01429

SEQUENCE DESCRIPTION:

GATCTTTGGG GAGATACATC TTATAGAGTT AGAAATAGAA TCTGAATTTC TAAAGGGAGA 60

TTCTGGCTTG GGAAGTACAT GTAGGAGTTA ATCCCTGTGT AGACTGTTGT AAAGAAACTG 120

TTGAAAATAA AGAGAAGCAA TGTGAAA 147

SEQ ID NO:1281

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01430

SEQUENCE DESCRIPTION:

GATCCTGACA CTAAGGAATG CTGAAGCTTT GGACTTCGGC AGTCTCCAC CTTCAAGTCAT 60

CAGCTACAGT TGGAATGAAT TTNAACGC TCGGGACCTG TTAATNTNTC CTGTAGNCTG 120

TATTATNTNA AAAATCTGGG CAACAAA 147

SEQ ID NO:1282

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01431

SEQUENCE DESCRIPTION:

GATCTCGCTC CCCCTTCGG TTCTTCGAC CGGTCCCCC TCCCTTTTTT GTTCTGTTTT 60

GTTTTTTTT GCTACGAGTC CACATTCCTG TTTGTAATCC TTGGTTCGCC CGGTTTTCTG 120

TTTTCAGTAA AGTCTCGTTA CGCCAAA 147

SEQ ID NO:1283

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01432

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTCAGTT CCTGGCTTTC CCCCCAGCCT TCTCACCCTT TGTGTCTGTG TAGTGATTG 60  
GTGAGAAATC GTTGCTGACC CTCCCCAGA CCATTATGA GTCNAAGTTT ATTATTCAAT 120  
AAAAGTGCTN TATGCGCTTT CTCAAA 146

5

SEQ ID NO:1284  
SEQUENCE LENGTH:146  
SEQUENCE TYPE:nucleic acid

10

TOPOLOGY:linear  
CLONE:HUMGS01433

SEQUENCE DESCRIPTION:

15

GATCCAAAGA TGAGGGGATT NTTTCAGAAA GACAATCTCG GCATGCATTA TTTCTTTNNT 60  
TTGAAGATTC ACTCATGTTG CATGCATCTN TAGCTTGTC CTTTTTAATT CCTAGTAGAT 120  
TCTGTCATAT GCCTATCTNC AATTNN 146

SEQ ID NO:1285  
SEQUENCE LENGTH:167  
SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear  
CLONE:HUMGS01434

SEQUENCE DESCRIPTION:

25

GATCCCCATG CTAAGAAAAT GCCCAAAAAA ATAGGCAAAA CACGAGAAGA GCTAGGGTAA 60  
GAGAAGGACG TAAACAGAAC CTGACACCAG CTCCTTTTCC TTCTATACAT TATTTAATAC 120  
CTATTAAATA AAATNATTTT TGGAATAAAG CTTGTGGGAA CATTAAA 167

SEQ ID NO:1286  
SEQUENCE LENGTH:179  
SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear  
CLONE:HUMGS01435

SEQUENCE DESCRIPTION:

35

GATCAAAAAG GCTTATAAAA CAGAGTAATC TTGTTGGTTC ACNCTTGNGA CCGTGAAGAT 60  
ACTTTGTATT GTCCTATTAG TGTTATATGN ACATNCAAAT GCATCTTNCA TGTGTTGTTT 120  
TTGGCAACAA ATTTTGAAAA GTAATATTTA TTAATNTTT TTGTATGCAA ACATGCAA 179

SEQ ID NO:1287  
SEQUENCE LENGTH:145  
SEQUENCE TYPE:nucleic acid

40

TOPOLOGY:linear  
CLONE:HUMGS01436

SEQUENCE DESCRIPTION:

45

GATCCGATGG GAGTGTAAT GTGAGACACA ATGTCTTGAT TATACCTGTT TGTGGTTTAG 60  
CTTTGTATTT AAATAAGGAA ATAACTTGA AAATNATTTG TCATCATAAA AATGAAACAA 120  
ATNAAAATAT TTATTGCCAG GCAAA 145

50

SEQ ID NO:1288

55



# EP 0 679 716 A1

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01437

SEQUENCE DESCRIPTION:

GATCAGGGCA TGCAACCAAA AGCAGCTTAA ATGAAATATT TAAAAATAAA ATATCAGGAA 60

GCTATTTTGA GATTTCTNCT GGCTTATGTT TCTACTTTAG GACCCTCATT GTNCTCTTAT 120

TAAAAAAAAT TATTCCTGT GCAAA 145

SEQ ID NO:1289

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01438

SEQUENCE DESCRIPTION:

GATCAGATTT TTTTGTACC TACGTAAGAG TACTTGAAGT TTTATTTAAA ATAAAATGTT 60

GTGGAAAAGG TAGCATTCTT TTTTAGGAG TGTTATTTT CACTATGTGT GGCACGGATA 120

CAATAAAAGA CTTTACAAA CTAAA 145

SEQ ID NO:1290

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01439

SEQUENCE DESCRIPTION:

GATCCCAGGG CTCCTGCCA TTTTAGTGTC TTGGTGTAGT GTAACCATTT AGTGGTTGGT 60

GCCATTTTT TTTTGTNCA AATGATTTAA ATNATTGGAA TNCACAATTT TTAAATATN 120

CAAATAAAN GTTAAAACC TTAAA 145

SEQ ID NO:1291

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01440

SEQUENCE DESCRIPTION:

GATCAGGAAT TCTAAATAAA TTTCCAGTT AAAGATTATT GTGACTTCAC TGTATATAAA 60

CATATTTTGA TACTTTATTG AAAGGGGACA CCTGTACATT CTTCCATCAT CACTGTAAAG 120

ACAAATAAAT GATTATATTN ACAA 145

SEQ ID NO:1292

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01441

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTGCCAG CACCCTGTGG GGCCAGACT ACAGGCTGAT GGCGGAGGCT TCGAGTGACC 60  
CGGGTGCCGA GGAGCGGGAA GAGTTGCTGG GGTAAGGGTC TGCGGCGACG CCGGCGCCCT 120  
GTGCCGTGTC CACGGGTGCA TAAA 144

5

SEQ ID NO:1293  
SEQUENCE LENGTH:144  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS01442  
SEQUENCE DESCRIPTION:  
GATCTAAATA TTTNNAGCT GAGTTATTAG GGAGTCATTA TTCTGTGGTA CAATGCTGCA 60  
AAAAGCATCA TGTGGAAGAA TGGGAACAT GCTTACTTTA TGAAGTGATG TATAACACAA 120  
TGAAATCTGT TTTACAATA CAAA 144

15

SEQ ID NO:1294  
SEQUENCE LENGTH:372  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01443

20

SEQUENCE DESCRIPTION:  
GATCTTGGTA GTATCCCTGG CTGCTAAGCC TATGGCAGGG GTGGTCCTTT CTACATTCCC 60  
ATTCATTAA CAGCTCTTTT GGGATTGGGT GTTTCATTCC ATTTCTGCCC ACTCCCTCTC 120  
CTCTCCTCTC TGGTAGGTTT AATTTTATGC TTTCCCTGAT TCCAGCTTTC TGCTTCCTGA 180  
GGACTCCCGC TCCCNCCACC CCAAAGTTTG TCTGTGGGTG TTATAGTGGT AACTGCAGTT 240  
CCCTCCTCTG GGAATNGTAG GCTGTAATAG GNTTAATAAA CTCNACNTNC TCTAATCNTT 300  
GCTNAAAANG TGGGGGTAAAN GGGGATGGCN TTGNCCCNNG GTGGGAAANT TAAANNTGGT 360  
GTTTANGGNA AA 372

30

SEQ ID NO:1295  
SEQUENCE LENGTH:145  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01444

35

SEQUENCE DESCRIPTION:  
GATCTTCTCT GTGGGGGAAA AGGAAGAGGA GGGTCTTGTT CTCCANTNT GTTTATTCTT 60  
TGGGCTCTGG GAACAGGGGA CTACTTTGGG GCTTCTCCA ATNCTNTTGT ATGNTGTTAT 120  
TAAAAGCGAG CTATTGCATT TCAAA 145

40

SEQ ID NO:1296  
SEQUENCE LENGTH:141  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01445

45

SEQUENCE DESCRIPTION:  
GATCTTATAT CCTGTGACCT GTCTAAATTC AATCTGTTAG TTTTATCATT TTTAAAAAA 60

50

55

ATGTCCGTGT GTGTCTTCCT TGAGATTTTC TACATTATCA TGTCATCTGC ANATAAAGAC 120  
ATTTACTTCT TTCTTTCCAA A 141

5

SEQ ID NO:1297  
SEQUENCE LENGTH:141  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01446

10

SEQUENCE DESCRIPTION:  
GATCCAGTTG TACTAAGGTG TACAGGATAT TTGCAGATAT AGGTAACTG AATGAAGCAT 60  
ATTAATAACT GCATTTNCCT AACTTTGAAA AATTTTNCAA ATGTCTAGGT GATTAAAAA 120  
ATGAGATTGG GCTATTGCAA A 141

15

SEQ ID NO:1298  
SEQUENCE LENGTH:140  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01447

20

SEQUENCE DESCRIPTION:  
GATCTAAAAT AGATATGTTG GATTGATATT CTCACGTGTT CGGTGTGGAA AACAAAACAA 60  
GTACATGCTT TAGAAGCAAC AACAAATGAAA TCCTTTTGAA ATNTGTGTGA ATATCGTTTA 120  
NTAAAATACC TAGTTTGAAA 140

25

SEQ ID NO:1299  
SEQUENCE LENGTH:140  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01448

30

SEQUENCE DESCRIPTION:  
GATCCATAGA AGGGCTTCCC AAACCTTGTT TTGCAACATC CCAAATTGTC TCCAGTTGAA 60  
GGAAGGCCTT TATCAGATTC ATAGATGAGC TTTCATTGTA AAAATAAATG TACTTTGCAC 120  
CACTTCATGA TGGAGGGAAA 140

35

SEQ ID NO:1300  
SEQUENCE LENGTH:140  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01449

40

SEQUENCE DESCRIPTION:  
GATCTGAGGT TTTTAGATTT TAAATATTTA TGTGGAATTA ATTAAAGGTA GTTGGCTATA 60  
TCGCTATCAT TTCATTCTTT TGACATTATT TGAATATTTT ACTGGAAAAT AAGACTAATA 120  
AATTGTAAAA AGTTTTTAAA 140

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SEQ ID NO:1301  
SEQUENCE LENGTH:139

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01450

SEQUENCE DESCRIPTION:

GATCTTCACA AAGTTGTCTT TTCACTGTGT TTTGTCAACG TGAAATTAAA TTGTAGTTAT 60  
AAGCAAAAGT TGGTTGCCTA GGGAAACAATT GTATATNCAG TTAAACAGAA ATAAAAGAAT 120  
ATTTGTCTTA AGATGCAAA 139

SEQ ID NO:1302

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01451

SEQUENCE DESCRIPTION:

GATCGNCACA TTCCCAAAA ATAATAAAAA AATCACTAAC CTTTTTTAAG GAAAATATTT 60  
AAAGTTTTAC AAAATTCAAT ATTGCAATNA TCAATGTAAA GTACATTNA NTGCCTTATN 120  
AAAACTTTCC CAATTAAA 138

SEQ ID NO:1303

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01452

SEQUENCE DESCRIPTION:

GATCATTTTT TCGGTCTCCG AGGTGAAATG ACTTATTAAT TAAAATTTGT AAACCTCAT 60  
ATGCATATTG TATATGTGTA GAAATGTAAT CACACTTTGT CTGGAATTA CATTAAACTG 120  
TTTGAAATCA CTGTAAA 137

SEQ ID NO:1304

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01453

SEQUENCE DESCRIPTION:

GATCTTTTTG TGATTGCTTT CCCGTCTCTA AGTAGTATTC TGTTGTGTCT AGAGAACTGA 60  
TTTTTTCCTA CATACGCAAA TTGTACATT GTAAAGTGAAA ATNTCAATAC ATTTAAAGCA 120  
TTANCCTAAA ANCAAA 136

SEQ ID NO:1305

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01454

SEQUENCE DESCRIPTION:

GATCAGCTGG GTTTTGGCCA GGAAGTTGTC TTTGTGGACT CTGCCTGCAT GGCTTAGTAG 60

TTGAAGGAAA TTTTTTTTGG GTTTTGTTTT TTATAATTCA GTTTAATCAA TAAACATGTA 120  
TTTATTGACT GTTAAA 136

5

SEQ ID NO:1306  
SEQUENCE LENGTH:136  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS01455  
SEQUENCE DESCRIPTION:  
GATCCCTTTA TGAGTTTTCG TATTTTGGCA TGCTACATGT AAGTTTTCCT TAATGTTTTT 60  
ATGTAAAGCA TCTTCCTCCT TTTACTTCTT TTATTGTGAT AAAACTCATA TAAAATTGAC 120  
CGTTTGAAG TGTAAG 136

15

SEQ ID NO:1307  
SEQUENCE LENGTH:136  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS01456  
SEQUENCE DESCRIPTION:  
GATCTGGGCC CGACCCTCAC TACCCCTGAG ATATTAGTTC CCAGGCCTGT TTTCCACAG 60  
GATTGTGGGC TCTCTGCTTC CTTAGTCGGA AGTNTTTTCA ACTAATCAAA TAAATGAATG 120  
AATGATGAAT AAGAAA 136

25

SEQ ID NO:1308  
SEQUENCE LENGTH:135  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS01457  
SEQUENCE DESCRIPTION:  
GATCCCAAAG ATATTAAATA TATGCAAATA TTCCAAAGTC TGAAAAATC CAACATCCAA 60  
AAACACTTCT GACCCAAGCA TTTCAGATAA GGGACCAGAA TTATTAGATT AAATAAGGTA 120  
TATTATTAAG TTAAG 135

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SEQ ID NO:1309  
SEQUENCE LENGTH:135  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40

CLONE:HUMGS01458  
SEQUENCE DESCRIPTION:  
GATCAGGCCA AGAGGTTGCA CAGGGCATGA TACTGCACCC TGCCTGACCC AGCTGGGCTC 60  
ACAGGTCAGG GGAGAGTTGG GGCAGGTGAA TGTCAGCATC AGGCTTCTNN TTTTAAACTT 120  
TTAAANAAAT ACAA 135

45

SEQ ID NO:1310  
SEQUENCE LENGTH:135

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55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01459

SEQUENCE DESCRIPTION:

GATCCTGCCT CAAAAAAAC AAAAAAATC TTTATTTTCT CCATAAACTA CAGTTTATAT 60  
AAGCAAAAGT TTCAGTACTA AGCAATTNA GTCTCTGCAG TCTCTNGTNT TGANTTAATA 120  
CAACTTTNGT NAATN 135

SEQ ID NO:1311

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01460

SEQUENCE DESCRIPTION:

GATCTACCTG TGGCCCGGCC TCCCTAATGT NATTCACATT GAATGGGGAT GAGGTCGGAC 60  
AGTGGCTCAT AGAGCGAGTA TGAGCCCTAG CTGTGGGCTA GAAATNTCT TAATAACAT 120  
CCTTATTTTC NTNTTTAAA 139

SEQ ID NO:1312

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01461

SEQUENCE DESCRIPTION:

GATCCTAGTA TGTGATAGC TTTNATTTG TGAGTGGTTT ACTAGTCATT TATTATGATT 60  
CCCATGANCT CTGATATGAT TCATTGTGGT TTAACTCAG GTTGAATAAA AGCATCCATT 120  
TCTTTTATAG GAAA 134

SEQ ID NO:1313

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01462

SEQUENCE DESCRIPTION:

GATCTCAAGG TTGATAGTGG TGTTCACTAG GAGACGTGGA ATTGAGACTA ATAACCTGGA 60  
TGTTAACTACT GTTACTGTT TTTTCACATG TAGAAATGTT CTTGTGTAT TTTTCTACA 120  
GAGGATTTTC TCTGATTTTA TTTTCTTTGT TTCTGACTCT AATAATTAGT TGGAACCTCA 180  
TATAAAATGA GCTTTCCTAA ATTAAATCTA TTTTAAATAA AGGTATTAC TATTAAT 237

SEQ ID NO:1314

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01463

SEQUENCE DESCRIPTION:

GATCTATAGG TTTATTAGAA NCCTNACCAC AGNATCCAGA TTATCTTCAG TATTCTNTCA 60  
 GTACAGCTCT CTGCAGCTTA AACTCGGTGG TACATAAAGA AGATGATGAA CCCCCAATGN 120  
 TGGNCACTGT ATAN 134

5

SEQ ID NO:1315  
 SEQUENCE LENGTH:133  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01464  
 SEQUENCE DESCRIPTION:

10

GATCAGAAAA TCCCTCTGAC ATCTCCACTG CCCCCAAAGA CCTCCGTTGA ACATTCTGTA 60  
 TGGAAAAGAG CCCTGGAGCA TCAGGTTCCC CAGATAGGCC CCAAATAAA GACCTGTCTA 120  
 TGGCTCTCCC AAA 133

15

SEQ ID NO:1316  
 SEQUENCE LENGTH:132  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01466  
 SEQUENCE DESCRIPTION:

20

GATCTAGCTG GCTGTAGTAT TGCNTTGATA ATTTTTTCT TTTAATTAC CTAATATATA 60  
 TAAGGAAGGG GTTTGGATAT ATTAATAAG GTGTTAATT TATCTATTTA CCAATAAATT 120  
 CATCTCTTTA AA 132

25

SEQ ID NO:1317  
 SEQUENCE LENGTH:130  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01467  
 SEQUENCE DESCRIPTION:

30

GATCCAGCCA TTCCTGAAGC CCACCCTGCA CCTCATTCCA ACTCCTACCG CGATACAGAC 60  
 CCACAGAGTG CCATCCCTGA GAGACCAGAC CGTTCCCCAA TACTCTCCTA AAATAAACAT 120  
 GAAGCACAAA 130

35

SEQ ID NO:1318  
 SEQUENCE LENGTH:130  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01468

40

SEQUENCE DESCRIPTION:  
 GATCTAAAAG CCAACTTTTT CTCAGNTTA CTCAGTGGAA AGATAAACTA AGTTTTAATG 60  
 TTATNTTTTT AAATNTAAGC AAAATTTATT TCTGTNCTNT AATAAATAAG AAAATGTGGT 120  
 CCACTGCAAA 130

45

SEQ ID NO:1319

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55

SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
5 TOPOLOGY:linear  
CLONE:HUMGS01469  
SEQUENCE DESCRIPTION:  
GATCCCCTGC TCCTGTTGTG TTCTGTTGTA AATCATTGCGAGACTGTA TTTTAGTAAC 60  
TGCTGCCTAA CTTCCCTGTG TTCTATTTGA GAGGCGCCTG TCTGGATAAA GTTGTCTTGA 120  
10 AATTTCAAA 129

SEQ ID NO:1320  
SEQUENCE LENGTH:128  
15 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01470  
SEQUENCE DESCRIPTION:  
GATCAGAATT TTAAAGCAG AATTTTGTCA AAAGGGTCAT TTTTGTCT ACCCCTTTTA 60  
20 CACTTTTCAG ATTCTCAAAG TGTCTCATCT CAACTTTTAA AAGAATAAAG AATATCTTGC 120  
TGGGCAAA 128

SEQ ID NO:1321  
25 SEQUENCE LENGTH:128  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01471  
SEQUENCE DESCRIPTION:  
30 GATCCTTGTC AGATGAAAAT GGATTCACAG CTCTGGCAGT TCCCAATGTC TGGGGAGGGG 60  
TATAGGTTTG AAAGGCTGTT TGAAAGAGGA ATGTTTAATA AAGGCTTTGA TTTAATCTTG 120  
AAAAGAAA 128

35 SEQ ID NO:1322  
SEQUENCE LENGTH:128  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01472  
40 SEQUENCE DESCRIPTION:  
GATCTCGAAG TNACTCCGGG CTGAGCAGTG GGGCGGCTGG GGGAGGGGTG ACGATTCTCC 60  
TCAGGCTTTG GCCCTGCAAG CAAACCCACA TATCTNCTCT GTATGTAATA AATNTNTTAA 120  
CGTCGAAA 128

45 SEQ ID NO:1323  
SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
50 CLONE:HUMGS01473  
SEQUENCE DESCRIPTION:

55



EP 0 679 716 A1

GATCCTGAAG CNGCACTTAC CTNTGAANAG TCTTCAAACCT TTAAACCTT GCCAGTNAGG 60  
ACTTTTNTCTA TTGCAAAATAG AAAACCCAAC TCAACCTGCT TAAGCAGAAA ATAAATTTAT 120  
TGATTCAAAA 129

5

SEQ ID NO:1324  
SEQUENCE LENGTH:127  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS01474

SEQUENCE DESCRIPTION:

GATCTGTGAA GTTATTTTGT AAGGACATAC ATTTGGTAAG TAAGTTTGTG TCCCAGGAAA 60  
TGTATGTNTT TTAAACCTT TTCTAAATAT GCAGGCCATT AATAAATAAG ATTGTTTCTT 120  
CCCTAAA 127

15

SEQ ID NO:1325  
SEQUENCE LENGTH:127  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS01475

SEQUENCE DESCRIPTION:

GATCAGAGAG ATTTTNTTTT TAACTACCA TGGTCCCAGG ATTCCATCCT GAAATNAATT 60  
TTCCTTTGTA TGAATATGTG TAAATAATTT AAAAATAAAA CTGTAAAANA TTTGTNCGAA 120  
GAATAAA 127

25

SEQ ID NO:1326  
SEQUENCE LENGTH:137  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS01476

SEQUENCE DESCRIPTION:

GATCCCCCTT CATTTGATGT TTGGAAAATN CCAGTAATTA TCATTTTTC AACGAATATG 60  
GATACCACAT AGTACTTTGG TGTACCTGC TTTTGAAAAA TAAAGTCTTT GGTTACCCCG 120  
GTGAACCTATT TATGAAA 137

35

SEQ ID NO:1327  
SEQUENCE LENGTH:126  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40

CLONE:HUMGS01477

SEQUENCE DESCRIPTION:

GATCCTCAGC CTCCCAGTGG TCTTTGTAGA CTGCCTGATG GAGTCTCATG GCACAAGAAG 60  
ATTAACACAG TGTCTCCAAT TTTAATAAAT TTTTGCCCAT TTCTTATTAA AAAAATTGT 120  
TGTAATA 126

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SEQ ID NO:1328

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SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01478

SEQUENCE DESCRIPTION:

GATCCATCTG TGTAGTTTCT GAACAGTCAG CGATTCCAGG TTTTAAATAG TTTGTAAATT 60  
TTCAGTTTCT ACACACTTTA TCATCCNCTC GTGATTTTTT AATTAAAGCG TTTTAATTCC 120  
TTTCTCAAA 129

SEQ ID NO:1329

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01479

SEQUENCE DESCRIPTION:

GATCCATGCT TTAAGTGTT TAATGGGGGT AACAGGGGTC CCTACAGCCC TCCCAGCTAA 60  
ACATTTGGAA CAAAACACCA GCCCTTTTGT AGTGGATGCA GAATAAAATT GTTAATCCAA 120  
TCAAA 125

SEQ ID NO:1330

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01481

SEQUENCE DESCRIPTION:

GATCTGTGTT GAAAGTNGTA TATTTTATC TGTNCGGTGC TGAGTGCAGG CCACCAGCTC 60  
CTAAATAGAG GTTCCCTATA TGC GCGTATG ACATGGTGAA TAAACACAAC TCTCTCCACT 120  
CAAA 124

SEQ ID NO:1331

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01482

SEQUENCE DESCRIPTION:

GATCGTTGTA ATTNNTTGAC ATTCCTTTNA GAAGTTGTGA AATGTTACAA CTTGTNCTTA 60  
TG TAGACACA ATCTCCTGTC TCAGTACAGA GGC ACTGACT TCAATAAAGT CTATTTATAC 120  
TAAA 124

SEQ ID NO:1332

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01483

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCAAAAAA TGGAAATGTA TAATTAAATC ATACTTAGCA AATCTAACAC ATGAAATGTA 60  
ACATCTGCAT ATGGAGAATC GTGTTACTTT ATTGAAAAAC ATTAAANGTT TGAGANCTTA 120  
AGTTGGAAA 129

5

SEQ ID NO:1333  
SEQUENCE LENGTH:122  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01484  
SEQUENCE DESCRIPTION:

10

GATCTGCCAA GATTCTTTGA ATACAGATAA TTAATGTAAA CAATTATCAT AAGTATACTA 60  
ACATGTTATN CTTTTTAAAT AAGAAGGTAT AATAAAATAT CCCATTGGTT TNATGTATTA 120  
AA 122

15

SEQ ID NO:1334  
SEQUENCE LENGTH:122  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01485  
SEQUENCE DESCRIPTION:

20

GATCGGGCCN TTGGCTGTAA GACCCGACCC TTCGAGAACC CGANACGAAA CGCTCCATTA 60  
CCACTGCNCA GTGAGATGAG GGACTCACAG TTCCAAGAGG NTTCTTTCCC GTGGNCCCCT 120  
NN 122

25

SEQ ID NO:1335  
SEQUENCE LENGTH:121  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01486  
SEQUENCE DESCRIPTION:

30

GATCCAACCC TGTACTGATA GTA CTCTCCA GTATGATATT GTGATGTTT ATACAATGCA 60  
GTGAACATAA CCAACTTGTT ACCTAAATAA AGANTTGATA AAAACAGTGT GACATATTAA 120  
A 121

35

SEQ ID NO:1336  
SEQUENCE LENGTH:120  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01487  
SEQUENCE DESCRIPTION:

40

GATCAAGGTC TGCAAGGGAA TTCTTGTGTG CTGCTTTCCA TTTGACACCG CAGTTCTGTT 60  
CAGCCATCAG AAGAGAGACA AGGNATTAAA AATTTCTTTT TAATCNNGTT ACCAAATAAA 120

45

SEQ ID NO:1337  
SEQUENCE LENGTH:119

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01488

SEQUENCE DESCRIPTION:

GATCTAGTAG GCACGTCTGT CAACAGGACA CATGCCTCCT CTGACTATAA CCTCTTAATA 60  
GTTGTGTATA ATGAAAACG TAAACTTTTT TAAATAAACN GTGTATATAC CTTGGCAAA 119

SEQ ID NO:1338

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01489

SEQUENCE DESCRIPTION:

GATCCTGAAG CCATGGTTTC TTCCCTGCCA GAAATGAAAG GTTCAGTTAT GAGGCAACCC 60  
TCTAGTAAGG CATTGTAAAA GTTACTGGAT TTGGTTTAAT AAAAGTTGAA ATAAAGTAAA 120

SEQ ID NO:1339

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01490

SEQUENCE DESCRIPTION:

GATCTTCCGA GTGCTTGGGG CCCACAGAGA CATCATCCTG GAGAGCATT CCACTGACAA 60  
CCCAGAGGCG CACAGCAACC TCTACATCCT CACGGGCCAC CAGAGCACCT ACTAAGAGCA 120  
GCGGGCCTGT CCAGGGGCTC CCCGNCCCAC CCCACGCCTT AGCTGCAGGC CCTTTTGGGC 180  
AAAGGGGCC ATCCTGGGCC ATCCATTCCA TTTTGTCCA CATTCCTTT CTACTCTTC 240  
TGCCAAGAGN CTGCCCTGC ATTTGTCCTG GGAAACACGG TATTTAAGAG AGAACTATAT 300  
TGGTATTAAA GNTGGTTTGT TN 322

SEQ ID NO:1340

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01491

SEQUENCE DESCRIPTION:

GATCTTTGGA GCAAAAGCCA ACGGCAGGAA AAAATAGTTT GTACCAGTTT CATGAAGTAT 60  
GTCTTTGGGT TTTGTAAAT AATTTTAACT CAAATAAAAT TGCTACTTTC AATACAAA 118

SEQ ID NO:1341

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01492

SEQUENCE DESCRIPTION:

GATCAGAATN AAATNTGTAT AGAGCAGAGT TTAAAATGA ATGTAAATAG CACTAAACGT 60

NTNCTTTCTG CAACCTGTAC TTACAGATTC TCCCTGTAAA CTAAATAAAA AAAAAANTN 118

5 SEQ ID NO:1342  
SEQUENCE LENGTH:118  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01493  
10 SEQUENCE DESCRIPTION:  
GATCACAAAA TGTGCATGAG NGTTATTNAC TTTATTCTNG TACAGTACTA GGATTCCTGT 60  
AACCACTCTT TTTTTTCTTC GNNGTATTGA AAAGTGGTTC AGTGTTAACC AGGCAAGN 118

15 SEQ ID NO:1343  
SEQUENCE LENGTH:118  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01494  
20 SEQUENCE DESCRIPTION:  
GATCAATTCA CTTAAAAGNA TGGCCCANAT AGCACNNATA GGACCAAGGG ACACATGTAG 60  
TCANTTTTAA AAAACATGTA CTTGGTCTTT TGTGTGTGTC TGTTATATTC CATTAGAN 118

25 SEQ ID NO:1344  
SEQUENCE LENGTH:117  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01495  
30 SEQUENCE DESCRIPTION:  
GATCCCAGGA GAGCTGGGCT ATGACTGCAA TAAGGAGTTG TTCCTTCACC TGAGATGTGC 60  
TTCTTTTGGT TCATTTCTGG CTTGACAACA AGAAATAAAC GTGGTATGTT CCTGAAA 117

35 SEQ ID NO:1345  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01496  
40 SEQUENCE DESCRIPTION:  
GATCTTGAGG GACCCAACAT TTGTAGGGGC ACTAATCCAG CCCTTAAATC CCCCAGCTTC 60  
CAAACCTGAG GCCCACCATC TCCACCATCT GGTAATAAAC TCATGTTTTT TCTGCTAAA 119

45 SEQ ID NO:1346  
SEQUENCE LENGTH:116  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01497  
50 SEQUENCE DESCRIPTION:  
GATCAGATTT GGGTGGGAGA AAGAAGTGGG TATCAAGGGT GATTGAATT TTCTGCAGCA 60

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TTAAAGTGGC GTTAATAAGA TAAGTAATAA TAAAGAATTC TAACATCCAT GTCAAA 116

SEQ ID NO:1347

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01498

SEQUENCE DESCRIPTION:

GATCCGGTGG AAATCCAAGC TCTGGGCTGG TAATTTTAT GAGCATTTTC AGCTTTTGCA 60  
AATACAAAAT ATAATNCTTT ACAAAAATAA ATTTTATNC TAATCTAAAT CTGAAA 116

SEQ ID NO:1348

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01499

SEQUENCE DESCRIPTION:

GATCTTCTCT ATGATTGATA CATGGCACAG TGAGAGATTA ATGGGCATTG TGTACAAATT 60  
GCTTCTCACC ATCCCCTTA GACCTACGAA TAAAGCATCC GGTCTAAAA TTAAA 115

SEQ ID NO:1349

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01500

SEQUENCE DESCRIPTION:

GATCTTTTGT TAAAAGGACC AAATGTTCTT TTATAAATGT AATAAGGAAT ATCTTGCTCT 60  
TTAAAATTTA TTAGGNNTTT AATGAGTAAT TTNATTAAA AGATTCTTT TTTTGAAA 118

SEQ ID NO:1350

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01501

SEQUENCE DESCRIPTION:

GATCCTATTT GTTTCATTTT ATTGTAAATN CCCATTTGCA TCAAAACCTA ATNATAGTGA 60  
TNGGTAAGTA AAAACAAATG GTGTATTGCT TTTCATACAA GTGTTTTCAC AAAAGCCATT 120  
TGCCTAGGCA GCAAAAAATA TTAATTTGTT AAAAAAATT TTCCTTCGTG TCCATCCNCA 180  
NAAANTGNG NN 192

SEQ ID NO:1351

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01502

## SEQUENCE DESCRIPTION:

GATCTGTGGA CTTTCATCAN ATTATGAGAC TNNCTCAATT TCATGACTGT ACTACCTGAA 60  
ACAAAGTGAG AAAGGACAGG TGTATTTTNN TAAGTCATCA AGATAAATCC TTAAN 115

SEQ ID NO:1352

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01503

## SEQUENCE DESCRIPTION:

GATCTTAGTT TGTAGCTTAT GACTTATTTA ATGAATGGAT GCCCAGCCAA GCTCAGAGTA 60  
GGCGCCCAAA GCATTGTGGA TTATTTTCCT GTTTTGTCTT TTTTTTTTTT TTTTITNAAG 120  
CCATGNCANC CCNGANGGGG CCAGNGANTN 150

SEQ ID NO:1353

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01505

## SEQUENCE DESCRIPTION:

GATCGNNAAG AGGTTACCCA GACCACACAC AGTTTGAGAA AACATNCCCA TTATNACCCA 60  
TCTAGCAAAG AGGCACCCTA AGTGGTCCAT GAAGAGTTTA ATTTATNTT AAN 113

SEQ ID NO:1354

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01506

## SEQUENCE DESCRIPTION:

GATCGGGTTT AGACGNNAGN TCATTTCAGTG AAGCAAGCCA AAAGCNCACA TTTGTATGCC 60  
TTAGGTCTTC TTAAATGGT ATCTGTAAAC ATGTGTCCAA TATAAANCT ATN 113

SEQ ID NO:1355

SEQUENCE LENGTH:411

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01507

## SEQUENCE DESCRIPTION:

GATCCTCCCT GCCCGGAAG TGNACAGTTT ACAAATTAT TTTCTGCAAA AAAGAAAAAA 60  
AAGTTAGGTT AAAAACCAAA AACTACATA TTTTATTATA GAAAAAGTAT TTTTCTCCA 120  
CCAGACAAAT GAAAAAAG AGGAAAGATT AACTATTTGC ACCGAAATGT CTTGTTTTGT 180  
TGCGACATAG GAAATAACC AAGCACAAAG TTATATTCCA TCCTTTTAC TGATTTTTTT 240  
TTCTTCTATC GTTCCATCT GCTGTATTCA TTTNTCCAAT CTCATGTCCA TTTTGGTGTG 300  
GGAGTCGGGG TAGGGGGTAC TCTGTCAAA AGGCACATTG GTGCATGTGT GTTTGCTAGC 360  
TCACTTGTC ATGANAATAT TTTATGATAT TAAGGNAAT CTTTGAAAA A 411

SEQ ID NO:1356  
SEQUENCE LENGTH:112  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01508  
SEQUENCE DESCRIPTION:  
GATCATGGTG TAATAAGACA TAACGTTTTT CCTTTAAAAA AATTTAAGTG CGTGTGTAGA 60  
GTTAAGAAGC TGTTGTACAT TTATGATTTA ATAAAATAAT TCTAAAGGNA AA 112

SEQ ID NO:1357  
SEQUENCE LENGTH:112  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01509  
SEQUENCE DESCRIPTION:  
GATCAAGTGC ATTTGACAGA AAAGTTCAGT TTCTTGGGAA GAAACACCTT TTAAGCTGAA 60  
TGGAGAAAAT NCCAAAATAA ATTATATCAC CACAATGGTG TATACTCAGA AA 112

SEQ ID NO:1358  
SEQUENCE LENGTH:112  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01510  
SEQUENCE DESCRIPTION:  
GATCTGGGAA AAAACAAGA GACTCAATGG AGACAGAAGA AAATCCAAG GTTCTAATAA 60  
CTNCNTTCTN AAAAANTATC TACCCCATTT GGTGAAGTGA AAANCAGAAA AN 112

SEQ ID NO:1359  
SEQUENCE LENGTH:112  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01511  
SEQUENCE DESCRIPTION:  
GATCCTGGTT GGAGTAAACA TTCCATGGGA ACTCGGGCTG TNAGAATNTC CTAACCACT 60  
GANTGCAGAA ACATCCTTAT CACATCCTNC TGGGAAAGNC CAACAGCCTG AN 112

SEQ ID NO:1360  
SEQUENCE LENGTH:112  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01512  
SEQUENCE DESCRIPTION:  
GATCCATCAC CTGNGCAGCA TAACTGGCTT CNCTCAGTC ATCCACACAA CACCAGGACT 60  
TAAGACAAAT GGGACTCCCT GTCATCTNGA GCTATNCATT TATTAAACT GN 112



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SEQ ID NO:1361

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01513

SEQUENCE DESCRIPTION:

GATCCCTTCA TTGATGTTTG GAAATTCCAT ATTACATTTT GCACGATATG GTACACATAG 60

TACTTTGGTG TACCTGCTTT TGAAAAATAA AGCTTTGGTC ACCCGGTGAA A 111

SEQ ID NO:1362

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01514

SEQUENCE DESCRIPTION:

GATCAGAGAA TGCAGCAGCA GTTTTTTCC TNGTTTNCCT ACCACTTTAT TCTTTCANAG 60

TTTAAAGAAA ATGGACTCAT GCACAGAACA CTATGCATT NAAACTNGT N 111

SEQ ID NO:1363

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01515

SEQUENCE DESCRIPTION:

GATCGGGGGC GTANATNCAT AGTAGTTTTT ACAGCTGTGT TATTCTTTCG GTGTAGCTAT 60

GGAAGTTGCA TAATTATTAT TATNATTATN ATAACANGTG TGTCTTACGT N 111

SEQ ID NO:1364

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01516

SEQUENCE DESCRIPTION:

GATCTCAAAA CAGTGCTAAA ATCAAAGNTG TNGACTGTAA AGAAAAACAT GTATATATAT 60

TGCACCTNAA AGTTGTCAGA AGNTAGAAAC TNAATAAAC TAACTTTAAA 110

SEQ ID NO:1365

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01517

SEQUENCE DESCRIPTION:

GATCCCACGC CACAGCCTTT TGNTNTGCAA CTGCCTTCTT CGGAAAGAAG AAGTGGGAGG 60

ATGTGAATTT TAGTTCTGAG TTTACCAAAT AAAGAGATAT AAGACGAAA 109

SEQ ID NO:1366

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS01518

SEQUENCE DESCRIPTION:

10 GATCATGTAC TGAAGTAGTT TAAGCAGGCT GGCTAACTTA GACTNATTGA TTCTGCNTTT 60  
GTACTNNAAT AGGGGTTATA ATTGTAAGAT AAAAATGTGT GTGTNCAAN 109

SEQ ID NO:1367

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01519

SEQUENCE DESCRIPTION:

20 GATCTGGGGG TTTCTTCATA TTCCTGCTGT TGGAAGCAGT TGACCAGAAA TGCTTGNCAG 60  
NACTGCCAAA GCACTGCTGT GAAATGTGAA GTACTTTGTT TTTTATTTT TAATNATTTT 120  
CTTTTGTGA TTAATATTTT TCTCTGTTCC TTGTTATTA CTTGCATGGT TTGGCGTCAG 180  
AAGTCCTTAC CTCTTTATAT TGTTTGCAGG TTAAATAAA ACAGTGTGGT GCCAAA 236

SEQ ID NO:1368

25 SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01520

SEQUENCE DESCRIPTION:

30 GATCTTGAAG TTATTTTAA GACATACATT TGGTAAGTAA GTTGGTCCCA GGAATGTATG 60  
TNNTTNAAC CCTTCTAAA TATGCAGNCA TTAATAAATA ANATTGTN 108

SEQ ID NO:1369

35 SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01521

SEQUENCE DESCRIPTION:

40 GATCCAACCC AAATCAAATT GTTAAATGCC CTCTGAATT TTTTGTCTG TTATTTAATT 60  
ATATGGTGGA ATTAATAATA AAATAAACTT CATGTCTCTG ATTCAAA 107

SEQ ID NO:1370

45 SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01522

SEQUENCE DESCRIPTION:

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GATCTNGAGC TCTGTCTTCA GCAGATTTCA GGTGTAACAT TTGTAACTC GTACTNGAAG 60  
GTGTGTCCTC AAGAAGAAAG TTTTCAAATT AAAAAAGCTG CTGCAAA 107

5 SEQ ID NO:1371  
SEQUENCE LENGTH:107  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS01523  
SEQUENCE DESCRIPTION:  
GATCATGTAC ATTGTAACGT GTGTCGTCAG TACTGCAGTT CCTCAACTTT NTTTGTCTNT 60  
NATTACCATG ACATTTTAA AGATACAGCT ATTTTNTCGA TGTNAAA 107

15 SEQ ID NO:1372  
SEQUENCE LENGTH:286  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20 CLONE:HUMGS01524  
SEQUENCE DESCRIPTION:  
GATCACATCT AAAGCTTTAT CTTTGTGTAA TCTAAGTATA TGTGAGAAAT CAGAATTGGC 60  
ATAATTTGTC TTAGTTGATA TTCAAGGCTT TAAAAGTCAT TATTCCTGGG CTTGGTAAGT 120  
GAATTTATGA GATTTACTGC TCTAGAAAGT ATAGATGGCG AAAGGACCGT TTTGTATTGC 180  
25 TTCCTGATTA CCAGTCTGAT TATACCATGT GTGCTAATAT ACTTTTTTTG TTATAGATTG 240  
TCTTAATGGT AGGTCAAGTA ATAAAAAGA GATGAAATAA TTAAA 286

30 SEQ ID NO:1373  
SEQUENCE LENGTH:107  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01525  
SEQUENCE DESCRIPTION:  
35 GATCCGCGCA CCTAAGCCTC CCAAAGTNCT GGAATTACAG GCATGANCTA CCATNCCTGG 60  
CCTTCTAATG TTTTCNTAA TTAAGGCTCT NAACTTCCA GACTGTN 107

40 SEQ ID NO:1374  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01526  
SEQUENCE DESCRIPTION:  
45 GATCTAGAGG NGAGAAAAAG ATGANTTGCT CCTTACATTC GATAATCAGT GACCACGAAA 60  
CACTCAGACC AGAGCCTGGC TTATCAAAA CCTNAGTGA GNNCTN 106

50 SEQ ID NO:1375  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid

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# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS01527

SEQUENCE DESCRIPTION:

5 GATCCACGTG CCATTGTGGA GGCAGAGAAA AGAGAAAGGN TTTATATACG GTACTTATTT 60  
AATATCCCTT TTTAATTAGA AATTAAAACA GTTAATNCNC TTCAAA 106

SEQ ID NO:1376

SEQUENCE LENGTH:117

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01528

SEQUENCE DESCRIPTION:

15 GATCCTGAGC TCCCTTTGCA GTCTGAAAAA GGTATTGCAG TCAGAACTGT GTACTGATGA 60  
TAAANGCCTC TGGTAGCAAT AAAAAGTTGT CCCTAACAAA AGAGGCAAAA AAATAAA 117

SEQ ID NO:1377

SEQUENCE LENGTH:105

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01529

SEQUENCE DESCRIPTION:

25 GATCCAGCAA ACAGGTTCTN TTAAAGAAAA ATAATTTATA CTAAATTNAG TAAAATGGAC 60  
TTCTTATTCA AAGCATCAAT AATTAAAAGA NTTATTTNAA TGAAA 105

SEQ ID NO:1378

SEQUENCE LENGTH:105

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01530

SEQUENCE DESCRIPTION:

35 GATCAGCAAA ATGAGATAAA TGTTTCTNTT TTCCTTTCTG ACTGCATTAA ATCAGATACA 60  
ACTCAGCATT AAAAAGCTAT CTNTGTAAAT NTNGTNACTA ATAAN 105

SEQ ID NO:1379

SEQUENCE LENGTH:105

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01531

SEQUENCE DESCRIPTION:

45 GATCTAACAC GAGGAACATA TCATGGAAAG TGCATNGTAT NTATTTTAGG GTTATGAGTT 60  
CTTTCAAGGG CTAAGNTGCA GAGNATTTC TCCANGAATC GTGTN 105

SEQ ID NO:1380

SEQUENCE LENGTH:105

50 SEQUENCE TYPE:nucleic acid

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EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS01532

SEQUENCE DESCRIPTION:

5 GATCAGGTGA CATGAGGGNT CACTCTTCTT GTTGACANN CTGTGAGTTC GGGCAAATNT 60  
GTAATGGCAT ATCTCCACTA TTACAGTNTC ACACAGAATT ATTTN 105

SEQ ID NO:1381

SEQUENCE LENGTH:332

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01533

SEQUENCE DESCRIPTION:

15 GATCGGTGCG TTCTCCTGAT GTTTTNCCNT GGCTTGGGGA TTGTACACGG GACCAGCTCA 60  
CGTAATGCAT TGCCTGTAAC AATGTAATAA AAAGCCTCTT TCTTTTGGG GTGGNNNTTG 120  
TCCTTCTGTC AGCTAAAATG GGAGCTCATG AGAGAAGGAC GTCAGGGAAA CGGGGTTGAG 180  
GGTGGTCTCG GTGCAGAGAG AAGGGTGTCA GGGAAACGGG GGGTGAGGGT GGTCTTGGTG 240  
20 CCAGACGTAG GGAATGGTGT TGGGAGTGGC CCGAGTGCCT GGCACAGTTG TCTNGTTCAT 300  
TCATGTAACA TGATAATTTT TAAATCATTA AA 332

SEQ ID NO:1382

SEQUENCE LENGTH:157

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01534

SEQUENCE DESCRIPTION:

30 GATCCTGCTG CTGTAATGGG AACCCCTCCC CCATTTACTT CTCCACCTCC CGTCCTCCCC 60  
ATCATTGGTT TTTTTTGTG TGTCAACTGT GCCGTTTTTA TTTTATTCCT TTTATTTTCC 120  
CCCTTTTCAC AGAGAAATAA AGGTCTAGAA GTAGAAA 157

SEQ ID NO:1383

SEQUENCE LENGTH:103

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01535

SEQUENCE DESCRIPTION:

40 GATCTACTGT TTGTTGAAGT GTGGGAAAAT AGCCTCTCTA AGGCAGCCCA GATGGGACCA 60  
AAATCAGTAC AAACATATTT AAGTAAATTT TAAATGCGT AAA 103

SEQ ID NO:1384

SEQUENCE LENGTH:284

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01537

SEQUENCE DESCRIPTION:

50 GATCCCCTTG TCCCTGGAGT AGGGACTAAC TATAGCACAA AGTAATATGT GCCAATGCTA 60

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5 TTTGTGAAAT GTTTGGGCTT TCTAAACGAC TAAAGGATTT GTNGGGTTTT TNCTTAAGTT 120  
TTGAACCAAA TCCTAGAGCC AGCTGATAAT ATTTAATAAT CTAGAGGAGA GAATAATGAT 180  
GTACCANTAA GTGGAGATTC CTCCTTATGA TGTATGCTAG GTTATGGAAG ATGTAAAATA 240  
TTCAACTTTT TCCTNCGTTT TTTGGACTTT GTATTTTACT GNAN 284

10 SEQ ID NO:1385  
SEQUENCE LENGTH:103  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01538  
SEQUENCE DESCRIPTION:  
15 GATCTGGAAC TCCTAAGCCA TCTACTCCTA CACCAACCNN TTCATCGAAC NCACACCCTN 60  
CTNATGCTCA GAGCTCAACT CCTAGTACCC CTTAGCCAC CCN 103

20 SEQ ID NO:1386  
SEQUENCE LENGTH:104  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01539  
SEQUENCE DESCRIPTION:  
25 GATCGCCGTT CTGTTTNGCA TNNTCCCACC GGGAGTTGCC NGGCAGGAGC ATGGGGTGCT 60  
TGGTTGTTTC CTTCTAATA AAATAAACGC GGGTCGCCAT GAAA 104

30 SEQ ID NO:1387  
SEQUENCE LENGTH:102  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01540  
SEQUENCE DESCRIPTION:  
35 GATCTTAGCC TTAGGGTAAG TAAAATGGGT CTTTAAATAT AANAGTGTGA AAATATTTTC 60  
NATCTAATAG TACTCTTTN AATAAAAGTC AGTAGTNGGA AA 102

40 SEQ ID NO:1388  
SEQUENCE LENGTH:378  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01541  
SEQUENCE DESCRIPTION:  
45 GATCCTNGGT TTTTGTGGTT TGA CTCTCTAT GGNGTTTAA AAAACACAG ATTTTATGTT 60  
TTAATATTGT GTAAATGTAC TCACCTTAGG GATTCATTG AATGATGGTN TTATACCATG 120  
ATTGNTTACA GTTTGTGAAA TTGTTGCAAG GGCAAAGATA ACTCTTAAA AACCGTCGAG 180  
ATTACAATGC TCTAGAATCA GCATATAAGA AAATAAATGA TATCTNCATG TNGANTNNGG 240  
GTGGATGGGG GGAGCACGCA TAATTTTAA GTGTGAAGCT TTGCATCANA GAAATTATTA 300  
50 AAANGCTTTT TTNCTCCNGT ATNTTCCTGT ATTAATCCTT AATGTTTATG GCAAATAAAA 360  
TGTAAGGGGN ACATGAAA 378

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SEQ ID NO:1389

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01542

SEQUENCE DESCRIPTION:

GATCGTAACC GTAACCGTAA CCGNNAAGCA CAAACGGGGG GAGCGGGGCA GTGAGCGGGG 60  
CAGGNATGAG NCCCGAGGTG GGGTCGGTGG CCAGNACAAC GN 102

SEQ ID NO:1390

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01543

SEQUENCE DESCRIPTION:

GATCCAGAGG TCCNNGTCAC TTGGAGAAAG NCCAGTCCCT GNGACGGGGC AGCCCTCTNT 60  
TGCCCTCGGG CAGCTCGTGT GAATCCTGGG ACCTCTTCCG GN 102

SEQ ID NO:1391

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01544

SEQUENCE DESCRIPTION:

GATCTCAGCA ATTTGAACAC TAACCTCTCC CCTCCTGGCT CAAGAATTAC TCCGAAGTCA 60  
GTCTGCAGAA AATAAATATT TAGTATGACA TGACACTTAA A 101

SEQ ID NO:1392

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01545

SEQUENCE DESCRIPTION:

GATCTACTCA GGCAACNACC AATCTTCTAN TCTGTCACTA TAGATTAATT TGCATTNTTA 60  
AAGAAATNNA CATACATGGA ACCATACATC ATCTATGCTT N 101

SEQ ID NO:1393

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01546

SEQUENCE DESCRIPTION:

GATCCTAGGA AGTNTGTCCC TGTCTCCCT GTGCAGGGTA TCCTGTAGGG TGACCTGGAA 60  
TTCGAATTCT NTTTCCCTTG TAAAAATTN NTNTGTCTCT N 101

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SEQ ID NO:1394

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01547

SEQUENCE DESCRIPTION:

GATCCACGTG CCATTGTGGA GGAGAGAAAG AGAAGTGTTC ATATACGGTA CTTATTTATA 60  
TCCCTTTTAA TTAGAATTAA AACAGTTAAT TTAATTCAAA 100

SEQ ID NO:1395

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01548

SEQUENCE DESCRIPTION:

GATCTTAGGT TACATAAAGT TTCTAAAGTT TCAAAGAGTC TTGATACAAA ATCAGTTTAT 60  
ATTCTGAAAA TATTTATAAT AAAGTATTCT AATTTCTAAA 100

SEQ ID NO:1396

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01549

SEQUENCE DESCRIPTION:

GATCAATTCT TCAATTTGAT TGAAGTGTTC AGCCTTTTCA AGATTTCTTT ATTTACAAAT 60  
GATTACATTT AAATGAATGT ACATTCTTCT CACTGAAA 98

SEQ ID NO:1397

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01550

SEQUENCE DESCRIPTION:

GATCTGTAAC ATTTGTTTCA AAATGCTGTT TCATTTTAT AAAGTACCAG TGTTTAGCTG 60  
CTTTTATAC ATTAAATTAG CAATTTGAAA AACTCAAA 98

SEQ ID NO:1398

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01551

SEQUENCE DESCRIPTION:

GATCCTCAGT GTCCTTACCC CCTCCTACCT CTTTCTGTG CCACCTGCTG TGGGTCCAGC 60  
AGGCNTTTAC TTGAGTACAA TAAAAAGTCT GAGTCAAA 98



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SEQ ID NO:1399  
SEQUENCE LENGTH:98  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01552  
SEQUENCE DESCRIPTION:  
GATCCAAGTG TAGTGGGACC CCCTACTAGG GTCAGGAAGT GGACACTAAC ATCTGTGCAG 60  
GTGTTGACTT GAAAAATAAA GTGTTGATTG GCTAGAAA 98

SEQ ID NO:1400  
SEQUENCE LENGTH:104  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01553  
SEQUENCE DESCRIPTION:  
GATCTCCAAA GTGGTGAGTT TATGTGTGAT TTTTATTTTG TTTATGCTCT TCTGTATTTT 60  
CCGAATTCA TACAATAAAT ATCTGTTACT TTTACAATAT GAAA 104

SEQ ID NO:1401  
SEQUENCE LENGTH:94  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01554  
SEQUENCE DESCRIPTION:  
GATCCAGAGA GTTCAAGGGA TTGGGGAAAG AGAGGCGTCA AGTCATTGTC ACTTTGTACC 60  
TGTAAGTTAG GTAATAAACT ATTATACTCG TAAA 94

SEQ ID NO:1402  
SEQUENCE LENGTH:92  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01555  
SEQUENCE DESCRIPTION:  
GATCTAGTNT CTNGCATTTT TATTATGTTG CTATATACTT TTGTTATCCG TATACTAAAA 60  
AAAAAGAATA AATAAATGTT TTGATTGTTA AA 92

SEQ ID NO:1403  
SEQUENCE LENGTH:92  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01556  
SEQUENCE DESCRIPTION:  
GATCTNTACA TTCTTCAGAC TCATCGTGTG TTTGANACTT TTTATAATGA ACATATATCA 60  
TTTTNNTTAA AAAAGAATAA AGTTTTTGAA AA 92

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SEQ ID NO:1404  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01557  
SEQUENCE DESCRIPTION:  
GATCCTCTGG GGAAGCCAGG ACCAGGAGAG AAGCAAGGTC AAGAAATCCC ACAGTTTGAT 60  
GTATTAAAGA AATNACTTAT TTCTACTCAA AATAAATGGC ATTGAAGTCT TTCTTTAAA 119

SEQ ID NO:1405  
SEQUENCE LENGTH:90  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01558  
SEQUENCE DESCRIPTION:  
GATCTTGTGT CTCCTCTCCA TCTCTGCCTT TGTTACCAGT GTGCATGTGT TTGTGTGTTT 60  
TTTAATAAAA TATTGACTCG GCCAGTTAAA 90

SEQ ID NO:1406  
SEQUENCE LENGTH:90  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01560  
SEQUENCE DESCRIPTION:  
GATCTGTTAT GGCATTCACT TCCAGATTAA TTTTCCGTGT TTGAAGTATG TNCATATGTN 60  
CTTTACAGAA TAAAACATCT GAATTTTAAA 90

SEQ ID NO:1407  
SEQUENCE LENGTH:87  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01561  
SEQUENCE DESCRIPTION:  
GATCCATTTT CTTTCAAAAT TTTCTTTATT GTAAAGTATG CAAAATATAT ATTCATACGA 60  
TTTATTAAAT CAGAATGTTT ATACAAA 87

SEQ ID NO:1408  
SEQUENCE LENGTH:85  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01562  
SEQUENCE DESCRIPTION:  
GATCTGGAAT CCTTTTCTG CATTGACAAG GACCACAGCT AAAGGACAAT AATATGAATG 60  
ACTCATTAAA ATCTCAAAAC TTAAC 85

SEQ ID NO:1409

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01563

SEQUENCE DESCRIPTION:

GATCCAAGTT ATNTTNAGAA GAAAAACCTA ATTGAACAGG TATGGGTTGG GAGCATAATA 60

AATGTGTTTT GAGAATTGTT CTAAT 85

SEQ ID NO:1410

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01564

SEQUENCE DESCRIPTION:

GATCATTATT TCATGACTGG TGCCTTCCTA AACTCTGAAA TCAGCCTTGC ACAAGTACTT 60

GAGAATAAAT GAGCATTTTT TAAAT 84

SEQ ID NO:1411

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01565

SEQUENCE DESCRIPTION:

GATCTAAGCC CATGAGCACA GGGACTGGCT ATCCCAAGAC CTGGCAGATG TGGCTGCTCA 60

ATAAACACTT GTTGAACCAT CAAAT 84

SEQ ID NO:1412

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01566

SEQUENCE DESCRIPTION:

GATCACCCAA GGGTTTTTTT GTGTCGGACT ATGTAATTGT AAACATATACC TCTGGTTCCC 60

CATTAATAAGT NCCCATTTNA GTTAAAT 86

SEQ ID NO:1413

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01567

SEQUENCE DESCRIPTION:

GATCTGTGTT TGTATCCCTT TATGTAATGT AAAATTTAAG GGTATTTTGA TTCTAAATAT 60

GATAAAATAA TTTCTCACCT AAAT 83

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SEQ ID NO:1414  
SEQUENCE LENGTH:83  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01568  
SEQUENCE DESCRIPTION:  
GATCAGCAGT CCACCACAAA AGCTTCTGTT AAAAGACCCT ACACAAATGC ACAAATTCAG 60  
ATTAAACAAG GAAAAGACGG AAA 83

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SEQ ID NO:1415  
SEQUENCE LENGTH:83  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01569  
SEQUENCE DESCRIPTION:  
GATCTTGGTG TTCAAAACAG AACTGTATTT TTGCCTTTAA AATTAAATAA TATAACGTGA 60  
ATAAATGACC CTATCTTTGT AAA 83

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SEQ ID NO:1416  
SEQUENCE LENGTH:82  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01570  
SEQUENCE DESCRIPTION:  
GATCCTTCTG TAAAGGTTTT TGGAATTATG TCTGCTGAAT AATAAACTTT TTTGAAATAA 60  
TAAATCTGGT AGAAAAATGA AA 82

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SEQ ID NO:1417  
SEQUENCE LENGTH:86  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01571  
SEQUENCE DESCRIPTION:  
GATCTGCATA TTTCTGTATA TTTGTCATGA CAGTGCTTGC ATCCTATTTG GTGTACTCAG 60  
CAAATAAACT TTTCAATTTA AACAAA 86

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SEQ ID NO:1418  
SEQUENCE LENGTH:81  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01572  
SEQUENCE DESCRIPTION:  
GATCCCAACA TGGTCCTAGC ACTGCACACT CAGTTTTNCT CTAAGAAGCT GCAATAAAGT 60  
TTTTTNAAGT CACTTTGTAA A 81

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SEQ ID NO:1419  
SEQUENCE LENGTH:81  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01573  
SEQUENCE DESCRIPTION:  
GATCTTCANT TAATCNCAC T TAAAAATGA CCAAAACATG TCTTTCTTGA ATTAAC TTG 60  
AATAAAAGTT TGTATATTAA A 81

SEQ ID NO:1420  
SEQUENCE LENGTH:81  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01574  
SEQUENCE DESCRIPTION:  
GATCAGAGCT CAGTTCCTGT AGAAAACGAA CTGTAAAAGA CCATGCAAGA GGCAAAATAA 60  
AACTTGAAGT GAATGCTTAA A 81

SEQ ID NO:1421  
SEQUENCE LENGTH:80  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01575  
SEQUENCE DESCRIPTION:  
GATCTTGGGT TTGGTCTACC CACCCAAGAG AAAAGACTGT TAACTGGAAG AAAAAATATA 60  
TATATNNAAT TTTATGTAAA 80

SEQ ID NO:1422  
SEQUENCE LENGTH:79  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01576  
SEQUENCE DESCRIPTION:  
GATCACAATT ACCTTTAGTT GTTTTTTTTG TAATAATTGT AGCCAAGTAA ATCTCCAATA 60  
AAGTTATCGT CTGTACAAA 79

SEQ ID NO:1423  
SEQUENCE LENGTH:79  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01577  
SEQUENCE DESCRIPTION:  
GATCCTTATG AATGACAGGT TACTGTTTTG CCTTATTGCT TAACTTAATG TAGTGAAATA 60  
AAGCAGACAA AGCTTGAAA 79

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5 SEQ ID NO:1424  
 SEQUENCE LENGTH:79  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01578  
 SEQUENCE DESCRIPTION:  
 GATCTTCTGC ATGAGACCTG GAGTTGGGGA AGCAAGGTTA CATTTGTATT NGTTTATCCT 60  
 10 ATGAATACTN TTCTTCAAA 79

15 SEQ ID NO:1425  
 SEQUENCE LENGTH:78  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01579  
 SEQUENCE DESCRIPTION:  
 GATCAGGCAG TCTGCTCAGA TACATTGAGT GGCGATTTTA AGTTTTGTTT TGAAAAAATA 60  
 20 AACAGATTAA CCTGCAAA 78

25 SEQ ID NO:1426  
 SEQUENCE LENGTH:78  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01580  
 SEQUENCE DESCRIPTION:  
 GATCTAAATT TCTAATGTGT TCTATGGGTT TCAATTCTGA AAAAAGAAAA TGAATAAAGA 60  
 30 TTTTAATAAA TATTGAAA 78

35 SEQ ID NO:1427  
 SEQUENCE LENGTH:78  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01581  
 SEQUENCE DESCRIPTION:  
 GATCTTCATT GTGCTGGGTG CCAGGNCAGT NATCCATTTT AAAATTGTGA ATTCAATAAA 60  
 40 GTTTTTTTTG TTNTTAAA 78

45 SEQ ID NO:1428  
 SEQUENCE LENGTH:77  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01582  
 SEQUENCE DESCRIPTION:  
 GATCTCCAGG CTTGGCCTCC AGAGCAGCCC ACACCAACNC CAAAATAAAA AAATGTATAT 60  
 50 ATTCCTTTAG CTCTAAA 77

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5 SEQ ID NO:1429  
 SEQUENCE LENGTH:76  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01583  
 SEQUENCE DESCRIPTION:  
 10 GATCCCAGGG ACCTCAGTCG GCTTAATCAG AGTGTGGCAT AGAAGCTATT TAATGATTAA 60  
 AGTCATTTGC AGTAAA 76

15 SEQ ID NO:1430  
 SEQUENCE LENGTH:76  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01584  
 SEQUENCE DESCRIPTION:  
 20 GATCAAACCT TTNATGTTCT TAATAAGCTT GCAATTGANT AAAATAGAAT ATAAAATAAA 60  
 GGTGAAATAA TATAAA 76

25 SEQ ID NO:1431  
 SEQUENCE LENGTH:79  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01585  
 SEQUENCE DESCRIPTION:  
 30 GATCCCAAGT ACAATGAAAA GTTTGCACTG TATGCTGGAC GGCATTCCTG CTTATCAATA 60  
 AACCTGTTTG TTTTACAAA 79

35 SEQ ID NO:1432  
 SEQUENCE LENGTH:75  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01586  
 SEQUENCE DESCRIPTION:  
 40 GATCTCCAAC NTTGGAAAAT ATACATGATG TGAAACTGNG GGTNCTATGT TAAAAATAAA 60  
 TGTATGATAA CTAAT 75

45 SEQ ID NO:1433  
 SEQUENCE LENGTH:74  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01587  
 SEQUENCE DESCRIPTION:  
 50 GATCCAAACA TTTTGTGTG TGTGTATGGC ATTGATGCAG AATAGAATAA AATTATACTT 60  
 AAGTTCTTTT TAAA 74

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SEQ ID NO:1434

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01588

SEQUENCE DESCRIPTION:

GATCCCGGCG CGGGAAAAGTC ACAGAGCTGC CTGGGCTTGT ACCTGGNCAC ATAAAGCCCC 60  
ANTTTAAAGC AAA 73

SEQ ID NO:1435

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01589

SEQUENCE DESCRIPTION:

GATCCCANAG CNATAAAATA AAATTTTATT CCAAATAAC AAAACAAATT NATCTACTGT 60  
ACACAATCTG AAA 73

SEQ ID NO:1436

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01590

SEQUENCE DESCRIPTION:

GATCCCAGGC TTCTGCGGAC CGACGATACG TTAAATGTT GTTCTAGTAA AGTTTTCGAT 60  
ATGTTTCTGA AA 72

SEQ ID NO:1437

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01591

SEQUENCE DESCRIPTION:

GATCCCTTGG NGGNCTAGTT CGTATTTTGG TTTAAACTA TTTGTTAGAA TAAAGTAATT 60  
TTGCTAATAA A 71

SEQ ID NO:1438

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01592

SEQUENCE DESCRIPTION:

GATCTTAAGT ATAAAAATTT TGTAATTGGG CCTTTACTCT CTCAATAATA AAGTATTTTG 60  
TTTATATAAA 70



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5 SEQ ID NO:1439  
 SEQUENCE LENGTH:68  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01593  
 SEQUENCE DESCRIPTION:  
 GATCTGTATT TTCTAAGTCC CCAGTTCTCC TGGCTCTCCT TTCTGAAATA AAGGATTGAA 60  
 AACNGAAA 68  
 10

15 SEQ ID NO:1440  
 SEQUENCE LENGTH:67  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01594  
 SEQUENCE DESCRIPTION:  
 GATCTGTTT TAAAAATCAT AAAGTGTGTG CAGACTCAAT AAAATCATGT ACATTCTGA 60  
 AATGAAA 67  
 20

25 SEQ ID NO:1441  
 SEQUENCE LENGTH:71  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01595  
 SEQUENCE DESCRIPTION:  
 GATCAACAGT TACTGTNACT GAGTCGGCCC ATTCTGTTTA GAAATATATT TNAAATGTTT 60  
 AGTAATTGAA A 71  
 30

35 SEQ ID NO:1442  
 SEQUENCE LENGTH:66  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01596  
 SEQUENCE DESCRIPTION:  
 GATCTGCCAT TTCATGCCNT GTGACTACNN ATCATTGGCC CTGCAATAAA ATCATTTATT 60  
 TTTAAA 66  
 40

45 SEQ ID NO:1443  
 SEQUENCE LENGTH:64  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01597  
 SEQUENCE DESCRIPTION:  
 GATCTGCGAT GCTACTCTTA GATAGAAGAT GGCAAAACCA TGGTATTAAA ATATGAATGA 60  
 TAAA 64  
 50

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SEQ ID NO:1444

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01598

SEQUENCE DESCRIPTION:

GATCAAGTCA CTNTTGACAA CATCCAGGNG AATATAAAAA CTTAATAAAG CTGTGGAAAG 60  
GAAA 64

SEQ ID NO:1445

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01599

SEQUENCE DESCRIPTION:

GATCAATTGG TTAACTTCT TTTATGTAAG TATGGTATAT AAATTTCAAG ACGAACACTA 60  
AA 62

SEQ ID NO:1446

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01600

SEQUENCE DESCRIPTION:

GATCACTTTT CACTTTTGG AATGTTTGT ATTGAACTT AATAAACTT TAACATGGCA 60  
AA 62

SEQ ID NO:1447

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01601

SEQUENCE DESCRIPTION:

GATCGNTCTC AGGCCCTCCC CCCGGAGTAC TTCAGAATGC AATAAATCAA AATAATGGCA 60  
AA 62

SEQ ID NO:1448

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01602

SEQUENCE DESCRIPTION:

GATCTGTATG TGTTCTATTC AGCACAAGGA AATAAAATTT TAGTTGAGGA TTCAGCACTA 60  
AA 62

SEQ ID NO:1449  
SEQUENCE LENGTH:62  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01603  
SEQUENCE DESCRIPTION:  
GATCCCCATT CTTTCAAAA ACAAATAAA ACAATAAAGA CTGCAAGGAA GACTGANGGA 60  
AA 62

SEQ ID NO:1450  
SEQUENCE LENGTH:62  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01604  
SEQUENCE DESCRIPTION:  
GATCCAGTCT GGAATAACAT TTTGTAAAAA AAAAATATAT ATATATATAT ATATNGCTGA 60  
AA 62

SEQ ID NO:1451  
SEQUENCE LENGTH:61  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01605  
SEQUENCE DESCRIPTION:  
GATCGGGGGC ACCAGAGGGG CAGAGGCACC AACATCTGAA TAAAGCCATT GTTCTCCCAA 60  
A 61

SEQ ID NO:1452  
SEQUENCE LENGTH:61  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01606  
SEQUENCE DESCRIPTION:  
GATCTTGGAC NTCTCGCATT CAGAACTGTG AGAAATAAAT ATCTATTATT TACAAATTAA 60  
A 61

SEQ ID NO:1453  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01607  
SEQUENCE DESCRIPTION:  
GATCTCCGTC TTGTATGGCT GAATGTTGGC CTAAAATAAA GATTACTGTT GTAAAATAAA 60

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5 SEQ ID NO:1454  
 SEQUENCE LENGTH:62  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01608  
 SEQUENCE DESCRIPTION:  
 GATCTGTGGA GAATGTACAC AGTTTAAACA CATCAATAAA TACTTTAACT TCCACCGAGA 60  
 10 AA 62

15 SEQ ID NO:1455  
 SEQUENCE LENGTH:72  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01609  
 SEQUENCE DESCRIPTION:  
 GATCAAGAAT CCTGCTCCAC TAAGAATGGT GCTAAAGTAA AACTAGTTTA ATAAGCAAAA 60  
 20 AAAAAAACCA AA 72

25 SEQ ID NO:1456  
 SEQUENCE LENGTH:59  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01610  
 SEQUENCE DESCRIPTION:  
 GATCTAGATG TTTCTTTAAC CAAGATGAAT TAAAATATAG TAGAGTTCCA CTGTNCAAA 59  
 30

35 SEQ ID NO:1457  
 SEQUENCE LENGTH:63  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01611  
 SEQUENCE DESCRIPTION:  
 GATCAAATTG TACCTTTTGA GAGAAAAGGA CCAAAATAAA AGAAAAATGA ATTATGAACT 60  
 AAA 63  
 40

45 SEQ ID NO:1458  
 SEQUENCE LENGTH:59  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01612  
 SEQUENCE DESCRIPTION:  
 GATCAGCAGT CTTGGATGGN AGGNAACAAA GCTAAATAAA TGTTAGTTTG GTGAGCAAA 59  
 50

55 SEQ ID NO:1459  
 SEQUENCE LENGTH:65

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SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01614  
 SEQUENCE DESCRIPTION:  
 5 GATCTCCCTT ATATTCTTAT GATGAGGCTA AATAAAAGTC TAATAAAAAT GTTAAATATG 60  
 TGAAA 65

SEQ ID NO:1460  
 10 SEQUENCE LENGTH:56  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01615  
 SEQUENCE DESCRIPTION:  
 15 GATCAAAATC AAGTTTAAAG TTTTTTTGAC CAGATAAATT TAATGATTTT GGCAAA 56

SEQ ID NO:1461  
 20 SEQUENCE LENGTH:58  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01616  
 SEQUENCE DESCRIPTION:  
 25 GATCTTAATT ACTTTCAGAA TATTTTCAAA ATAGATATAT TTNAAAATC CTTACAAA 58

SEQ ID NO:1462  
 30 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01617  
 SEQUENCE DESCRIPTION:  
 GATCGTTCTT CTCTCCGTAT TGGGGAGTGA GAGGGAGAGA ACGCGGTCTG AGAAA 55

SEQ ID NO:1463  
 40 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01618  
 SEQUENCE DESCRIPTION:  
 GATCCCTGAG ACGGGGTAAG TTATAATAAA CAGAAATGTA TTGGCTCAGA AGAAA 55

SEQ ID NO:1464  
 45 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01619  
 50 SEQUENCE DESCRIPTION:

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GATCTGTTAT GTATTTCAAC ATAATCATGT TTCATAAAGA TTTAGTCTTC TGAAA 55

SEQ ID NO:1465

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01620

SEQUENCE DESCRIPTION:

GATCCACCT TTGCTCCTGA CAACCCTCAT TTCAATAAAG ACCAGTGAAG ACCAAA 56

SEQ ID NO:1466

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01621

SEQUENCE DESCRIPTION:

GATCAGAATC CTGCTCCACT AAGAACGGTG TAAAGTAAAT TAGTTATAAG CAAA 54

SEQ ID NO:1467

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01622

SEQUENCE DESCRIPTION:

GATCTTGAGC CTTAACTGGA CATGAGGGGC ATGAAAATAA AGCTGAACTG CAGCCTCCTG 60  
AAA 63

SEQ ID NO:1468

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01623

SEQUENCE DESCRIPTION:

GATCTTTTCT AAATGTTATT ACTTGTAAT AAAGTCTATT TTTCTCCCGT GAAA 54

SEQ ID NO:1469

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01624

SEQUENCE DESCRIPTION:

GATCTGTATA TTTTCTTA AGAGAAAATG TAAATAAAGG ATTTCTAGAT GAAA 54

SEQ ID NO:1470

SEQUENCE LENGTH:54

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SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01625  
 SEQUENCE DESCRIPTION:  
 GATCTGCGCA TATATATATA TGTATAAAAA ATAATAAAAT AATGGAAGNT GAAA 54

SEQ ID NO:1471  
 SEQUENCE LENGTH:54  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01626  
 SEQUENCE DESCRIPTION:  
 GATCCTAAAT NCACGCACCC CGTGGGAGCN CAATAAAGAT TTACTGAATT GAAA 54

SEQ ID NO:1472  
 SEQUENCE LENGTH:53  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01627  
 SEQUENCE DESCRIPTION:  
 GATCCGCCAT CTGTAATGTC CTTGGCACAA TAAACCAAA TGTCAGTTTC AAA 53

SEQ ID NO:1473  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01628  
 SEQUENCE DESCRIPTION:  
 GATCCCTAGT GATTACAGCC CTGAAGAAAA TTAAATCTGA ATTAATTTTA AA 52

SEQ ID NO:1474  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01629  
 SEQUENCE DESCRIPTION:  
 GATCCAGTGT GGATTCTTNG AGTAATAACG TTGGTTTTAT TTATCATATA AA 52

SEQ ID NO:1475  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01630  
 SEQUENCE DESCRIPTION:  
 GATCTTCAAT GTTTATTTTA AAATAAAATA AAATAAGTTC TTGACTTTTA AA 52

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5 SEQ ID NO:1476  
 SEQUENCE LENGTH:56  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01632  
 SEQUENCE DESCRIPTION:  
 GATCTTGAAT GAAAGTCTTC TCAGGCTGTA GGGTGGTTCC TACAACCACA GCCAAA 56

10 SEQ ID NO:1477  
 SEQUENCE LENGTH:51  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 15 CLONE:HUMGS01633  
 SEQUENCE DESCRIPTION:  
 GATCTCATCT GAATCCCCAA CACCCAATAA AGTTCCTTTT TAACACACAA A 51

20 SEQ ID NO:1478  
 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01642  
 25 SEQUENCE DESCRIPTION:  
 GATCAAAATC CTATTTAGAA AAAATAAAAC TACTTTCTGT TTATCTCTTT AGAAA 55

30 SEQ ID NO:1479  
 SEQUENCE LENGTH:34  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01671  
 SEQUENCE DESCRIPTION:  
 35 GATCCAAAAA CATCCGTGAA CCTCTGTCTG TAAA 34

40 SEQ ID NO:1480  
 SEQUENCE LENGTH:305  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01673  
 SEQUENCE DESCRIPTION:  
 45 GATCAAAATA AAGGATGATA ATAGATATTA TTTTNCCTTA TGACAGAAGC AAATGATGTG 60  
 ATTTATAGAA AAACGGGAA ATACAGGTAC CCAAAGAGTA AATCAACATC TGTATACCCC 120  
 CTTCCCAGGG GTAAGCACTG TTACCAATTT AGCATATGTC CTTGCAGAAT TTTTCTTTCT 180  
 ATATATACAT ATATATTTT AACCAAAATG AATCATTACT CTATGTTGTT TTACTATTTG 240  
 TTTGACATAT CAGTATATCT GAAACACCTT TTCATGTCAA TAAATGTTCT TCTCTAACAT 300  
 TTAAA 305

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SEQ ID NO:1481

SEQUENCE LENGTH:734

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01686

SEQUENCE DESCRIPTION:

GATCCAGCCC ATTCTCTACT CTTACTCCTT TCATGGGCCA CCAGAGCCAG TACTCTTGGA 60  
TAGCAGCAGC ATTCTAGCTG ACAGAATTTT GCTGATGGAT ACTTTCTTTC AAATTGTCAT 120  
TTATCTTGGT GAGACCATAG CCCAGTGGCG TAAAGCTGGC TACCAGGACA TGCCCAGTA 180  
TGAAACTTC AAGCACCTTC TGCAGGCACC ACTGGATGAT GCTCAAGAAA TTCTGCAAGC 240  
ACGCTTCCNG ATGCCACGTT ACATCAACAC GGAGCATGGA GGCAGTCAGG CTCGATTCCT 300  
TTTGTCCAAA GTGAACCCAT CTCAGACACA CAATAACCTG TATGCTTGGG GACAGGAAAC 360  
TGGAGCACCC ATCCTAAGT ATGATGTTAG CCTGCAGGTG TTCATGGACC ATTTGAANGA 420  
AGCTGGCTGT CTTCCAGTGG CCTGTAAAG CTGAGGATAC AACCAGGGAA ATGCAAACGG 480  
TNTCAAGATT TGGTGGTTCA AAATTGTCTA GAAAGGGTTT GATAACCATT CCNGGTTACT 540  
TTTTCTTNGG ANGTTTAAAC CAAATAATCA ANGGCNATTT TATTATGGAA CCTCTTTAGG 600  
TTATAATTNA TTNGGAATNC CGNCNTTGGC CTTTTCTTGN CCTTTAAATT TTAAGGGAAN 660  
AAANNTTTGG GCNTNAGGNG GTTNNGGNTT TTTGGNNCNA ACTTTNGGGN TTAATAAANC 720  
NGGGGNNTNT TAAA 734

SEQ ID NO:1482

SEQUENCE LENGTH:731

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01687

SEQUENCE DESCRIPTION:

GATCAACCGG AGCGCTTCCG AGCCATCCTT GCATCGGGCA GCCCACACTG AGGATATCAA 60  
TGCTTGACG CTGACCACGT CCCCAGGGCT GCCTGTNTTC TAGTTGACTT TGCACCTGTN 120  
TTCAGGCTGC CAGGGGAGGA GGAGAAGCCA GCAGGCACCA CTTTTCTGCT CCCTTTCTCC 180  
AGAGGCAGAA CACATGTTTT CAGAGAAGCT GCTGCTAAGG ACCTTCTAGA CTGCTCACAG 240  
GGCCTTAACT TCATGTTGCC TTCTTTTCTA TCCCTTTGGG CCCTGGGAGA AGGAAGCCAT 300  
TTGCAGTGCT GGTGTGTCCT GTCCTCTCCC CACATTCCCC ATGCTCAAGG CCCAGCCTTC 360  
TGTAAGTGC CAAGTGGGAT GTTGATGGTA GTACAAAAAG CAGGGGCCCA GCCAGCTGT 420  
TGGCTACATG AGTATTTAGN GGAAGTAAG GTAGCAGGCA GTCCAGCCCT GANNTTGGAG 480  
ACACATGGGG TTTTGGAAA TAAGNTTCTT GNGGGATGAA TGTAACAGGN GGGNTTCTT 540  
CANGGAGTGG TNCAGCNCAG ACATTTNNAC ATAAGGACCA AACAGCCCAG NNTNCCGNAT 600  
TTGNCNCCC AAGNGCCTTT TTTGGACTTG GANCTTTNTT NGGGGAAAGC CNCTTNAANG 660  
TTTAAGNGCC AGNATNGGTG TTTGNGAAG NATTGCCATC CGATTTAGCC TTTANGGAN 720  
GTTCCANAAG N 731

SEQ ID NO:1483

SEQUENCE LENGTH:687

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01688

SEQUENCE DESCRIPTION:

5 GATCGGTGGC TCCATCCTGG CCTCACTGTC CACCTTCCAG CAGATGTGGA TTAGCAAGCA 60  
 GGAGTACGAC GAGTCGGGCC CCTCCATCGT CCACCGCAAA TGCTTCTAAA CGGACTCAGC 120  
 AGATGCGTAN ATTNTGCTGC ATGGGTAAAT TGAGAATAGA AATTGCCCC TGGCAAATGC 180  
 ACACACCTCA TGCTAGCCTC ACGAAACTGG AATAAGCCTT CGAAAAGAAA TTGTCCTTGA 240  
 AGCTTGATC TGATATCAGC ACTGGATTGT AGAACTTGTT GCTGATTTTN ACTTTGTATT 300  
 10 GAAGTAACT GTTCCCCTTG GTATTAACGT GTCAGGGCTG AGTGTCTGG GATTCTCTA 360  
 GAGGCTGGCA AGAACCAGTT GTTTGTCTT GCGGGGTCTT GTCAGGGTTG GAAAAGTCCA 420  
 AGCCGTAGGA CCCAGTTTC CTTCTTAAG CTGATGTCTT TTGGCCAGAA CACCGTGGGC 480  
 TNGTTAATTG CTTTAAAGTT GGAAGCGGT TTGCAATTAC GGCNCTAAA NGTATTCATC 540  
 CTNAATTNAA GGAAAGGGT TTTTGTGAC CGAAANNNG ATTCTTTGAA GNGNTGNAC 600  
 15 CAAATTTTGG GTTTCANCC GGTAAAGGGN GACATTAGGN CCCAGNACAA GGNATTNTGA 660  
 AAGGGAANAN AANGGCNCC GAAAAAN 687

SEQ ID NO:1484

SEQUENCE LENGTH:649

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01689

SEQUENCE DESCRIPTION:

25 GATCAAAGTG TATTGCCAG GCCAGCTCCT GAAGAACTGT GAACTATGAA CGTCTCAGCC 60  
 TAGAAGGATA ATGTGACCTT CAATTTGCAC ACCATCCATT GTCTCTTTCA AACTAAGAGC 120  
 CTCTCTAAGC TAGATAGGCC AAGGATTATT TTTTAACTT TTATTTTAGG TTCAGGGGTA 180  
 CATATACAGG TTTGTTACAT AGGTAACCTC ATGTCATGAG GGATTTTGTA TAGATTATTT 240  
 GGTGACCCAG GACTAAACC TAGTACCCAT TAGTTGTTTT TNCTGCTCCT CTCCCTCCTC 300  
 30 TCACCCTCCA CCCTCAGTTA GTTCCAGTG TGTGTTGTTT CCCCACATCT ATCCATGTGT 360  
 TCTTATTATT TAAGTCCCA CTTATAAGTA AGAACATGCA GTGTTTGGTT TTCTGTTCCC 420  
 GATTAGGTAA TGCTAGGGA TAATGGCTTC CAATTNCCAT CCATNGTTTC TGCAAAGGAN 480  
 CATGNNCTCA TTNCTTTAAA TATGGGCTNG CATAGNNGT CCATGGGNGG TGAATGTACC 540  
 35 ACATTTTCCT TTNANCCAGG TCTNATCAAT TGGNGGGCCA TTGNGGGTGA TTCCAAGGCT 600  
 TNGGTAATGG TGAANAGGGC ACAATAANCC AGTACCATGG GGCATGAAA 649

SEQ ID NO:1485

SEQUENCE LENGTH:549

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01691

SEQUENCE DESCRIPTION:

45 GATCCTCTGA TGGGAGCTGA AAGGATGAGA GGTGGGCATC TAGATTTAGG GAGGCTGTTC 60  
 AGGCTTTGCA GGTCCCTTAC CTGAACACAT AGAAACCCTG GAGCTGTGAC TGTGTCCATG 120  
 TGTGTGTGTT TGTCTGTGTG TGTGCGGGG GATGGGCACC TGCATGAATG TGGTAGAGAA 180  
 AATGGCTCTG CTCAGAGGGA AGATACGCAT AGCAAGGCAG GGACCAGAGG AATCACAGGC 240  
 GCCTGGAGAG CAGCCGGGCA ACGNCTCCAG GGACCTGCCG GCTTCCCTCA GTCCTCCAGG 300  
 50 GGCCAGCAC TCTCCTTTA GGCCCTGTGA GCGTCCCTTG TCAGGATACA TTCTCTCATT 360

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5 TTGCTGAAGC TGATTTGATT GGGTGTCTGT TTCTCGCAGC CAAAAGAGCT CTGAAATGAG 420  
GAAAGTGCTT CTGTGCTAAC TCCCCGGGTC TCCTGAATT CAGTCATTCA TGTACCCGCC 480  
TCGAAATTTT TTGCAATATC TGTGTACCCA ATGTCCATT AATTAATAAA GAAGTTTCT 540  
TAAATTAAT 549

10 SEQ ID NO:1486  
SEQUENCE LENGTH:543  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01692  
SEQUENCE DESCRIPTION:  
15 GATCGANGTT TACCTTGTGT CAGGAAAAAA TGTGGGGTAT GCCAAGTATG CCGATAGAAT 60  
AAGTNCTAAT GATGCCACTN GCCACTCTAC ATNGAAAGAT TCTGAATGGG GTGAGACTTA 120  
AAGTTATGCT GGCAGATTCTG CCAAGAGAAG AATCTAACAA ACGGCAAAGA ACTTACTGAT 180  
TCTTGAGAAC ACCCGACTAA ATAATGACAT ANTCTCAGC TGACTGACTG AAAATGTGAC 240  
TGGACGCATT CCCTGTGGAC AGTTGACAGC TTTTTTTTTT TCCATATACC TGNTAGTCTG 300  
20 TGTCCAGCAT TGTTTTGTCT GGGAAAGCAGG GTTTGCTGNC ATGTATTTN NATTCATAC 360  
ATTANTGCTA AACCGNTTAT AGTAGTTGTN CCTTAGNGCA NTATGTTGTT ACGTGTAGCA 420  
GAANTAAAGT TTTCTTTGCT TTANCTAAAT CATGNCTTTA TTTNTGNAA GGCCAGGACC 480  
GGGAAATTTT ATTNGNCAGT CTTTGGNTTT TGCCTAATGN CATTGNCATG NNTTTGGGGT 540  
NCN 543  
25

30 SEQ ID NO:1487  
SEQUENCE LENGTH:533  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01693  
SEQUENCE DESCRIPTION:  
35 GATCCAGAGT TGCATACAGA CCAATTTCTG CATCAGTGTT ATCTCGACCA GAGGCTAGTA 60  
GGACTGGAGA GGGCTCTACG GTATTTAATG GGGCCCAGAA TGGTGTGTCT CAGCTAATCC 120  
AAAGGGAGTT TCAGACCAGT GCAATCAGCA GAGACATTGA TACTGCTGCC AAATTTATTG 180  
GTGCAGGTGC TGCAACAGTA GGAGTGGCTG GTTCTGGTGC TGGTATTGGA ACAGTCTTTG 240  
GCAGCCTTAT CATTGGTTAT GCCAGAAACC CTTGCTGAA GCAGCAGCTG TTCTCATATG 300  
CTATCCTGGG ATTTGCCTTG TCTGAAGCTA TGGGTCTCTN TTGTTTGATG GTTGCTTTCT 360  
40 TGATTTTNTT TGCCATGTAA CAAATTACTG CTTGACATGT TGGCATNCAT ATTAATTACG 420  
GATGNAATCC TGGGNANCTA CTTGTNCCTC CGAAAACCTG TAGGTANTTG GGGGTCANGG 480  
GGAATTGNNC GGTAATTCCC AAAGCCATT NATTAAGGN GGAAACCTTT AAA 533

45 SEQ ID NO:1488  
SEQUENCE LENGTH:531  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01694  
50 SEQUENCE DESCRIPTION:  
GATCCAAAAG ANCTGCTTTC TGAAGCAAGT TTCCAAGANG CTCTTCAGGA AAGCATTCTT 60

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GACATTCAAG CGCACGAGTG GGTGCCGCTG TGGCTACTGC GGTATTCGGT CATTGTGAAA 120  
 AGTAGAGGAA TTATCAAATC AAAAGGCTAC ATTTTACAAG CTAAGAAG GGGTTCTTAA 180  
 CTGACTTAGG AGCATAACTT ACCTGTAATT TCCTTCAATA TGAGAGAAAA TTGAGATGTG 240  
 TAAAANTCTA GTTACTGCCT GTAAATGGTG TCATTGAGGC AGATATTCTT TCGTCATATT 300  
 TGACAGTATG TTGTCTGTCA AGTTTTAAAT ACTTATCTNG CCTCCATATC AATCCATTCT 360  
 CATGAACCTC TGTATTGCTT TCCTTAAACT ATTGNTTTTC TAATTGANAT TGTCTATANG 420  
 GANATNCTTG CAATATATTT NNNCNTTANT TTTTATGNCT AATATNAATN CAGGNNAATT 480  
 TGTTGTTTGG TATTTTTGGG CNNGGGTTCC GGGGAATGNT TNTNCANTTT N 531

SEQ ID NO:1489

SEQUENCE LENGTH:526

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01695

SEQUENCE DESCRIPTION:

GATCGGCGTG ACCANCCCTT GCCGGAGGTG GCCCATGTCA AGCACCTGTN TGCCAGCCAG 60  
 AAGGCACTGA NAGGAGAAGG AGAAGGCCTC CTGGAGCAGC CTCTCCATGG ATGAGAAAAGT 120  
 CGAGTTGTAT CGCATTAAAGT TCAAGGAGAG CTTTGCTGAG ATGAACAGGG GCTCGAACGA 180  
 GTGGAAGACG GTTGTGGGCG GTGCCATGTT CTTCATCGGT TTCACCGCGC TCGTTATCAT 240  
 GTGGCAGAAG CACTATGTGT ACGGCCCCCT CCCGCAAAGC TTTGACAAAG AGTGGGTGGC 300  
 CAAGCAGACC AAGAGGATGC TGGACATGAA GGTGAACCCC ATCCAGGGCT TAGCCTCCAA 360  
 GTGGGACTAC GAAAAGAACG AGTGAAGAA GTGAGAGATG CTTGGCCTNC GGCTTCAACT 420  
 TGCGGCTGGC TCTTTCACCG CCATGCAAAC TCCATGCCTA TTTACTNGGA AACCTGTTAT 480  
 NCCAAACAGT TGTNCNCTGC TAATAAATTG NCCAGTTTAC CTGAAA 526

SEQ ID NO:1490

SEQUENCE LENGTH:525

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01696

SEQUENCE DESCRIPTION:

GATCAGCAGA GGNATCAAAC CAACACCTTC TTTGGCTCCC CTCCCGCAGC CACAGAGGCA 60  
 ACCCACGTTG TCAGCACCAT CCCTGAGTCA TTACAATAGC ACCCTGCAGC TATGCTGGAA 120  
 AACTGAGCGT GGGACCTGCG CAGACTGAAG AGCAGGTGAG CAAAATGCTG CTTTCTGCCT 180  
 TGGTGGCAGG CAGAGAACTG TCTCGTACTA GAATTCAAGG AGAAAAGAAG AAGAAATAAA 240  
 AGAAGCTGCT CCATTTTTC TCACTACCC ATCTATTTGG AAAGCACTGG AATTCAGATG 300  
 CAAGAGAACA ATGTTTCTTC AGTGGCAAAT GTAGCCCTGC ATCCTCCAGT GTTACCTGGT 360  
 GTAGATTTTT TTTTCTGTAC CTTTCTAAAC CTCTCTTCCC TCTGTGATGG TTTTGTGTTT 420  
 AAACAGTCAT CTNCTTTTAA ATAATATCCA CCTNTCCTTT TTGCCATTTT ACTTATTGGN 480  
 TCCATAANGT GAATTTTAA TTAAGGTTAT GCCACACATG CATGN 525

SEQ ID NO:1491

SEQUENCE LENGTH:522

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01697

SEQUENCE DESCRIPTION:

5 GATCAGCTGT TTGTCATAGG GCAGTTGGAA ACGGCCTCCT AGGGAAAAGT TCATAGGGTC 60  
TCTTCAGGT CTTAGTGTC CTTACCTAGA TTTACAGCCT CACTTGAATG TGCTACTACT 120  
CACAGTCTCT TTAATCTTCA GTTTTATCTT TAATCTCCTC TTTTATCTTG GACTGACATT 180  
TAGCGTAGTA AGGTGAAAAG GTCATAGCTG AGATTCTGG TTCGGGTGTT ACGCACACGT 240  
ACTTAAATGA AAGCATGTGG CATGTTTCATC GTATAACACA ATATGAATAC AGGGCATGCA 300  
10 TTTTGCAGCA GTGAGTCTCT TCAGAAAACC CTTTCTTACA GTTAGGGTTG AGTTACTTCC 360  
TATCAAGCCA GTACGTGCTA ACAGGCTCAA TATTCCTGAA TGAAATATCA GNCTAGTNGN 420  
CAAGCTCTG GTCTTGAGAT GTCTTCTCGT TAAGGAGATG GGCCTTTTGG GGGTAAAGGN 480  
TAAATGGAT GAGGTCTGNC ATGNTTCACT ATTCTAGGAC TN 522

SEQ ID NO:1492

SEQUENCE LENGTH:509

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01698

SEQUENCE DESCRIPTION:

20 GATCCCAACA ATATTCCCAA GGCCTCAATG ACAAGTGGTT TGGTTCAGCA GTTCCAACAC 60  
ACAGTCCTTC CCTCAGTGAC TCCCTTGGNN CCCTCATCTG CACACTGATT GCCATATTGC 120  
25 CCTCTATTTT CTGTCTTTGG TTTAAACCCC AAGGGCCAG AGGCTTTCTC CGATGTCTAA 180  
CTCTTTGTGC CTTGAGCTCC TTTATGTTTG GGTGGCATGT TCATGAAAAA GCCATACTTC 240  
TAGCAATTCT CCAATGAGC CTTTGTCTG TGGGAAAAGC AGGAGACGCT TCGATTTTTC 300  
TGATTCTGAC CACAACAGGA CATTATTCCC TCTTCTCT GCTCTTCACT GCACCAGAAC 360  
TTCCATTAA AATCTTACTC ATGTTACTAT TCACCATATA TAGTATTTTCG TCACTGAAGG 420  
30 ACTTTATTCA GAAAAGGAAA AACCTCTTTT TTAATTGGGA TGGGAACCTT CTANCCTGCT 480  
TTGGNCNGGG GGCCTCTGGG AAGGNCTTN 509

SEQ ID NO:1493

SEQUENCE LENGTH:497

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01699

SEQUENCE DESCRIPTION:

40 GATCCTGTCA AAATAGTCCG ATGCCATGAA CATATAGAAT CCTTACAGTA AATGGAGAAT 60  
TACTCTTTTT TAGACAAAGA GAAGGGCCTT TTTATCCAAC CCTAAGATTA CTTCACAAAT 120  
ATCCTTTTAT CCTGCCACAC CAGCAGGTG ATAAAGGAGC CATCAAATTT GACTCAGTG 180  
GAGCAAATAT CATGTGTCCA GGCTTAACTT CTCCTGGAGC TAAGCTTTAC CCTGCTGCAG 240  
45 TAGATACCAT TGTGCTATC ATGGCAGAAG GAAAACAGCC TGCTCTATGT GTTGGAGTCA 300  
TGAGATGTCT GCAGAGNCAT TGNGAAGTCA CCAAAGGATT GGCATTGAAA ATATCCATTA 360  
TTTAAATGAT GGGCTGTGGN TATGAGGCAT ATAAATGNGC TCAGAGGGAT GCACTTGGGT 420  
NAATATGGNT ATTGTGCTGT ATCTGTGTTG TGNCCTGTGT TGCANCTGAG GTATGCCTGT 480  
50 GGTNTGCTGA TAAATCN 497

SEQ ID NO:1494

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SEQUENCE LENGTH:472

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01700

SEQUENCE DESCRIPTION:

GATCAAAATA TCATGGATTG AACCTCATCA ATTGATAGCA GTGAGTGACT GANGCTTCCA 60  
 AATCAAGAAA AGCCGGCACC AAGAAGTTCC ATTCTAATCT AGAGCTGACC AGTTTGAGCT 120  
 GATTCTNTCT TTGAAGAGTC CTTCTTGATT GCAGTGACGT ACTGGCATTT CTGAATGGAT 180  
 GTANGNGGAG TATTTTAGTC TAAAGGCTTT TCAAATTACT TGAATTTTTT TAAAAATTGA 240  
 GGAGCTTTAT TTCTATTTAC CCTTCCATTT TTGTATATCA AATTTCCATN GTCATTAAAA 300  
 ACTGTATCTT GAAAGTTTGT GAACTGACTT GCTGTATTTG CACTTTGAGC TCTTGAAATA 360  
 ANTGTGATTT TNGTGTGATT ATCTGGTTTC CNGTTTTAAC CATTACCTGT CACCNTTNAT 420  
 CCTTAACCTT GAAAGTCCAG AAACCATNNN ATTATTAAGG TNGTCCAATA AA 472

SEQ ID NO:1495

SEQUENCE LENGTH:496

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01701

SEQUENCE DESCRIPTION:

GATCTGTGTG GATGGCAAAC TCCCCAGGCC ATTCTGGGAC CTAAGTTTAA GAAGTGCCGT 60  
 CCTCGAACTT NCTGACTCTA AGCTCCTGAG CGGGAGTNAG ACTTAGCCCT GAGCCTGCAC 120  
 TTCCTGTTCA GGTGCAGACA CTGAACAGGG TCTCAAACAC CTTCAGCATG TNTNTTGTGT 180  
 GCTCACGTGC CACACAGTGT CTCATGCACA CAACCCAGTG TACACACCAC CTACATGCAC 240  
 ACAGCGTCTT TNCACACTGT GTATGTGAAC AGCTTGGGCC CTGCAACACA ACCATCTACA 300  
 CACATCTACA ACCNNNAGGA CACACACATG GGTCCGTGCC ATGTCACCTC CNTAGGGGAN 360  
 GGNTTTCTTT CCAAGGTGTN GCCAGGCCAG GCAAGCCTTC CAGGCCATGA ATTCCTTACT 420  
 TAGGTACCTN GGGGTTTGGG GTGGGNGNCC CAGNCAAAAT TCTNGGGTTN CGTNCNCTTT 480  
 GGTNNNGNCC AGNTTN 496

SEQ ID NO:1496

SEQUENCE LENGTH:492

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01702

SEQUENCE DESCRIPTION:

GATCCTGTAC AGCCAGTGTG GGGATGTGAT GAGGGCCCTG GGCCAGAACC CTACCAACGC 60  
 CGAGGTGCTC AAGGTCCTGG GGAACCCCAA GAGTGATGAG ATGAATGTNA AGGTGCTGGA 120  
 CTTTGAGCAC TTTCTGCCA TGCTGCAGAC AGTGCCAAG AACAAGGACC AGGGCACCTA 180  
 TGAGGATTAT GTCGAAGGAC TTCGGGTGTT TGACAAGGAA GGAAATGGCA CCGTCATGGG 240  
 TGCTGAAATC CGGCATGTTT TTGTCACACT GGGTGAGAAG ATGACAGAGG AAGAAGTAGA 300  
 GATGCTGGTG GCAGGGCATG AGGACAGCAA TGGTTTGTAT CAACTATGAA GAGCTCGTCC 360  
 GNATGGGTGC TGAATGGCTG ANGGACCTTT CCCAGTNTTC CCCAGATTNC CGTTGCCTTT 420  
 CCNTNGTGTG AATTTTGGTN ATCTAAGCCT AAAAGTTTTC CCTAAGGCTT TCTTGTCTTC 480  
 AAGCAACTTT CN 492

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SEQ ID NO:1497

SEQUENCE LENGTH:490

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01703

SEQUENCE DESCRIPTION:

GATCCAAATA CACAGAATCA AGGGAAGGAG TTGCTTCTTC TAAGAGTGAT GCTTAATCTT 60  
 TTGGGTCATG GATGAATTGA AGATTTGATT AAAGTTACAA TAAAAAGAGN CCCCNTCAAA 120  
 GCACGTACAN NCTGTATCAC GAACGGTGCC TGGCCTACTT TTTCCTTTTC TACCCACCCC 180  
 ACCCCAACCC CCCCTGTCTC AGTGAAGAAC TGGTTGTAC TAAAGTGAAA CTTAATAAAG 240  
 GATATTGCCT AGGGAAGATT AGTTGTTTTT CTTGTTCATC AAGTTCATTC TGGACCTCTT 300  
 CCTCTGAGCT GTTAATCAGT GTTGCTAAAC AGACAGGGAA AGACAAGGGA GAGAAAAATG 360  
 CTGATTCAAT CTCAGAACT TTTAACCNCT TTAACCNCTA ATTCTTCTCC TTGAGAAGCT 420  
 ATTCTTTGAT TGTGAAAGCT TTGTTGTTCA GGGNAATATG GGGTAATAAA AATAGCTAAC 480  
 CATTTTTAAA 490

SEQ ID NO:1498

SEQUENCE LENGTH:477

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01704

SEQUENCE DESCRIPTION:

GATCAAACTT CCATATTTGC CTTGGGAATA ATGGACAAAG GGAAATACTC TTAATTCATG 60  
 AATAAAAACT TTGCAGAAAA TTAGACAGTG TTTAATTTTC GAAAACTTCC CTCTCTAGAC 120  
 AGTAGATACC ACCTACTGAT GGTACATAT ACTAGGGAAA TTTTAAATTT AGGAAATGCT 180  
 GATAGCTCAT ATTATAAATT TCTAAATCCT AGGAAGAAAC GCTTGGAGTG CTTCTGAATA 240  
 TACAGAAAGT CCATTTAAGG GCAAGTTTCC CCGTAGATGT ATCAAAATAC TACCAACTGT 300  
 AAATTGAGGT TTAATTTCCA AATGTATTCT ACTTGTCTTA AAACAATCTG TCCNCAATA 360  
 TANAACATA AAGTAATAAA TTGTTATTTT CCGCACCAAT GGGGNATCTC TAATGGTGGA 420  
 AAATGGTAAT CCTATGGAAA ATTAATTTTT TTTAANTAAA ANGGTNATTT TAATAAA 477

SEQ ID NO:1499

SEQUENCE LENGTH:476

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01705

SEQUENCE DESCRIPTION:

GATCCCCGAG TCTTCACAAA TNCTCACTGA AGAAAATTCC TGGAACAATT CAGGGTCCTT 60  
 TCATAACCTC TACTCTGAGG TGTTANTAAA AAACCTTAGT AACTTAAAAA AAATGAGCTG 120  
 TACACAAATA CTGAACAATA ATGCTNCNTA TGTTAAGTAT GTANGAAAAA TATATACTTT 180  
 GACATANATA AGAAACGGTG AGTTGATAAT TGGATAGAAT GGTGGATAGA GTGATAGATA 240  
 TGTAATAAAG CAAATATAAC AAAATGATAA TTGTACAATC TAAGTGGTTG GACTATAAAT 300  
 ATGCACTTCC CACAACNTTT TTATATGNTT AAACAGTTTT ATAATACCAT ATTANGGGAA 360  
 ACTGTTTGTG TCAAGGAAAT AGAGNTTGTG ATATGTTCTA GTNCAATGNA GGTGTAATCA 420

TGGTNAAATT AAAAGCTTTT ACTTCCTGGG CAATTAAAGG TAATCCTGGT AGGAAA 476

5 SEQ ID NO:1500  
SEQUENCE LENGTH:488  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01706

10 SEQUENCE DESCRIPTION:  
GATCCTGACT GCTGTCATGG CGTGGCCCTCT GGAGAAGGCN CTGGATGTGA TGGTGTCCAC 60  
CTTCNANAAG TACTCGGGCA AAGAGGGTGA CAAGTTCAAG NTCAACAAGT CAGAACTAAA 120  
GGAGCTGCTG ACCCGGGAGC TGCCCACTT CTTGGGGAAA AGGACAGATG AAGCTGCTTT 180  
15 CCAGAAGCTG ATGAGCAACT TGGACAGCAA CAGGGACAAC GAGGTGGACT TCCAAGAGTA 240  
CTGTGTCTTC CTGTCTGCA TCGCCATGNG GTNTAACGAA TTCTTTGAAG GCTTCCCAGA 300  
TAAGCAGCCC AGGANGGAAA TGAAACTCC TCTGATGTGG TTTNGGGGGG TCTGCCAGCT 360  
GGGGGCCCTT CTGNGTNGNC CANTGGGGNA CTTTTTTTTT TTTCCCACC NTGGGNTCCT 420  
TTNANGANA NGGGCTTNGA TTGCTTGAGC AAAGTTTCAA ATAAAAGNTT TNTNGGGAAG 480  
20 NTTTTAAA 488

25 SEQ ID NO:1501  
SEQUENCE LENGTH:472  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01707

30 SEQUENCE DESCRIPTION:  
GATCCAGAAG CTGATGGATG TGGGTCTGAT TGCAATTCGG TGATGACTTG TTCATACCCC 60  
CTTCCTTTCG CCCTCATGTG GAAAGAGGAG CTGGGACCGC GCGAGCAGC ACGGAGCGGA 120  
AGGGAGAGCA GGGGAGAGAA GGCCTCATNT CTCTATATT ATACATAACC CCGGGGAAGA 180  
CACAGAGACT CGTACCTGCG CTGTTTGTGC CGCCGCTGCC TCTGGGCCCT CCCAGCACAC 240  
GCATGGTCTC TTCACCGCTG CCCTCGAGTT CCATGTCTCT TTCCCCTGCC CCTAGTTGCT 300  
35 GTCTCGGCTG CTCTCCCATA GTTGGTTTTT TTTTNNATT GGGGCAGTGG GCATGTTAAT 360  
GGGGGAGGGG AGGGGGTTCT TCCAGCCTNA GGTCCCAGTT GGTCTNACGT NGTTTAATTC 420  
TTGGGTCCCC TTTTCCAAT TAAAACAAGC CANTNGGGGC GTGGGTTNTA AA 472

40 SEQ ID NO:1502  
SEQUENCE LENGTH:469  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01708

45 SEQUENCE DESCRIPTION:  
GATCGCAAAT TGCTNGAGCT GTTGTGGAAT AAATACTGGG TGAATACGTT GAGTTCTTCT 60  
AGCTTGCTTA CTAATGCAGA CTATACCACT GGTCAGGTCT TTGATTGTC TGAAAAGTTA 120  
GAGCAGTCAG AAGCCCAGCT GGGACGAGGG AGTTTCATGT TGGGTTTAGA AACGCATGAC 180  
CGAAAATCAG AAGACAAACT TGCCAAAGCT ACAAGAGACA GCTGTAAAAC TACCATAGAA 240  
50 GCTATCCATG GATTGATGTC TCAGGTAAAT TAAGGATAAA CTGTTTAATC AAATTAACAT 300  
CTCTTCCACA GTCTCTGAGA AGGGCTNTAC CTGAAAGACA GTATGNNGGA AAATATTCAA 360

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GGTAACACTT TTAAANCCAG TTNCCNAAAA TCTGATTAGG ANGNTTANGG TTCTCTGAAG 420  
TGGTCCTAAA TATTANTATC CCTGTAATAA ANGCTCTTTA AANTGGAAA 469

5 SEQ ID NO:1503  
SEQUENCE LENGTH:466  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01709

10 SEQUENCE DESCRIPTION:  
GATCTGCAGT GGCTGTTTGA CCAGACCACA AAGTTCACAT CTCCTGAGCT TAGTGTCCGT 60  
GGCTGTCCAC CTCCAGCCA TACTTGACTG TCCCCAACT CTCCCTGCAG CCACATGTTT 120  
CCCATGACCT GTGGGCTCTG CAGATGGACC TCTCTCCGCT AGAGATGCCC TTCTCCAAA 180  
15 TGGCTTCCCT CCTGGAAGGC CCAGCCTGAG TCCTCGTCTC CTTTCCAGTG CTTCTGCCAG 240  
AAGCATCCCC ATGATGTTGT GACCGCACAG CACTTTGTGT CTTGCTTTGA GCACTTGCCA 300  
CTCTGGCTGG TGCTGCTGCC ACTGATTGTG TACTGTCTTG CTGCCCTTTC TAGACTGTGA 360  
GCTCCTCGTG GGCAGGGACC GCCTGTGTTC TCTGTATTTC CCACGGAGCC TAAGNACAGT 420  
GCCTTGCACT TGATAAGGTG CTTAATAAAT GTCTGNTCAA CTGAAA 466

20 SEQ ID NO:1504  
SEQUENCE LENGTH:465  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01710

25 SEQUENCE DESCRIPTION:  
GATCACTGTG TTCAGTGTG TTGGAATGGA TTCAGACTGG CTAATGGGGG AAAGGGGAAA 60  
CCAGAAGGGC AAGGTGCCAA TTACCTACTT AGAACTGCTC AATTAAGTAG GTGGACTATG 120  
30 GAAAGGTTGC CCATCATGAC TTTGTATTTA TATACAATTA ACTCTAAATA AAGCAGGTTA 180  
AGTATCTTCC ATGTTAATGT GTTAAGAGAC TGAAAATACC AGCCATCAGA AACTGGCCTT 240  
TCTGCCAATA AAGTTGCATG GTAAATATTT CATTACAGAA TTTATGTTAG AGCTTTCATG 300  
CCAAGAATGT TTTCTTACAA AATTCTCTTT TTATTGAGGT TTCACTAATA AGCAGCTTCT 360  
35 ACTTTTGAGC CTCAACTTAA AGCAGANCTG TTTTCTACTG GGATTTTTC TTAACAGCAA 420  
GCCTTTTCCT TTTATGTAAA ATTAAATCTA TTGTGGAATT TGAAA 465

40 SEQ ID NO:1505  
SEQUENCE LENGTH:462  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01711

45 SEQUENCE DESCRIPTION:  
GATCTTGTCT TTAAACATG ATAGTCCTTT CAGTATAATG TCTTAGATTA AAGACGTTGC 60  
CTTTAATATC TGTGGGAAG GAAATGTCCA GACTTTTCAA ATCTCTTATT ATATGTTTCC 120  
TTTTNTTGT TACATAGGGA ACAATGTTTA TAGTCGTGTG TACAGTGGGG GTCTACANCN 180  
NGAAGTGAT ATTTCAAAC AATTTTTTAA NGATTTAACA ATTTTGTAA ATCATTTTCA 240  
GGCTTCTGCA GCTGTAGATT CTCACTGTGA ATCCCTTGCT TGCTCATGCA TAAGTGTATT 300  
50 TGCAATACCA NATATACAGG TTTAGTATTT TTGCTGTGA GTNGATTGTT TCACATGNGT 360

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AACGTNTTGG GTGAGATGTT ANATGGTTGG NCGAGGTACT GTGGANGTGA ATGTGGGNAG 420  
 TAATTTTAAN NCATATGNAA TTGGTCACCA GGGCCNAATT TN 462

SEQ ID NO:1506

SEQUENCE LENGTH:459

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01713

SEQUENCE DESCRIPTION:

GATCCCAAGC AGGCTCACAA ATTTAAATGA GGGCTTTGTG TGCAGAAAGA GGAATAAGTA 60  
 CAGATTATTT TCCTACCACT AGATTTTGGG GGAGAGTCAC CATGGAATGT TGACAATTAC 120  
 TTTAAATATT TTAAGCTCCC TTGCTGAATT CCTGTCCTGT CCCTGAGGAA TCAGATGGTC 180  
 ATACAGCCAT AGGCACCCAC CCGAAATTC CCTAGGAGTT GGAGTAATGC TAGAATTGAA 240  
 GACCTTCTGA GTAAAGGGCT TCTCTGCCTT CTCAGAGGCA GGAGAATTG CACTGGTTGT 300  
 GTTAAATGTA TAAAAAGCTA TATGTTACC AGTTTACTCA TTTCCAATGT GTAGATGAAT 360  
 AAAATGTAGT GTACAAATTA TTTGAAATC CCAGAAGGGA AGGTACTTTT CAAANACAGT 420  
 ATTTTTTTTA ACAAATAAAC TTACGNTTTT TACAGCAAA 459

SEQ ID NO:1507

SEQUENCE LENGTH:454

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01714

SEQUENCE DESCRIPTION:

GATCTCCTGT CCATCAGCCA GGACAGTCAG CTCTCTCCTT TNAGGGCCAA TCCCCAGCCC 60  
 TTTTNTNGAG CCAGGCCTCT CTCACCTCTC CTACTCACTT AAAGCCCGCC TGACAGAAAC 120  
 CACGGCCACA TTTGGTTCTA AGAAACCCTC TGTCATTGCG TCCCACATTC TGATGAGCAA 180  
 CCGCTTCCCT ATTTATTNAT TTATTTGTTT GTTTGTTTTA TTCATTGGTC TAATTTATTC 240  
 AAAGGGGGCA AGAAGTAGCA GTGTCTGTAA AAGAGCCTAG TTTTAAATAG CTATGGAATC 300  
 AATTCAATTT GGAAGTGTGT GCTCTCTTAA AATCAAGTCC TTTANTTAAC ACTGAAAATA 360  
 TATAAGCTCA GATTATTTTA ANTGGGNATA TTTATAANTG NGCAAATATC ATACTGTTCA 420  
 NTGGGTCTG GAATAAACTT CACTGGAGGG NAAA 454

SEQ ID NO:1508

SEQUENCE LENGTH:453

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01715

SEQUENCE DESCRIPTION:

GATCGAGCAG TGTGACTACC CCCCACTCCC CGGGGAGCAC TACTCCGAGA AGTTACGAGA 60  
 ACTGGTCAGC ATGTGCATCT GCCCTGACCC CCACCAGAGA CCTGACATCG GATACGTGCA 120  
 CCAGGTGGCC AAGCAGATGC ACATNTGGAT GTCCAGCACC TGAGCGTGGA TGCACCGTGC 180  
 CTTATCAAAG CCAGCACCAC TTTGCCTTAC TTGAGTCGTC TTCTCTTCGA GTGGCCACCT 240  
 GGTAGCCTAG AACAGCTAAG ACCACAGGGT TCAGCAGGTT CCCCCAAAGG CTGCCCAGNC 300  
 TTACAGCAGA TGCTGAAGGA GAGCAGCTGA GGGAGNGGN GCTGGCCACA TGTCAGTNT 360

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GGGTCAGNTT CCAAAGTCCT TTNNTTANCA CTGTTGTGGA CAATNTNANN TNGGGTCAAN 420  
TNAAGGGCAG GTNGGTTNAA GNGGNGCCNN GGN 453

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SEQ ID NO:1509  
SEQUENCE LENGTH:450  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS01718

SEQUENCE DESCRIPTION:

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GATCCTGGGG AAGGTGGGGA ACATGCTTGC AGTATCTNTC CCTGTNTGTN TGCTCACATA 60  
AGCATTCCGT CCATCTGAGC TCATCGTGCT ACTGGTATGT GTATGTNCAG TTACACAGTT 120  
TTNTGTATCA TAGATTCTAG TGTGTTTATA CAAGGNGACA TCTGTGGTTT CCCCACCGT 180  
TCCAAAAGGC TATTTCAAAG GAACCAGCCA ACGTATGAGA AATGANTGTA AACTGTGGA 240  
CATTGACTTC CCGCATAAGG CAGGGTGACC CCCTGAACTC CAGATGTNTG CACAGTATCT 300  
NATGTGTTGT TTTCCGTTGT GACGAATGTG NATTGGAACA TTTGGGGGAG CACCCAGAGG 360  
GATTTNTNAG TGGGAAGCAT TACACTTTGC TAAATCANGT ATTTNNTTCC TGNTTAAACC 420  
AACCTANTTA ANTNTTTANC CCTTGGCAAA 450

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SEQ ID NO:1510  
SEQUENCE LENGTH:449  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

25

CLONE:HUMGS01719

SEQUENCE DESCRIPTION:

30

GATCCATGGA TGAGTGGGG AGTGGAAAAT GGCACAATAT CAAGTGTGAG ANAGGNGATA 60  
NACTTCGACT CTNCTGCCTT CAACTGAGAN CAGTTGACCG CAAGCTGAAA CTGGTGTGTG 120  
GNAGTCACAG CTTATCAAG GTCATCAAGG CCAAGAAAA CAAGGAAGGA CCAATGAATG 180  
TTAATTGAAA TATGAAAGCT GAAATGCAAC AAACAACCTC CGCTTAAAAC AATTAAGTTG 240  
TTAATAACTG TGATTTTGTA AATTTAGTA ATTCATTTAA ATGATGTTT AGTAGATATA 300  
TTCTAGCATA TTANGAGCTT TTATACTGA GTTATAGATT AGTTTGCTTT CTGGAATAAA 360  
ATTTTCTTCT TATACTCTTC CTTTTTTTGA GATATNACAT TTTGCTTTTA TGNCATTAC 420  
GGGGGCAAAA ANTAAAATAT CTTTTTTTNN 449

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SEQ ID NO:1511  
SEQUENCE LENGTH:464  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01720

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SEQUENCE DESCRIPTION:

45

GATCAGAATC ATGGTCTCCC GCAGTGAAGT GGACATGTTG AAAATNAGGT CTGAATTCAA 60  
GAGAAAGTAC GGCAAGTCCC TGTACTATTA TATCCAGCAA GACACTAAGG GCGACTACCA 120  
GAAAGCGCTG CTGTACCTGT GTGGTGGAGA TGAAGTGAAG CCGACACGGC CTGAGCGTCC 180  
AGAAATGGTG CTCACCATGC TTCCAGCTAA CAGGTCTAGA AAACCAGCTT GCGAATAACA 240  
GTCCCCGTGG CCATCCCTGT NAGGGTGACG TTAGCATTAC CCCCACCTC ATTTTAGTTG 300  
CCTAAGCATT NCCTGGCCTT CCTGTCTAGT CTCTCCTGTA AGCCAAAGAA ATGANCATTN 360

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CAAGGGAGTT TGGAAGTNAA GTCTATGANT GTGAAACAAC TTTTNNCCTC CTGTNGTNCT 420  
GTGTTAATAA ANCAGGTGNA TTAAACTGGN TTTNGTACTT TAAA 464

SEQ ID NO:1512  
SEQUENCE LENGTH:445  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01721

SEQUENCE DESCRIPTION:

GATCTTGCCA TGGAAGATAC TAGCCCAGCC TAGCAGAAAA GTGCAATATG TATAGCATAC 60  
TTTGACATTT TAAACATGAT AGTCCATAAC CATTTTGAAA TGCTGGGCAA ACTACATGAA 120  
GTTATTTTATA ATTAATTCAC AGCTAATCAG GCATTTTGAA AGCTTAATTG GATTCAAAAA 180  
CCATAATGTT GGAATTTGGT AAAATTTTAA TGTGTATTTT TACTGTGAAA AGGTTTTTAT 240  
AAGATATACA CACCCTAGTT TAATGTTGTG TCTTGGTGTG GATTACAGA TTTACTACAG 300  
GTATTCTGAA CCAGGAACAC ANTCAGGTTT TCAGGCCAGT TTGAATACTG GCTGGCCTTA 360  
AATTCTAATT ATNNGGAGTA GGGACATCAT ACCTAAATNT TTATGTCAGT GGGGNCCTGA 420  
CTGTCTGTG GGANCTTAGC AAATN 445

SEQ ID NO:1513  
SEQUENCE LENGTH:435  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01722

SEQUENCE DESCRIPTION:

GATCAATCGG ATTGAGAAGA ACATCCTGAG CTCAGCGGAC TACGTGGAAC GTGGGCAGGA 60  
GCACGTCAAG ACGGCCCTGG AGAACCAGAA GAAGGCGAGG AAGAAGAAAG TCTTGATTGC 120  
CATCTGTGTG TCCATCACCG TCGTCCTCCT AGCAGTCATC ATTGGCGTCA CAGTGGTTGG 180  
ATAATGTCGC ACATTGTTGG CACTAGGAGC ACCAGGAACC CAGGGCCTGG CCTTCTCTCC 240  
CAGCAGCCTG GGGGCAGGGC AGAGCCTCCA GTCGGACCCC TTCCTCACAC TGGCCCTAT 300  
GCAGANGGTN AGACAGTTCT TCTGGGGTTG GNAGCTGCTC ATTCATGATG GCCTNCTCCT 360  
TNAGGCCTCA ATGCCTGGGG GGANGGCTGC ACTGTCCTAT TTGGNCGGGA CANACGGTTT 420  
TNTAAAAATT TAAA 435

SEQ ID NO:1514  
SEQUENCE LENGTH:434  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01724

SEQUENCE DESCRIPTION:

GATCTAACCT AGACTAAAAT TGGGAACCTA TTTGCAATTT TTGACCCNGN CCACTAACTA 60  
GTGATTCTNC TCCAAAATTG AGAAAGACAG CACCCATTGA AGCAGATATG TGTGTGAAAG 120  
TATATTTTTC AATTCCAGAT TTTTAATTTT AAGGCTCCAG GAAAGAAAGG AGAGTAGAAC 180  
ATTTTCTCTC ATTTTATCAA ATCCTCTCTT GCCCTCCCTC AATTCCTCTG TAACATTCCT 240  
GAAGCTGTTT CCACTCCCAG ATGGTTTTAT CAATAGCCTA GAGGTAAAGA ACTGTCTTTT 300  
TCTCTGATTC TTTAATAAAT TATCTTTATA GGAATATGCA CAAGTTTTTT TTACACTCAG 360

TGTTAAAAGT ATTTATTAAT NGGGAAGTCA ACTTAATGTT TTGAAATAAA NTATATGNCT 420  
CTGGTTAATG CAAA 434

5 SEQ ID NO:1515  
SEQUENCE LENGTH:423  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS01726

## SEQUENCE DESCRIPTION:

GATCCAGTGA TTCANTCACT TAAATNAAGT CTTTGGTCA GAAATNACCT TTTTGACACA 60  
AGCCTACTGA ATGCTGTGTA TATATTTATA TATAAATATA TCTATTTGAG TGAAACCTTG 120  
15 TGAACCTCTT AATTAGAGTT TNCTTGATA GTGGCAGAGA TGTCTATTTT TGCATTCAAA 180  
AGTGAATGA TGTACTTATT CATGCTAAAC TTTTATAAA AGTTTAGTTG TAAACTTAAC 240  
CCTTTTATAC AAAATAAATC ANGTGTGTTT ATTGAATGGT GATTGCCTGC TTTATTTTCAAG 300  
AGGACCAGTG CTTTGATTTT GATTATGCTA TGTNATAACT GACCCNAAAT AAATNCAAGT 360  
20 NCAAAATTTAT GTNGNCTGTA TAAGGTTTGT AATAANCCAT GNCTGAGGNC AAAAAAGGNG 420  
AAA 423

SEQ ID NO:1516  
SEQUENCE LENGTH:419  
25 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01727

## SEQUENCE DESCRIPTION:

GATCTGTAAT CTCCACTGCT TGGATGTCTG CCCTCTACCC CAGAGGAATT TACAGAAACT 60  
30 TGCCCTGTGC CTGTGTCCCC CATGCTAGGG GCGGAGGGGT CTTTCCTTC TTCTTCCTA 120  
CCTACCCCTT TTCTCTTGGC CAGGGGCCCTC GTATCCTACC TTTCCTTGTG CCCTGGGCTG 180  
GCTGCACAGA GGATTGCCCC TTCTCTTTTC AGAGCTGGCC CTCGATGCCA AATTAGCATT 240  
TAGTATTTTG CACAAAGTCT AAGGGACCAT GGCTGCCTGC CTTGGGGAGG AACCATAGCT 300  
35 CCNTCTGGGC CGCTTCTGGC CTCTTGAGC CATGGGCCAA AGGCAAGGGG ATGGGCAGAG 360  
GTCTGTGTTT GGTCTGGCCC AGTTCCNCAT CATTAACTC AGCCTGACTG CTGCCTAAA 419

SEQ ID NO:1517  
SEQUENCE LENGTH:419  
40 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01728

## SEQUENCE DESCRIPTION:

GATCCTCAGT AGANCAGTCC AGAAGCCTGA NAGACAGTGG CCCCTTGATA ATCTGGGTCT 60  
45 CACGGGNCCA GCTAGGGGTC CAGGTTTCAN TCAGTAAATA AGAGTGGTCC ACGTCCTAAA 120  
GACACCTCTC CTNNACAAAG ACTTGTGATG CTCTGGGGNT TCTNTGGCCA AGCCCCACCC 180  
TTTCCTGGTC ATGGTACCCG TACAGCGTTG ATGGCCACAG CTCGAAGGGG GGCTTTCGTG 240  
TCCCCCTGTG CGGTCAGTGT TTTCAGTACC ACCTCTCTCC CGTGCCCACT TGGCTATTTA 300  
50 CTTATTTATT TATTGTGTGC CAGTNATGGT GGGTGGGGGC TGGCCCTCC CCGCCACCTN 360  
CANCCCTGTT GTGACCTGTC CTTCCGTACT TAATAAAGTG CGCGTGNGGA GTTGTTAAA 419

SEQ ID NO:1518

SEQUENCE LENGTH:418

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01729

SEQUENCE DESCRIPTION:

5 GATCTNAGCC CTCCGGTTCC TGGGCAGAGA GAAAGGCTAC AGGTTCAATTT NCCTGACGAC 60  
 10 AGCAGTCACA AACAGCGCTC GCNTTATGGA GGCCATNAGT GAGGTGAAAG CCTGATGTTT 120  
 TTCCCGGCCA NTNTTGACAT CTTCCCTGAA CACATTCTC AGTGAGATGC AGGCATCTGG 180  
 CACCCAGCTG CTATAACCAA GTGTCCACCA ACTACCTGCT AAGAGCCGGG AGCATGGAAC 240  
 GTGTTGGGAT TTAGAGAACA TTATCTGAGA AAAGAGTTCA CTTCTGCTC CCAGGATATT 300  
 TCTCTTTTCT GTTTATGAAG TACAACCCAT GCTGCTAAGA TGCAGCAGG AAGAGGCATC 360  
 15 CTTTGCTAAA TCCTGTTTGA ATGTCATTGT AAATAAGCC TCTGCTCTCA GATGTAAA 418

SEQ ID NO:1519

SEQUENCE LENGTH:404

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01730

SEQUENCE DESCRIPTION:

25 GATCCAATTT ACAGAAATCA GAGTTAGCTA CAGCTAGGAC TCGTTTGGTT GGGGTTTTTTT 60  
 AGTTTGTCTT TCTAAAGTCA TGTGGACCTT AATTTAATTA CAAAAGTCTA CCCTGGTGGT 120  
 CATAAAATAG GCAGGCCAT GAAGAAAGGC CTTTACTCT TCCATCTCGT CCCAGCCCCG 180  
 AGTTGACCCA CGTTGCTGCT CCTCACACCA TGGTGATGCA GGTCTCGTAG TGTGGGCACA 240  
 GGCTGGCTA CCTCATCTTT TTAGTGCTC TCTCTCTTC CACAGGATGG GGTCCCACAG 300  
 CTGCAGCAGC TGGCCCGGTA GTTGAGCATG TGTGGTTATC CTGTAGAGCT TTTCCCAAGA 360  
 30 AGGGTGTTTG AACTTAGAGT CTTAATAAAA TCTTACCAA TAAA 404

SEQ ID NO:1520

SEQUENCE LENGTH:402

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01731

SEQUENCE DESCRIPTION:

40 GATCTACAGA TACGTGATAT TNTGGTATAA CTAGAATCTT GATTTCTTTC ATAAAGTTCT 60  
 GCCATGTTCT ATTTCTTTCC TTAATGTTTT TTTCTCCCT ACTGTTTTAT CCTCCCTTTG 120  
 CTTTGGAAGG ATATTNCTGC ATATCGAGCT AAAGGAAAGC CTGATGCAGC AAAAAAGGGA 180  
 GTTGTCAAGG CTGAAAAAG CAAGAAAAAG AAGGAAGAGG AGGAAGATGA GGAAGATGAA 240  
 GAGGATGAGG AGGAGGAGGA AGATGAAGAA GATGAAGATG AAGAAGAAGA TGATGATGAT 300  
 45 GAATAAGTTG GTTCTAGCGC AGTTCTTTTT NNCTTGCTA TAAAGCATTT AACCCCCCTG 360  
 TACACAACCTC ACTCCTTTTA NNGAAAAAAA TTGAAATNTA AA 402

SEQ ID NO:1521

SEQUENCE LENGTH:407

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01732

SEQUENCE DESCRIPTION:

GATCTCAGCT GAACAAATTA GATGTTTCAG TTGCTCTTGG GTCAACTGGC TTACAGATTT 60  
ACATGTGCAC ACACACACAA ATTTCTTATC ACATTTTCGC CTTCTTCACT TGACCTAACT 120  
GATTATGCGA AATACCCAAG ATTCATGCTA CTGTACCACA GATTGTGTTT CACAGCAATA 180  
AATCTTCAGT TCTTTGTTTA TGATTCCACT TAACAAAAGG CCTGCAGAAG TGATTTATTA 240  
TTTGGGTATT TGGAGATAAT ACATTGTATG GTTTTTTGGG AAACCTTTT CACTCCATAC 300  
TCAGATATGC TTCATTGTCA AATGCATATT TAGGNTAGGT TAATNGAATT GTAATGTTTA 360  
ACCTGCTGCT TTTTTTTAA ATAAAAATTT GACTGAAAAT GGTTAAA 407

SEQ ID NO:1522

SEQUENCE LENGTH:397

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01733

SEQUENCE DESCRIPTION:

GATCTAGTAG CCACGCTAAA AAACAAGTAA AATTAATTTT AATATATTTA ACTCAATACA 60  
TTGGAGATAT TATTTAGAA CGATATTTT CATTCTTATG AAATAAGTC TGTCTGGTTT 120  
GCATATCTCA GTTGAGACAC TAAAGTTTTA CTGATAATAC TTAATCCATN NATTAGATTT 180  
CATAAAATCT AAATTGCAA AGTAAATTTA CATACCATG TNGGTCTAAA TGTGCTTAAA 240  
AGTTTTCCAA TAACTGAAAT GAGTATCAGT TTTAAATTTA AAAATTTGTT ACTTGTTAC 300  
TCCATATTTT AGGTATTAGT GGCTACCATA TTGGTCAGAG CAGATTCATA GGGATGATTT 360  
CCCAGGTTTG AAGTGTGTGT ATATTGCTGG TATTATN 397

SEQ ID NO:1523

SEQUENCE LENGTH:395

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01734

SEQUENCE DESCRIPTION:

GATCTGTACG AAATGTGAAA TTTTTAGGGA CATCTCCATG CTGTCACTTG TNATTTGCCC 60  
TCTNATGTAT TTNGGTCATA TTGCCAACTG GAAAGTCAAA ATTTCTAAC AACTTTAAGT 120  
AAGTCCTTTN AAGACTNAGT GCTGTTTTNA ATCCAGTTTA GAAAGTAACT TAATTTTAAT 180  
ACCGCTACTA AAAATNCGAA AATTTCTCCT TTAATCACAT TCAATATGGT TAAANGAACA 240  
ACACTAATTG ACATTGCGTG GGCTTTTCCT CCCTTTGTTT AAANANGTCA TTTTGTTGAG 300  
CAAGNGGTTG TATAGTATTA TCTACTNNCT TGAGGCTGTT AAATTTNCNA TTCCAGNGGT 360  
TTTGTAATG TATCCCGGGG CCNTGNTGCA TTGGN 395

SEQ ID NO:1524

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01735

## SEQUENCE DESCRIPTION:

5 GATCTCAATG ACCTGGCGAA GACTGGAAAA TACAACTCCC ATCACCAGCA GAGTTGCTAG 60  
 GCTGCTGCTG TATGGGTACA GAGAAGGGTT TGACAAAATT GACCTGACTG TGAAGAAGCT 120  
 TCCAGCAGTT TACACAGGAC TGTTTTATAA ACTCTATCAT AAGGAACTGC CAGAGAATTA 180  
 TAAAACTATG AAAGGAATTG ATTAAATTCA CATTATATG TTTAGAAACA TGTAGACTAA 240  
 CGAATGACAT AAGAAATAGT GGACATTTTG GATTGATTAA ACATCTGACT GTGATTTTCT 300  
 AATGTATATG ATTTCCATGA AGAAATTTTG TTTCTAAACA TGCACATTTT AAAAGCCTCT 360  
 10 TTTCGAATAA AGCAAATGCG TGAAAANGAA A 391

SEQ ID NO:1525

SEQUENCE LENGTH:388

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01736

## SEQUENCE DESCRIPTION:

20 GATCCGGCGC CACAAGACCA CCATCTTCAC GGACGCCAAG GAGTCCAGCA CGGTGTTCTGA 60  
 ACTGAAGCGC ATCGTCGAGG GCATCCTCAA GCGGCCTCCT GACGAGCAGC GGCTGTACAA 120  
 GGATGACCAA CTCTTGGATG ATGGCAAGAC ACTGGGCGAG TNTGGCTTCA CCAGTCAAAC 180  
 AGCACGGCCA CAGGCCAGC CACAGTGGGG CTGGCCTTCC GGGCAGATGA CACCTTTGAG 240  
 GCCCTGTGCA TCGAGCCGTT TTCCAGCCCG CCAGAGCTGC CCGATGTGAT GAAGCNCCAG 300  
 GACTCGGGA GCAGTGCCAA TGAACAAGCC GTGCAGTGAG ACCCCCAAGA GGCCCATTTT 360  
 25 CCCCATAAAA AGAGATTTGG GAGTCAAA 388

SEQ ID NO:1526

SEQUENCE LENGTH:388

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS01737

## SEQUENCE DESCRIPTION:

35 GATCTTATTT CTCTACTCA ATTGTATATT TATACCCATT AATCAACTTC TGTTCTTGCT 60  
 CTCTCCGTGC TACCCTTCTG GCCTTTGGTA ATCGCCAATC AATCTACTCT CTATCTTCAT 120  
 GAGACCAGCG TATTTTAGCT CCCACATATG AATGAAAACA TATAATATTT GTCTTTCTGT 180  
 GCTTGACTTA TTTTACTTAA CATAATGACC TCCAATTCCA TCCATCTTGT GGCAGTGACA 240  
 GTATTTTCAAT CATTTTGTG TGAATTATAT TTCGTTGTGA ATATACATTA CATTTTCTTT 300  
 ATCCATTCAT CACTGATGTG CACTTAGGTT GATTCCATAT TTGGGCTATT GTGAATAGTG 360  
 40 TGTTAATAAA CATGAGAGTG CAGTAAAA 388

SEQ ID NO:1527

SEQUENCE LENGTH:385

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS01738

## SEQUENCE DESCRIPTION:

50 GATCTTCCTG GTCAGCGCTC TCTCTAGCAT ACTCTTCCTC TATTTGGCTC ACAAACAGGC 60  
 ACCAGAGAAG CAAATGGCAC CTTGAACTTA AGCCTACTAC AGACTGTTAG AGGTGATACT 120

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ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAAGTCAAG ACAATACTCA 180  
GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG CCAAGAAACT 240  
AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGAGATGT CTATGGTAGC TGAGCCAAAC 300  
ACGTAGGATT TCCGTTTTAA GGTTCACATG GAAAAGGTGA TAGCTTTGCC TTGAGATTGG 360  
CCTCATTAAA ATCAGNGACT GTAAA 385

SEQ ID NO:1528

SEQUENCE LENGTH:377

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01739

SEQUENCE DESCRIPTION:

GATCCGTA CT CAGAACGTCC AGGAGAGACG CATGGCCCGA AGTCAAAGTG CTGGAATTTT 60  
CCAAAACAGC CTGTTCTCTC CTCTCTCCTC CCCAGAGCAC CCCCTGCCAT CAGGGGGGTT 120  
GAAATCCCTC TCCCCCAGGA GCCCTGCTGC TTTGCTTGGT GGTAGGGCAG GAGAGCAAAC 180  
AAACAGTCAT GGTCTAAAAC CCACATAGCA CTTTGCTCTT AGTTACATGT AAAATTTTAG 240  
ATTTCTAAAA CAGGTGGGCA ATCATTTTGA ATACTGTTCT GTGACCCTGA CTGCTAGTTC 300  
TGAGGACACT GGTGGCTGTG CTATNGTGTG GCCATGCTCC NTTGTCCCG TNCCTGTTGG 360  
CTGCTTCTGT TTAGGTN 377

SEQ ID NO:1529

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01740

SEQUENCE DESCRIPTION:

GATCCAAGGC CTGTGGTAAA CGGGAGANCT TGTNTTTTTC AAGTGGAAAA AAACCCAAGA 60  
GTTTGTNCAG ACATCCTGTC TTCCAGAGA AGGTGGACAC TCTTGGNCTC ATTGTAAAGT 120  
GCCTGCTGNA TCAATAAAGC TCTTGGCTTA TTAGTCTATA AAACAAA 167

SEQ ID NO:1530

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01741

SEQUENCE DESCRIPTION:

GATCCACACG TTCCGGGACT ACCTGCACTA CCACATCAAG TGCTCTAAGG CCTATATTCA 60  
CACACGTATG CGGGCGAAAA CGTCTGANTT CCTCAAGGTG CTGAACCGCG CACGACCAGA 120  
TGCCGAGAAA AAAGAAATGA AAACAATCAC GGGGAAGACG TTTTCATCCC GCTAATCTTG 180  
GGAATAAGAG GAGGAAGCGG CTGGCAACTG AAGGCTGGAA CACTTGCTAC TGGATAATCG 240  
TAGCTTTTAA TGTTGCGCCT CTTCAAGGTTT TTAAGGGATT CTCCGTTTGT GTTCCATTTT 300  
GTACACGTTT GGAAAATAAT CTGCAGAAAC GAGCTGTGCT TGCAAAGACT TTCATAGTTC 360  
CCAAGANTTA AA 372

SEQ ID NO:1531

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01742

SEQUENCE DESCRIPTION:

GATCCACTGT TGGGGCCTCG ACGAGTTCCT GTCCTGGGAA AGGAGTACAC CGAGAAGACC 60  
CCCATTCTG AGCATGCTGT TTTCAATGTG GACCTCATGA GCAAGAAAAT TCATCTGACT 120  
GAGAATGGGA TAAGGGTGGA TATTGGCGAT ACAATAATCT ATCTGGTCA TTAAACTCAT 180  
GCACATTGGA GATTTATCCT GGTTCCTTAG GAATACTACT ACTCTGATTG TGTCTACTGA 240  
TTGGCTATCA GAACCTTAGG CTGGACCTAA ATAGATTGAT TTCATTCTA ACCATCCAAT 300  
TCTGCATGTA TTCATAATTC TATCAAGTCA TCTTGATTG CTGGACCTAA TAAATTTTTT 360  
TTCCCTTTCA AA 372

SEQ ID NO:1532

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01745

SEQUENCE DESCRIPTION:

GATCCCAGTC ACAATTATCA CCGGGTATTT AGGTGCTGGG AAGACAACAC TTCTGAACTA 60  
TATTTTGACA GAGCAACATA GTAAAAGAGT AGCGGTCATT TTAAATGAAT CTGGGGAAGG 120  
AAGTCCGCTG GAGAAATCCT TAGCTGTCAG CCAAGGTGGA GAGCTCTATG AAGAGTGGCT 180  
GGAACCTAGA AACGGTTGCC TCTNCTGTTC AGTGAAGTGA GGAATGTGTT TACTGTGTAC 240  
ATGGTTTACT AGAAATGTTT ATTGATTATA TTTCCAGCTT TAATTTTCTT GAGTAATTTA 300  
ACTGAATTTA CACAGTTTGC TTCATTGTAT TTTCAAACAA ATAGAAAATA AACTTATTAG 360  
GAAGCAAA 368

SEQ ID NO:1533

SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01746

SEQUENCE DESCRIPTION:

GATCGTCCCC GTATGATGAT TGTNAGAAGA CAGGACTAAG TAGCAGAGAA TAGCTAAGAG 60  
ATAAATTGGG CTGGGGAAAC TTGTCAGAAA GCACTGAACA ATTAAGAAAT TTTCCAAGAA 120  
AATGTGCAGT ATTCTCTGCT ACTTCTGAAT CTGTTTTGTC TTCCTAATCT ATCACAATTG 180  
CCACCCATCG GGTTTTGGGT GTGTGTTTTT ATAGCGTGGT TACTTTCTAT AATGCTGTAC 240  
CCAGATTCTA AGAACCTGGA GAAGGATTAG CAGTTCCTAG TAAGTTTACT GTGTATAGGA 300  
ACGGTTTGTA TTTTATTACA GCTATTTCATC TTTTCTACAT TAAAAATATT TTTCTCTAAA 360  
GAAA 364

SEQ ID NO:1534

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01747

SEQUENCE DESCRIPTION:

5 GATCTGTGCC ATAAAATTTC AGTGTAATAA GACTTCTTCA ATACATCTTC CAATAAGGGG 60  
 TGCTTCTTTG TGACAGTATT TTTATTTCTG ACATTCATTT TATTTGGGTA CATAGTGTGG 120  
 TTGTTGATAC CTTGCAATAG TATTGCTTCT GAAAGTAATA AAAAAATTTA GGAGAATTTG 180  
 AGAAGTTTAC AGAATTACTT ATTCATTGTT TTCTTAGTAA GTCAGTTTAA TGTTTATTTT 240  
 TCTCATTATT TCATCACTGC AATAAAGAAT AAGGGTGTTT GAGCTCACCT CCATGCAAAG 300  
 10 ACTTCAGTTT TAAAACATTA TTTGCCTAAA ATTAGCATTG TGATGCTTTC TGAAAGAAAT 360  
 AN 362

SEQ ID NO:1535

SEQUENCE LENGTH:361

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01748

SEQUENCE DESCRIPTION:

20 GATCCACCTC TCCTGTGCTA AGATTAAGAN GACCAACGTC CCCGANTTCT TTNATTGCCA 60  
 GAAATGCAAG GAACTGAGGC CAGAGGCCNN GCGGTTAGGG GGGCCTCCCA AATCTGGAGA 120  
 GCCCTGATGG CACCAACTTT AGCCTGGAAC TTCCAAATNA CAACATGATT TGGGAACTGA 180  
 GCCTCAGGGT CCTCAGCCTA TCCCCTGGAG CTTGGATACT GTCTGCACTT CAAGGCAGGA 240  
 ATTCTCAAGG GAGACTTGTT TGAAAATNAG TGTCTCACTT TCCCACCCTA TCCTTCCTCC 300  
 25 CCACTCTGTG GACTTGAAAT TGAATCCATT ACGGTTGGGG ATGGGAGGCT GTCTGTGTCC 360  
 N 361

SEQ ID NO:1536

SEQUENCE LENGTH:360

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01749

SEQUENCE DESCRIPTION:

35 GATCGATTCT CTCTATGAAG GAATCGACTT CTATACNTCC ATTACCNGTG CCCGATTNNA 60  
 AGAACTGAAT GCTGACCTGT TCCGTGGCAC CCTGGACCCA GTAGAGAAAG CCCTTCGAGA 120  
 TGCCAAACTA GACAAGTCAC AGATTAATGA TATTNTCCTG GTTGGTGGTT CTACTCGTAT 180  
 CCCCAAGATT CAGANGCTTC TCCANGACTT CTTCAATGGA AAAGAACTGA ATANGAGCAT 240  
 CAACCCTGAT GAAGCTGTTG CTTATGGTGC AGCTGTCCAG GCAGCCATCT TNNNTGGAGA 300  
 40 CAAGTNTNNG AATGTTCAAG ATTNNGCTGGC TCTTAGGNTG TCACTACTCT TTTCCCTTAN 360

SEQ ID NO:1537

SEQUENCE LENGTH:358

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01750

SEQUENCE DESCRIPTION:

50 GATCCCAGTG AATCCTGGGT CCAGGAGTAC GTGTATGACC TGGAAGTGAN CTGAGCTGCT 60  
 CAGAGACAGG AAGTCTTCAG GGGAGGTCAC CTGAGCCCGG ATGCTTCTCC ATGAGACACA 120

55

# EP 0 679 716 A1

TCTCTCCAT ACTCAGGACT CCTCTCCGCA GTTCCTGTCC CTTCTCTTAA TTTAATCTTT 180  
 TTTATGTGCC GTGTTATTGT ATTAGGTGTC ATTTCCATTA TTTATATTAG TTTAGCCAAA 240  
 GGATAAGTGT CCCCTATGGG GATGGTCCAC TGTCAGTGTT TCTCTGCTGT TGCAAATACA 300  
 TGGATAACAC ATTTGATTCT GTGTGTTTTT ATAATAAAAC TTAAATAA AATGCAAA 358

SEQ ID NO:1538

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01751

SEQUENCE DESCRIPTION:

GATCCCTCCT CTAGGGGCCT GGGGACTTTN ACTGATGCTC TTCCTGATTC TAGAGCAAAG 60  
 GTGTGGGAAG GGGAAATGGA GGAATGCCCT CCTGTCTGTN TCGTTCTCTG TGCCACAGCT 120  
 ACAGATGCAG AAGGTTTCTC TGGATAGCAC ACCTCTGANT GTAAATCATG ATAAAATGGA 180  
 TATTTGGAAA CTTACTCCTA AGCTGTGATT TAGGGTGTAT TTCTACTTCT GGACTGCCTC 240  
 AATATCAAGG GCTGAGACTT TTGAATTTTG AATATTCGTT GGGTTTCATG TTAAGANGCC 300  
 TGTGGTCTAG GAGTGCTATT CAGTGTTCCT TTCCTGATA AACACTTGA ATAN 354

SEQ ID NO:1539

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01752

SEQUENCE DESCRIPTION:

GATCTCAGTA TGGACAGTGT AACAAACAAA CCAAAATGGC TGGACAGACT TCTTGTGTTT 60  
 TGTAATATA AACTAGGACA GTTCTGTAGG TTTGTTCAGT GTGCTAGTGG AGTATTTCTT 120  
 TAATGTAAAA CTTCACTTAA CAGAGAGATT CTTTGTTTAG CAAGCTTGGN GTGATGATAN 180  
 AGNGGTAAGA AATAATATA ATGTTGAAGA AAGCATCACA ACAGAACTAT AGGAGTCTAA 240  
 ATTTAATAAA TCTTTAAAA AAACCACTGT CTAGAATATA TACCATGTTT TATTATTTAA 300  
 AATCATTGTC TTAAATTTTT GTTCAAAAA TAAAAATTTG AATACAATCA AA 352

SEQ ID NO:1540

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01753

SEQUENCE DESCRIPTION:

GATCAGACAA GCCCAAACTG AGAGACACTC TACAAAATAA CTGGCCAGTA CGTTTTNCAA 60  
 GTNCCAAGGC CGTGAACAAT AAGGAAAGAC TGAGGAACAG TCATGGACTG GAAGAGAGTA 120  
 AAGAAATATG ATAACAACT GCATTGTGAG ATACCGATTT AGATGTTGGA TTAGAAAAAG 180  
 GACCAGAAAT AAGATTTTCA CAATGTCAAT TATTTGGTTT TGATAATTGT ACTGTGGTTA 240  
 TGTAAGATGT TAACATTAGT AAGAGCTGGG TGAAGGGTAC ATGGAACTA TTATTTTTGC 300  
 CACCCTTGA AAGTCTAACT TTTTCAAAA TAAAAAGTTT TAAAAATAA A 351

SEQ ID NO:1541

SEQUENCE LENGTH:357

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01754

SEQUENCE DESCRIPTION:

GATCCCAGAT GCAGTGACTG GTTACTACCT GAACCGTGCT GGCTTTGAGG CCTCAGACCC 60  
 ACGCATAATT GGGCTCATCT CCTTAGCTGC CCAGAAATTC ATCTCAGATA TTGCCAATGA 120  
 TGCCCTACAG CACTGCAAAA TGAAGGGCAC GGCCTCCGGC AGCTCCCGGA GCAAGAGCAA 180  
 GGACCGCAAG TACACTCTAA CCATGGAGGA CTTGACCCCT GCCCTCAGCG AGTATGGCAT 240  
 CAATGTGAAG AAGCCGCACT ACTTNACCTG AGCCACCCAA CCTAAATGGT ACTTATCTGT 300  
 NCCCATGTNC NTACACCAGC CTGTTTNNAT AATAAACTTT ATTGGTGGTA GGGNAAA 357

SEQ ID NO:1542

SEQUENCE LENGTH:412

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01755

SEQUENCE DESCRIPTION:

GATCAGGGCA GTAGGCATAA TTCAGCAACA AACAATCTTC CTTGGGAGA AACCTNTTCA 60  
 TTCCAATCTT CTAATTACAG TGGTTCCTAT CTCAGGGATA CTGGACTTN TGACGCAGAT 120  
 GAACAATTAA GGGGAAAAGC TTCCCTTTTC CCTCTGTGGC AGTTACGATT TTNACTTCAG 180  
 TCCTGAGAAA AACTTCAGGT TTTGAAAATC AGATGATGTC TTCTCCTTTT CCAANCACCA 240  
 CACGTTGAAA GCNTTTATAA ATCCAAGTCT GAAACTCTGC GCTCTAGTAC TGCTGTTAAG 300  
 NTACACAAC TGTTTTCTNN GTTCATATAA TCTNGGGGTA CNCACNCACA CACNCNTGTA 360  
 TGGGGGGGGG GGNNTGGCGN TTNCCACCGC GCGTTCNTT TTTGNNGGGT CN 412

SEQ ID NO:1543

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01756

SEQUENCE DESCRIPTION:

GATCCCAAAA TGCTGCGGGG CAATGACAGC TCAGTTCCCA GAAATAAAAA TCCATTCCAA 60  
 GAGGCCATTG TTTTGTGGT GGGAGGAGGC AACTACATTG AATATCAGAA TCTTGTGAC 120  
 TACATAAAGG GGAAACAAGG CAAACACATT TTATATGGCT GCAGTGAGCT TTTTAATGCT 180  
 ACACAGTTCA TAAACAGTT GTCACAACCT GGACAAAAGT AACACAGAAG AACCTTACTA 240  
 TGATAATCTA CTTGGAATGT GGATAAATGT AAAANGNAGA AAAGTTAGAA NGNGCANTAT 300  
 GTTTCCTTCT CTGTAACAGT GTCCTAACAG TGAATTTCA GGN 343

SEQ ID NO:1544

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01758

SEQUENCE DESCRIPTION:

GATCGANCTT NCTATGGACT CAAGCAGGTG NNGAAGGCCA ATNAAGCCAT GGCAATTGAC 60  
 ACATTGCTCA TCAGCGATGA GCTCTTCAGG CATCAGGATG TAGCCACACG GAGCCGGTAT 120  
 GTNAGGCTGG TGGACAGTGT GAAAGAGAAT NCAGGCACCG TTAGGATATN CTCTAGTCTT 180  
 CACGTTTCTG GGGAACAGNT CAGCCAGTTG ACTGGGGTAG CTGCCATTCT CCGCTTCCCT 240  
 GTTCCCGAAC TTTCTGACCA AGAGGGTGAT TCCAGTTCTG AAGAGGATTA NTGATTGAAA 300  
 CTTAAAATTT GNGACAATCT TTGTGTTTTT CTAAACTGTN 340

SEQ ID NO:1545  
 SEQUENCE LENGTH:339  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01759

SEQUENCE DESCRIPTION:  
 GATCTGCTTT CATTAACTGG AATTCTGTAG GAGATACTGG TGACCTAAGC TAAGTTGCAC 60  
 TCAGCATACT CAGTGTCAAG CTAATGAGGT TCTATTATAA AGGTTCTACT TTTAATCTGA 120  
 GGGAAAACAT GTTCAGGGCT TCTAGAACAC TAAAAAATTN GGNTTAAACC AGTGTNCAGT 180  
 CTGGTGCCAA ACTTCGAATG GAATACAAAT NNACATAATC TGANCTTTGT NCACAGGTGA 240  
 TCCTAATAGA GTAATTCTCC ACTTTGCTCT ATTGAACTGT CTTAAGGGAT TTGTTTAAAC 300  
 AGCTAAGTTA CTTGATTAAA ATAATGATAA AATTGTAAA 339

SEQ ID NO:1546  
 SEQUENCE LENGTH:362  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01760

SEQUENCE DESCRIPTION:  
 GATCTGGTAG AAGGTACCAG CTTCTTTTCC AGCTGGAGAG GCCCAACAC TGGATGGTTC 60  
 TGTAGGGAGC CTAGGGAGCC TGGTCATCAA CTTGCAATAC CTCACAGAGC CAGTTCACAT 120  
 CCCACTCTGA GCTCCCACGA GAAACACTGC TTCTCCAGGC CCGGGGTGTG TGGGGAGAGA 180  
 GGCAGAGGCA GCTGGAGCGC CGTTCTCTCC TGCTGGGACA CCGCTTGGGC TTTGGTATTG 240  
 ACTGAGTGGC TGACAGTTAT CTTCCAACCC CAACTGGCTT GGGGGCAGGA CAAGGGCTTA 300  
 GGCTTGATGG TGGNCAGGCT TGNCTGCTCC CCACCTGNGA TGCCCTGCT CTGGGACCTC 362  
 TN

SEQ ID NO:1547  
 SEQUENCE LENGTH:335  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01761

SEQUENCE DESCRIPTION:  
 GATCCTTTCA GAAAAGAAAC ACTGGGTCCC ATAGCTAAAT TCTCAACCGC CANGCACCTT 60  
 CAGAAGAATC CAGCCTAATA CTGGAATTG TGCTATTATC TTCCTCTCCA GCCCCCAAC 120  
 TCCATCCCTC ACCACAGTTG TCTAGGAAAT GACATGAATT CAATATCTAA TGTCAACCAA 180  
 TGGGGAGAGC CACAACCTCA GGAGAGGTTT CTGAGCTGAG TCCCTTAATT TCTGGATGAA 240  
 GAAGACCAAC AAGTTTTGTC CAATGTATTT GTTCTCAGA CCTTGCCTAG GCACTAAAAA 300

TAAAATACTA GGTCATTGGA GGCTAATGTG GGAAA

335

SEQ ID NO:1548

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01763

SEQUENCE DESCRIPTION:

5  
10  
15  
GATCATTAAAG GAAGGCGATG TAGATGTTTC AGATTCTGAT GATGAAGATG ATAATCTTCC 60  
TGCAAATNTT GACACATATC ACAGAGCCTT GCAAATAATA GCAAGATATG TACCATCATG 120  
AGTATACTGN TCCTTATTTT GAATGTTTAA TTCTCAAGAA AATTGTAATC AATTAGTAAA 180  
AATTATAAAA TGTTAATAGT ATTAAAGCTT GAGTCTTACA TTGCATTTT TTTTNGNA 240  
NCCACTTGGG GAACCATTC ATNCTCCAAA ANGGGGCATT CCCATTTCT NTTNATCCCC 300  
TNNAATGGTT TTNCAAAGTN NGTNTGCNGN 330

SEQ ID NO:1549

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01764

SEQUENCE DESCRIPTION:

20  
25  
30  
GATCATGGTG GATGAGGAAG CCTCAACGTA GATTCCTGAA CTCAAGGTAC CAGCAAGANT 60  
GCNTTCTCCC AGTGTGCTCT CCCCAACATC CTAGGCACAG CTTTCATAAC CCAGTTTCTT 120  
AGGTGTAAGA AACTGTTTTN ATCTCATTTA TTAAGTCTCA GAACTTAACA GAAAAGGAAG 180  
CCTTTTAAAT ATTCTTTTAA ATNTTATTTT AGATTAACAG TTTTGNACTT TACATTTTTT 240  
TATACAACCA NCCAGTTTCT TTNCTAGCCA ATCATCTCTG ANGAGTTGCT GTTTCTTACT 300  
GACAATAAAA NNTGTNCTCT TGGTTCGAAA 330

SEQ ID NO:1550

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01765

SEQUENCE DESCRIPTION:

35  
40  
45  
GATCAACATC TTTCCTTGCC TCTGTCCCT TCTCTCATCT CTTAGCTCCC CTCCAACCTG 60  
GGGGGCAGTG GTGTGGAGAA GCCACAGGCC TGAGATTCA TCTGCTCTCC TTCCTGGAGC 120  
CCAGAGGAGG GCAGCAGAAG GGGGTGGTGT CTCCAACCCC CCAGCACTGA GGAAGAACGG 180  
GGCTCTTCTC ATTTACCCC TCCCTTCTC CCCTGCCCCC AGGACTGGGC CACTTNTGGG 240  
TGGGGCAGTG GGTCCCAGAT TGGCTCACAC TGAGAATGTA AGAACTACAA ACAAATTTT 300  
TATTAATTA AAATTTNTGT GTCTCCAAA 329

SEQ ID NO:1551

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01766

SEQUENCE DESCRIPTION:

5 GATCCCAACT GCTCCCTNCC CTCGCCGGTG ACTCCTGCAC CTGCGCCGGC TCCTGCAAAT 60  
 GCAAAGAGTG CAAATNCACC TCCTGCAAGA AAAGCTGCTG CTCCTGCTGC CCTGTGGGCT 120  
 GTGCCAAGTG TGCCCAGGGC TGCATCTGCA AAGGGGCGTC GGACAAGTGC AGCTGCTGCG 180  
 CCTGATGCTG GGACAGCCCC GCTCCAGAT GTAAAGAACG CGACTTCCAC AAACCTGGAT 240  
 TTTTATGTA CAACNTGAC CGTGACCGTT TGCTATATTC CTTTTCTAT GAAATAATGT 300  
 10 GAATGNTAAT AAAACAGCTT TNACTTGAAA CAAA 334

SEQ ID NO:1552

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01767

SEQUENCE DESCRIPTION:

20 GATCTGTTTG GACTATGTTT TCTTTTCTTC TCCCACTTGC TCAGCAGCTT GGGCTTCCAT 60  
 TCTAGTTCTT TTACCAAGAT TTTTGTGTGA CCATGTTGAC TTCATTTGGA TTGCCCTCTT 120  
 TCAATTTCTT TGTGAAAACA CCCTTAACTT TCTCTTTACC CTTAGCTGAA ATGTTTACAT 180  
 AGCTTCTGGT GATATCTTTN CATGATTTTA TATCTCTTAA AATGGTGATG GATGTGACAC 240  
 CTCATAAAG TGAGCTTTGA ACTGTAGATA ACTCTTAAAG AAAATGTCAT TTTAGACAAT 300  
 25 TAAAATATTT GTGCTCAACT GCTTGAAA 328

SEQ ID NO:1553

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS01768

SEQUENCE DESCRIPTION:

35 GATCGAAATG TTAACACCGG GAGCTCTNCA GGACACTCAC CCAGCGACGC TCGTGGGGGA 60  
 AACATACTAA ACGGACAGAC TCCAAGANCT GCCACCGCTG GGCCTGCACT GCGGCCCCCC 120  
 ACGTGAATC GGTGTAAACG GGCCNGGGAA GAAAAGCAGA GAGAGAATTG CAGAGAATCA 180  
 GACTCCTTTT CCAGGGCCTC AGCTCCCTCC AGTGGTGGCC GCCCTGTACT CCCTGACGAT 240  
 TCCACTGTAA CTACCAATCT TCTACTTGGT TAAGACAGTT TTGTATCATT TTGCTAAAAA 300  
 40 TTATTGGCTT AAATCTGTGT AAAGAAA 327

SEQ ID NO:1554

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS01769

SEQUENCE DESCRIPTION:

50 GATCAGCAGA CCACGTATTT AAAATTCTGA ATCTTCTGGG ACAGGGTTGT AACTCAGCCT 60  
 TCCAAAGGGA AGAGTGCAGG GGGACGGGGC CATGATATGG GGAAATGGTG TAAACTAATG 120  
 TATTTNTTTA TTGGCTGTTA TTCTGTATAA CACTCATATC TTTGCCAAAG TTCAATTTTA 180  
 TATTTAGGCA ACTGATGGTC CTTTGCATT TAGGATTTTN GTTGTGTGTA CCTTATACCT 240

55



CATGATATAA GGAATGGGCT CATGTGTCTT CCGTCTTTTG GAAGGAGGTT GACATATTTT 300  
AAATAAATGC TTTTAAATAC AGTAAA 326

5

SEQ ID NO:1555  
SEQUENCE LENGTH:387  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS01770

SEQUENCE DESCRIPTION:

GATCAAAAAG AACAGAACCC TCTCCAGCCT GCTGACCCGA ACCCAACCAC ACAATGGTTT 60  
GTCTCAATCT GACCCAGCGG CTGGACCCTC CGTAAATTGT TGACGCTCTT CCCCCTTCCC 120  
GAGGTCCCGC AGGAGCCTAG CGCCTGGCTG TGTGTGCGGC CGCTCCTCCA GGCCTGGCCG 180  
TGCCCGCTCA GGACCTGCTC CACTGTTTAA CACTAAACCA AGGTCATGAG CATTCTGTCT 240  
AAGATAACAG ACTCCAGCTC CTGGTCCACC CGGCATGTCA GTCAGCACTC TGGCCTTCAT 300  
CACGAGAGCT CCGCAGCCGT GGCTAGGATT CCACTTCCTG TGTCATGACC TCAGGAAATA 360  
AACGTCCTTG ACTTTATAAA AGCCAAA 387

20

SEQ ID NO:1556  
SEQUENCE LENGTH:325  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

25

CLONE:HUMGS01771

SEQUENCE DESCRIPTION:

GATCACAGAT GGATNTTGTT ATAAGCATCA ATGTGACACT TGCAGGNCAC TACAACGTGG 60  
NACATTGTTT GTTCTTCCA TATTTGGAAG ATAAATTTAT GTGTAGACTT TTTTGTAAAG 120  
TACGGTTAAT AACTAAAATT TATTGAAATG GTCTTGCAAT GACTCGTATT CAGATGCTTA 180  
AAGAAAAGCAT TGCTGCTACA AATATTTCTA TTTTAAGAAA GGGTTTTTAT GGACCAATGC 240  
CCCAGTTGTC AGTCAGAGCC GTTGGTGTTT TTCATTGTTT AAAATGTCAC CTGTAAAATG 300  
GGCATTATTT ATGTTTTTTT TTTN 325

35

SEQ ID NO:1557  
SEQUENCE LENGTH:322  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40

CLONE:HUMGS01772

SEQUENCE DESCRIPTION:

GATCTGTAAT TCATAGTCAC ATCAAGGTCA TCAAGACCAG GAAAAACAAG AAAGACATAC 60  
TCAATCCTGA TTCAAGTATG GAAACTTCAC CAGACTTTTC CTTCTAAAAT CTGGATGTCA 120  
TTGACGATAA TGTTTATGGN GATAAGGTCT AAGTGCCTAA NAAAATGTAC ATATACCTGG 180  
TTGAAATACA ACACTATACA TACACACCAC CATATATNCT AGCTGTTAAT CCTATGGAAT 240  
GGGGTATTGG GAGTNCTTTT TTAATTTNCC ATAGTTTTTT TTAATAAAAT GGCATATTTN 300  
GCATCTACAA CTTCTATAAT TN 322

50

SEQ ID NO:1558  
SEQUENCE LENGTH:319

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01773

SEQUENCE DESCRIPTION:

GATCTTTCTT TAATAGTGAA CCCCTGGGCC ACTGAAGAGT AACATGGCTC CACTGGACAC 60  
AAAAGAGGGA TGGAATCAAC AGGCAGGGGG CCTTTTATAA GCCTTAGGAA AAGAAAATGA 120  
AACTATTTCA TCTTTGGACT TTTCAATACT ATTGGAGTGA TTTTTTTTTT TCTAAACAGG 180  
GAAAATAATG TTACAAAAGC ATCTTTTTTG TNATTTGTTT GCATCCCTCC CCCACACCT 240  
GGTGTTTTAA ANTGANGAAA AAAANCCATC ACCTTTTGTA CAAAANCTCT TAATGNTTAA 300  
CAAACAAACA AANCAGAAA 319

SEQ ID NO:1559

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01774

SEQUENCE DESCRIPTION:

GATCTGGCTG CGCTATGACT CCGGGAGCGN CACCCACAAC ATGTACCGGG AATACCGGGA 60  
CCTGACCACC GCAGCGCTGT CACCCAGTGC TACCGAGACA TGGGTGCCCG GCACGCGCCC 120  
GAGCCCACTC CATTANATC TNACAGCAGT GTTCTTGCAA TATGAGGAGA CAGTTACAGC 180  
CACATTATGG CTCTCATTGA ACAGTACGCA GCACCCCTGC CCCAGCCGT NTTTTGGGG 240  
CTTGCGCGAA AATCTACAAG CGGGAANGTG ACCTNGGATT CAAGGGCGGG GAGAGANGCT 300  
TNAATAAATA ATCGTN 316

SEQ ID NO:1560

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01775

SEQUENCE DESCRIPTION:

GATCTAGAGG GTCGGACCCA CATATTTAAG ATTCACGNTC GTTCAATGAG TGTTGAAAGA 60  
GATATCAGAT TTGAACTGTT AGCACGACTG TGNCCAAATA GCACTGGTGC TGAGATTAGA 120  
AGCGTCTGCA CAGAGGCTGG TATGTTGCC ATCAGAGCAC GGCGAAAAAT TGCTACCGAG 180  
AAGGATTCTT TGAAGCTGT AAATAAGGTC ATTAAGTCTT ATGCCAAATT CAGTGCTACT 240  
CCTCGTTACA TGACATACAA CTGAACCCTG ANGGCTTTCA AGTGAAAACT TTAAATTGGA 300  
ATCCTAACCN TATATAGACT TGTTAATAAC CAATTCATAA ACAAATAAAT GGCTTCAAAA 360  
TTGAAAAAAA NNNGANNNN NNNNAGNNNN 390

SEQ ID NO:1561

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01776

SEQUENCE DESCRIPTION:

GATCTGCTTA GAGTGGATTT TCACTCAAGT CCTTAGTAAG TGGATTTTGG GGAAAAAAGC 60

# EP 0 679 716 A1

ACCTGGGCTT CTGGTTCTTT TTGATAATAT ATAAAATTAT TCATTATGAG GTTGCAGTTG 120  
 TTTGCAAAGG AGAGGCACTC AAATTTGAAA GGTATTTTTA ATGTGATAAT TTGGAAGACT 180  
 TACTCAGATG TTGGTCATTG ACCACTCTGT GCATATATTT CTGCAGAGCT CTGTGAAGGC 240  
 AATGAGTGTG ACTTCCCTCT GCTCTAATAA AGCAATAAAT AATAGCTAAA GGGCTGACTT 300  
 TCACTTCGAA A 311

SEQ ID NO:1562  
 SEQUENCE LENGTH:310  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01777

SEQUENCE DESCRIPTION:  
 GATCTTTCTA CAACATTTAT CCTGGTTGTT AAGCCCTCCT TACAACATTC TTCTCTCTTT 60  
 GTTTTTATAG CTCCATCTCT CCTGCTTCTT TAAGTTGATA ATGCATACTT GATTTTCCTA 120  
 TTTGTNATTT CATAAACCAA TTAATACACA GATAAAATGA CTGTATATCA AACCATGTTT 180  
 GTATAGAAAA ANTGGATTN GGATGCCTCT CATATGTAAT TAGTTCTATT AAACATATTA 240  
 ATNGTATTGT TTAATTNGTC AGGTTTTTGA CAGANTTTTG TTTACAGGTA ATAAANNNTNT 300  
 TATCTCCAAA 310

SEQ ID NO:1563  
 SEQUENCE LENGTH:307  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01778

SEQUENCE DESCRIPTION:  
 GATCGAAAAA AAAATCCAGA ACCTTGGGAA ACTGTGGACC CTACTGTACC TCAAAAGCTT 60  
 ATAACAATCA ACCAACAAATG GAAACCCATT GAAGAGTTGC AAAATGTCCA AAGGGTGACC 120  
 AAATGACGAG CCCTCGCCTC TTTCTTCTGA AGAGTACTCT ATAAATCTAG TGGAACATT 180  
 TCTGCACAAA CTAGATTCTG GACACCAGTG TCGGAAATG CTCTGCTAC ATTTTATAGG 240  
 TTTGTCTACA TTTTNGGGC TCTGGATAAG GAATTAAAGG AGTGCAGCAA TAACTGCACT 300  
 GTCTAAA 307

SEQ ID NO:1564  
 SEQUENCE LENGTH:305  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01779

SEQUENCE DESCRIPTION:  
 GATCCTGTGG TTGCCACTG GCCATAGCTG CTGCCAGCT CTACCCCTCC CAGGGACCTA 60  
 CCCCTCCCAG GGACCGACCC CTGGCCCAAG CTCCCTTGC TGGCGGGCGC TGCCTGGGCC 120  
 CTGCACTTGC TGAGGTTCCT CATCATGGGC AAGGAAGGGA ATTCCACAG CCCTCCAGTG 180  
 NACTGAGGGT ACTGGCCTAG CCATGTGGAA TTCCCTACNC TGACTCCTTC CCCAAACCCA 240  
 GGGAAAANAG CTCTCAATTT TTNATTTTTA ATTTTGTIT GAAATAAAGT CCTTAGTTAG 300  
 CNAAN 305

SEQ ID NO:1565  
SEQUENCE LENGTH:304  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01780

## SEQUENCE DESCRIPTION:

GATCACAGCT AGAGAATTGA GAATTAAC TA TACTACTAGC CATT TTTAGGG CACCAAACT 60  
TGGGATTAAA CACTTCCTAC TTCCCACTCC CAACCTCTGA AATGAAGTCT TGCTATCTGT 120  
GACTAGTTTT ATTTTGTGC TTTAATAGT CCGAGCAGTC TTACCTGTT TACACATGTA 180  
TTGACACCAT TTGCTTCAGG CCATGGAGCA CTGTTTCTCC CN TTTTACTA TTTATAGGAT 240  
TCCGTTTTTT CACAAGACTT TTAATAAAAA GAAATTGTAG AAATAAACAC ATTAAAATTT 300  
GAAA 304

SEQ ID NO:1566  
SEQUENCE LENGTH:304  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01781

## SEQUENCE DESCRIPTION:

GATCTGCTTT CTCGTAATTA TAGATTGGTT TGCATTTTCT AGAAATTTT AAATAAATGG 60  
AAACATATAG TGAGTACTCT TCTTGGGGTG GAAGGAAGTG TGTGTGGCTT TTTCACTCA 120  
AGCATAATTA ATTTGATACT CATCCAGATT ATGCATGTAT CAATAGTTTA TTCCTTTTTT 180  
ATTGCAGAGT AGTAGTTANN NNCCTGGGTA TNCACAATTT GTTACCTGTT CATCTATTGA 240  
TGGNCAATTG GGGTATTTCC AGTTT TAGCT ATTACAAATA AACCTGCTGT GACATCATGN 300  
CAAA 304

SEQ ID NO:1567  
SEQUENCE LENGTH:304  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01782

## SEQUENCE DESCRIPTION:

GATCTGCTAT AGCTGTCCAT CAGAGAGAAT ACACGTGGCT ATAACATCTA TAACAAAACG 60  
ACGATTCCCTC TACAAGAGGC TGTTTCTNAC TGCTAACGTT GGTGTTTCTG GCGTGGGAAG 120  
AAATGCACAG GCGTG CATGG CATGCACGTN CAGACAGCTG CATTGTAAGA NTNCTGTCAT 180  
GCAGTCTGAA AAGGGAAGAA ACAGGATGGC TTTCTGTAGC CACACCTGTG AGGCGTGATG 240  
ATTGTNGTAT TATTAGATTA CTGATTTTCC TTTTCTGAAA ATACATTTGN NTTTTAATCA 300  
CAAA 304

SEQ ID NO:1568  
SEQUENCE LENGTH:304  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01783

## SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCTGCTGT TGCTGAGAGT NTGAGCGTGG ACTTGATGCA GTNATGACAA ATCATTGCTT 60  
 AGAATTAATG TTTTCAAATG TGCAACTCTA GTTTTTAAAA CAAAATTTGG TTCTTTACAT 120  
 TCATTATTTT GTTTTTGTTC CCCTTTAGTA TTAAATGGTC TTTGGAGAAA AAATAATAAA 180  
 ACAGAGTGTT ATATATATAT TTTTGGTGC AAGATAAGAT TTTCTGTTT TTGAAATAAG 240  
 TCTGTAGCAT AAAAGGTAA ACTATTTTAA GGACANANTA AAAATAGGAG TGTATTTAAA 300  
 CAAA 304

10 SEQ ID NO:1569  
 SEQUENCE LENGTH:303  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01784

15 SEQUENCE DESCRIPTION:  
 GATCCAGGGA TGAGGATAGA GTGGCCTGAG AGCAGTGCTT GGATTCAGCC TCCTGCTGGG 60  
 TCCTTCTGCT GGATACAGGC ACCAAGAGGC GGGGGTGGAG CAGGGAGCTG CGCCTTCCTG 120  
 GGGTGCCNGG TGGTGTGTAG AGAAAAGCTG CTTGTTTACT CCTTAAGTCA ATGTATTGGT 180  
 20 GACTGTTGAT TTGTTGAACA ATTCAGGAAT CAAGGGCTGT GGAGAACTC CCTCATGTTG 240  
 TTGGCAACAG GTGAATGAAC CTAGAGCGGT GACATGAAAA TAAAGCTCAC TGTTACTCGC 300  
 AAA 303

25 SEQ ID NO:1570  
 SEQUENCE LENGTH:302  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01785

30 SEQUENCE DESCRIPTION:  
 GATCCCCGA CGACGTGCTC GAGTTCCTGA AGGTGTATGA GANGCACTCT GCCCAGTGAG 60  
 CACCTGCCCT GCCTGCATCC GGAGAATTGC CTCTACCTGG ACCTTTTGTC TCACACAGCA 120  
 GTACCCTGAC CTGCTGTGCA CCTTACATTC CTAGAGAGCA GAAATAAAAA GCATGACTAT 180  
 35 TTCCACCATC AAATGCTGTA GAATGCTTGG CACTCCCTAA CCAAATGCTG TCTCCATAAT 240  
 GCCACTGGTG TTAAGATATA TTTTGAGTGG ATGGAGGAGA AATAAACTTA TTCCTCCTTA 300  
 AA 302

40 SEQ ID NO:1571  
 SEQUENCE LENGTH:307  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01786

45 SEQUENCE DESCRIPTION:  
 GATCCATTTT GCTTACACTG TTGCATCACA AGGGACTCAC CCAGGGACCA TGACCTGCTG 60  
 GTGTGTGTGT ATATTTACAA AAACAAAACA AACAAACCAC CCATTGGGAT ATAAGGTAGC 120  
 AATCACAAC TAAAGACTGC GGCTTGTTGA GGTGCAATAC CCTGACTCCC AAAGTTAGTT 180  
 ACAGTGGGTT TTATTGTTT TGTGACTGAA GGATTATTTC AGACTGCTGT ACTCTTCATT 240  
 50 TGATGTAACA AAATGCTATT AATCTAAATA TTTGTAAATA AAGTACCTGT ATCTAGATTA 300  
 AATTAAA 307

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SEQ ID NO:1572  
SEQUENCE LENGTH:301  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01787

SEQUENCE DESCRIPTION:

GATCCATTAC CTAGGGTAAA ATTCTCCTGA ATGTCAAACA AAGAGATAAA CTACATTTGG 60  
GTTTGGGAA GTCCCCTGTA ATGATGAATC AAGAATCCTC AAGTCTGTCT TGCCACCCAT 120  
TTAATACGTA TTTTGTGTA GGCTGAAGTT TAGAGTTAGA ATCAGGACAT TTTGGCCTAT 180  
TGAGAGGTTT TGAATTCCAA CAGAAGATGC CATGTAAATC AGTGAATTTN ATTCTTTTAA 240  
AAGCAACTTA CAAAATTTAC AAGATGTATT CAATAAAGCA GTTTAGCTTT GGTATATCAA 300  
A 301

SEQ ID NO:1573  
SEQUENCE LENGTH:303  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01788

SEQUENCE DESCRIPTION:

GATCCTCAGT GTGCTCACGG GGCTGCTGTT CGGCAGCNAT GGCTACTACG TGGCGCTGGC 60  
CTGGACCTCA TCGGCGCTCA TGTACTTNAT TGTGCGCTCT TTGCGGACAG CAGCCCTGGG 120  
CCCCGACAGC ATGGGGGGCC CCGTCCCCCG GNAGCGTCTC CAGCTCTACC TGACTCTGGG 180  
AGCTGCAGCC TTTNCAGCCC CTCATNATAT ACTGGCTGAC TTTCCACCTG GTCCGGTGAC 240  
GTCTNGCCCC AGATGGNAAT NAGTTTTTTA ATTTTCATTGN AAGGATTTTG AANTTCCTTG 300  
AAA 303

SEQ ID NO:1574  
SEQUENCE LENGTH:297  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01789

SEQUENCE DESCRIPTION:

GATCTGTGTT CGAATCCTCC CCACCCCTTT CTTTGTGGAG TTTCCCTAACC TGCTGCTGAA 60  
GCACAATGTT TTGGTGCTTT CTTTCTCNN TTGTTAAAGG CAGTGTCCAA AAGCCATTCC 120  
AGATGCCAAG ACCAGGGGCT TATTTCTAGG GAAGGTAGGT CGGTTTCCAT GTTCCCTCC 180  
CGTTATTTTT ATTTTINACT TTTTGCCTGA GACAAGCCGA GTATGAGGTG GTTTGATTTA 240  
AGAAAAATCA ATGAAATTGT TTACTACTGT TTAAAAATAA AACCGTAAAC TCTGAAA 297

SEQ ID NO:1575  
SEQUENCE LENGTH:299  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS01790

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCAGGCCG TTNCTGAGCT CAACGGGACC CAGGTGGAGT CTGTACAGCT CAAAGTCAAC 60  
 ATAGCCCGAA AACAGCCCAT GCTGGATGCC GCTACTGGCA AGTTTGTNTG GGGCTCCCTC 120  
 GCTGTCCAGA ACAGCCCTAA GGNTTGCCAC CGGGACAAGA GGACCCAGAT TGTTTACAGT 180  
 GATGACGTCT ACAAGGAAAA CTTTGTGGAT GGCTTCTAGG GAACAGNGCT GGATTCCTTG 240  
 TGCCTCATAT GCCCCAAATG CTGGTTTTCA GTAAANCACT TGAGGGTGGA AGCTTNAAA 299

SEQ ID NO:1576

SEQUENCE LENGTH:300

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01791

SEQUENCE DESCRIPTION:

GATCCAAGAT AAAGAAGGCA TCCCCCCGA CCAGCAGAGG CTCATCTTTG CAGGCAAGCA 60  
 GCTGGAAGAT GGCCGCACTC TTTCTGACTA CAACATCCAG AAAGAGTCGA CCCTGCACCT 120  
 GGCTCTGCGC CTGAGGNGGT GGCTGTTAAT TCTNCAGTCA TGGCATTGCG AGTGCCCACT 180  
 GATGGCATT A CTCTGACTA TAGCCATTG NCCCAACTTA AGTTTAGAAA TTACAGGTTT 240  
 CAGTAATAGC TNGAACCTGT TCAAAATGTT AATANAGGTT TCGTTGNATG GGAGCATAAA 300

SEQ ID NO:1577

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01792

SEQUENCE DESCRIPTION:

GATCTGGCTT CTTTCCCAAG GNGGGGGTGG GGTGTNCCTN GCGTCCCTGT CCTTGANGGA 60  
 CCTCCTTCCC CCAGCCTCAT CACCGTGCTC TTCTCAGCGC CACCCTCAGC AGCCAGATTG 120  
 CAACACCAGG GAGAGGCGGA TGCAGAGCCC CACCGGTGGG AAAGTTGCCT GTGGAAGGGA 180  
 GCCTTTTGCT ACAATTTGTA ACTTATTNC TAAAGTCTAT TTTGTAACAA TTTATTTAAG 240  
 TTTAAAAAAA GGAAGACTGC TGCCCNCCAA AAAAAGAAAT TTTCAAAACA AGAAA 295

SEQ ID NO:1578

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01793

SEQUENCE DESCRIPTION:

GATCTAAAGT TCTGGCTGTC CATTAACTC CAACTATGGT CTTTATTTCT TGTGGTAATA 60  
 TGATGTGCCT TTCCTTGCCT AAATCCCTTC CTGGTGTGTA TCAACATTAT TTAATGTCTT 120  
 CTAATTCAGT CATTTTTTTA TAAGTATGTC TATAAACATT GAACTTAAA AACTTATTT 180  
 ATTTATTCCA CTAATGTAGC AATTGACAGA TTAATAAAAT GTAACATCAT AATTTCTTAC 240  
 CATAACCTCA ATGCTNNNTT TTAATAANATA AAAATTAATA ATGAAAAGNG NTANAAA 297

SEQ ID NO:1579

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01794

SEQUENCE DESCRIPTION:

5 GATCTCTCTT GTCCNCTNCT GCTCTTTNCT TGGTGCTCTT TTNCTCGGT GGGGTGTGGG 60  
 TAATAGAACA GCCGTGGGCT TTTGGGGACC TTAACTTTT TTNCTCTCT TTTGTTTATA 120  
 AAAAACACTA AACATTCAAT TCCAGAGAAC CAAAAATCCC ACCTTCCCAC CGAACACTAC 180  
 10 TAAGGGGCTT GTGTTCTGCN CCATACCTTT NCTCTTTNCT TTCTGTCTTG TTAATGCTTT 240  
 TAAAAACAAA TGAGTTTTTT ATATAAATAA AGTTTTTAAA GTGTGTAAA 289

SEQ ID NO:1580

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01795

SEQUENCE DESCRIPTION:

20 GATCCCATCC GCATGGAGTT TGAAAATAAG GAAGACTTGT CGGGAACACA GGCAGGGCTC 60  
 AACGTCATTA AAGAGGCAGA GGCGCACNCC NGGTGGGCAG CCAAGGAGCT GAGAAGANCG 120  
 AAGAAGCTTT CAGACTACGT GGGGAAGANT GAAAAANCCA AAATTATCGC CAAGNTTCAG 180  
 CAAAGGGGAC AGGGAGCTCC AGCCCCGAGAG CCTATTATTA GCAGTNAGGA GCAGAAGCAG 240  
 CTGATGCTGT ACTATCACAG AAGNCANGAG GNGCTCANGA GATTGGN 287

25 SEQ ID NO:1581

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS01796

SEQUENCE DESCRIPTION:

GATCTATTGG CATATTCGGG AGCTTCTTAG AGGGATGAGG TTCTTTGAAC ACAGTGAAAA 60  
 TTAAATTAG TAACTTTTTT GCAAGCAGTT TATTGACTGT TATTGCTAAG AAGAAGTAAG 120  
 35 AAAGAAAAAG CCTGTGGCA ATCTTGTTA TTTCTTTAAG ATTTCTGGCA GTGTGGGATG 180  
 GATGAATGAA GTGGAATGTG AACTTTGGGC AAGTTAAATG GGACAGCCTT CCATGTTCAT 240  
 TTGTCTACCT CTAACTGAA TAAAAAGCC TACAGTTTTT AGAAA 285

SEQ ID NO:1582

40 SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01797

SEQUENCE DESCRIPTION:

45 GATCCTCCCC TTTTGAAATG GCCCTGCTGT GTCAGTTTCC CTGTGGCCTT TTGAACTGTA 60  
 CATCTCATAT GTTGGGAAAC GCTGGCCACT GGGAAATCAT TAGAAAGGAG GCTGTAGAAT 120  
 ATTTGCCGAG CCTCTACTGT ATACCAGGGG CTAATCACC AAGCACATTC TAGGAATTGG 180  
 GCCCTGCTCA TGAGGAGCCT TAGTGGAGAT TCCAGGTGAA TATTTATGAA AAAGTCAACA 240  
 50 TTGAACTGA AAATGGAAAT AACTGCTTG AAAAGACAAA 280

55



SEQ ID NO:1583

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01798

SEQUENCE DESCRIPTION:

GATCAGAATG GACTTCTNCC ACTGAGCATG ACANGCACTC GAAAGGCTAA ATCAACCAGA 60  
AACATCGAAA CAAAAGCTCA GGTGTGCCCC CCGGCACGCT CCACANCTGG TGACCCGACA 120  
GTTCTGGCT CTTGTTTCAG ACAGCTTGTC AGTNAAGAAG ACANCACGTC TGCACCTNCA 180  
TTATTCAAAC TTGGCTGGCT CTCTAGTATG ACTACGNACA TGGAACACAT CTGTCTCTCC 240  
CTAAATAANT ACTACCACAT TATTNCTTCT AAA 273

SEQ ID NO:1584

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01799

SEQUENCE DESCRIPTION:

GATCCATATT TGTTTTGTGT TCTGCTTAAA TCAGCAAGAA TGATAAATTT GATGGTGTGA 60  
AATTGGAAGT ATCAAGGGCT TTCTTTGGTG ATTGAGGGAA ATAATGTCTC TACTTGTAAT 120  
TTATTGTGAC CCTTTTTCAC TGTATATGCT TTGTATGTCT AATATTTATT TCAATGCAAA 180  
TTCAATTNNC CCTTCATCTG TATTGTTATA TCTAAGATTT TATTGATGTT AAAATCTAAT 240  
TGTGGAATAA AAATCTCTCT GGAATTTAAA 270

SEQ ID NO:1585

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01800

SEQUENCE DESCRIPTION:

GATCTGCTTG ACAGTGATTA AATCCTTAGC TCACATCCAT TCCCATCTTT NGGGCTCCTT 60  
AGGCCCAAGG ATGGCATGTG ACTGGTCCCT GCAAGGTCCT TTCTTTGTCA CCAGCCAAGG 120  
CATTGATAAC CAAGTAGCCA TTTTCTCTT AAGGTTTCCT CTACAACCCC AAGGACTTTC 180  
ATGATTATCC TCAGGGACAG GATTGGAGGC ATTGAGCGTG TTTATTAACA AATTGTTTTT 240  
GGTAATAAAA TAAATGCTTG GACTCTTAAA 270

SEQ ID NO:1586

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01801

SEQUENCE DESCRIPTION:

GATCTNGTAA ACTCTCTGTA TATCTTCCTA CCTTTCAAAA TCGTTCTTAG GGTTAGTCAA 60  
GTCTGGAATA TAATTGCTGA CTATAAAGTT AGCAATTATG CTTTAAAGGT GTTGTCACAT 120  
CAACCTAAG AGAACCATCT ATGGAAGGTA TGTTGAAAC ATCTGTAGGA ACACAGAACT 180

GGGATTTTAC TGAGTTTACC ANNTCAACTG TGTGAACTGT TTCTGCACTG CTTGCTAATG 240  
GCTTCATCTA ATAAATGTTT ACTTATAAA 269

5 SEQ ID NO:1587  
SEQUENCE LENGTH:267  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS01802  
SEQUENCE DESCRIPTION:  
GATCTAGGGA AGTCAACACA TAGTGTAATA TAATTACATG CCTAATGAAA AGAAGATGTC 60  
ATTTCCCTAAT TTTNATATCT CATTTTCGGC ATTTTTTAAA ATGTAAAAGG AAAACCTCTT 120  
GTGTTACACAC AGATTGCTGA ATTGATTTCT CCATATTTGT TAATAATTTA CTATTATTTA 180  
15 CAAAGATTCA AATGCTTTTA TGACTAATGT AAAATGAAAA GAGGCTTACA TTTTAAATGT 240  
TATTAATAATT ATGTACTTAA ATCTAAA 267

20 SEQ ID NO:1588  
SEQUENCE LENGTH:288  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01803  
SEQUENCE DESCRIPTION:  
25 GATCGCTTTG AGGTCAATAT TAGTGAGCTG CCTGATGAGA TAGACATCTC CTCCTACATT 60  
GAACAGACAC GGTAGAAGAC TCGCCCATTT TGGAATGTGA CCGTCTNTCC TTCAGGNGAG 120  
GACACCAGGN TGGGGGTGAA GGAGACACTA CTGCCCCAC CCCTGACAGC CCCCACCCCA 180  
TGGCTTNCAT CTTTTGCATN ACCANCACTC CTGAACCCCN ATTTCTNATT TGTCAGAATT 240  
30 TTTTNNNTTA ACAAACACTAG AAATGNANCA CATGGGGTCT GTGGTAAA 288

35 SEQ ID NO:1589  
SEQUENCE LENGTH:266  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01804  
SEQUENCE DESCRIPTION:  
GATCTTGCCT GTTTCACAAT GTAACAAGAC TCTACCTGGG TCCCCTGGTG ATGAGTTTCA 60  
40 GCATAGAATA ATGTTCAAGG AAAAGAAAAC GAAAACAGTT TAAATCTCTA CCACAGCCTC 120  
ACAAGCAAAT GCTAAGGGGA ACATACATGT AAAANGCCAG CAAACTATCT TCAAACCTCT 180  
CCGTCCTTAA TGTCTTCCAT GGCTATTGCC CCCACAATGG TCTCTTNNNT CCCTGCTCCC 240  
TTATTAANGA ACTCTTTCTG AAGAAA 266

45 SEQ ID NO:1590  
SEQUENCE LENGTH:266  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01805  
50 SEQUENCE DESCRIPTION:

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GATCTATGAC TCCAACCGTA TGATTTTNTT GCCTCCCCAG TTTTCATCCC AGTGGTAACG 60  
 CCTGATTTT GGTAGCTATG CCATCTTCTG CTGAGGATTA CCATTACTGG GTGTATCACC 120  
 CCAGTACTTC CAAATNCCTC TCCTCTATTG ATTCAGTTGT TATTGCAGTG TCTGCTTCAT 180  
 CCGTGGAAGT TGAGGCTCAG ATGCCCCCTG CTCTGTAACC CTGGGGAATG TCAGAGGCAG 240  
 GTAATAAAGG TTGTTTAAAC AATAAA 266

SEQ ID NO:1591

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01806

SEQUENCE DESCRIPTION:

GATCAGGAGA CTTTGAATTN ATATATTTTA ATCCTNATTA AGCTTAAATA GGAAAGTTTC 60  
 TTCAACAGGA TTACAGTGTA GCTACCTACA TGCTGAAAAA TATAGCCTTT AAATCATTTT 120  
 NATATTATAA CTCTGTATAA TAGAGATAAG TCCATTTTTT AAAAATGTTT TCCCCAAACC 180  
 ATAAAACCTT ATACAAGTTG TTCTAGTAAC AATACATGAG ANAGATGTCT ATGTAGCTGA 240  
 AAATAAAATG ACGTCACAGG GCAAA 265

SEQ ID NO:1592

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01807

SEQUENCE DESCRIPTION:

GATCTGAGAG AAGCCCTGTC CTCCACTCAC CTCACCCGCC GCTGCCACCA TCTCCTCTGT 60  
 GCCAACTCCT TGTGGACCGC AAGAAAGCAT GACTTTGAAA AAGGGAAGCC ATTCCGAGAT 120  
 TTTAAATGT TCATGGACTA TTCCATATTA AAAGCTGTTT TTGTTGTACA AAATTCACCTG 180  
 ATGTTTCAGT CTATTTTATT TTGCCTTCAG AAAAGAAGAA AGTCAAAAAT AAAACTTTTG 240  
 TGTATTACAG CAAA 254

SEQ ID NO:1593

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01808

SEQUENCE DESCRIPTION:

GATCCTGGAG GATTCCTAC CCCCCTCCTC TTCGAGNCCC CAGTCGTGAT GTGGAGGAAG 60  
 AGCCACCTGC AAGATGGACA CGAGCCACAA GCTGCACTGT GAACCTGGGC ACTCCGCGCC 120  
 GATGCCACCG GCCTGTGGGT CTCTGAAGGG ACCCCCCCCC AATCGGACTG CCAAATTCTC 180  
 CGGTTTGCCC CGGGATATAA TAGAAAATTA TTTNTATGAA TAATGNAAAT AAAACACACC 240  
 TNGTGGCATG GCAAA 255

SEQ ID NO:1594

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01809

SEQUENCE DESCRIPTION:

5 GATCCATGAA GGAGGGCTGT GTGGAGAAGA TTGGGGACTG GCTGAGGAAA AATGTGCTGG 60  
 TGGTAGCTGC AGCAGCCCTN GNAAATTNCT TTTGTCGAGG TTTTGGGAAT TGTCTTTNCC 120  
 TGCTGCCTCG TGAAGAGTAT CAGAAAGTGGC TACGAGGTGA TGTAGGGGTC TNGGCTCCTC 180  
 AGCCTNCTCA TCTGGGGGAG TGGAATAGTA TCCTCCAGGT TTTTCAATTA AACGGATTAT 240  
 10 TTTTTCAGNC CGAAAAGNGA TGGTCTGAGT TTNTCTTAGA AA 282

SEQ ID NO:1595

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01810

SEQUENCE DESCRIPTION:

20 GATCAAATAA ACCAGTGTAG GATATTAAGA CTATCAATTG GTGGGATTAG GCTTGACATT 60  
 TTATTTTTAT AAATATATAT TTNTCCTGAA TGTGTCTGAG TCCAAGAGTG GGCAAAAAAT 120  
 AATTNCTAC TTTGGACTAA TCTATAGAGG TTTTGGAAAG TCTGCATTAC TAAC TTGTTG 180  
 AATTCATGAT ATTCTGCCTA TGGCACAAAT TGTAACCTT TGT TTTNCTA AAATAANGTA 240  
 ATTGAAAACC TGNAAA 256

25 SEQ ID NO:1596

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01811

30 SEQUENCE DESCRIPTION:

GATCTGCGCT TCCAGAGCGC ACTAATNCGG TGCTTTGCAG GAGGCAAGTG AGGCCTATCT 60  
 GGT TGGCCTT TTTGAAGACA CCAACCTGTG TGCTATCCAT GCCAAACGTG TAACAATTAT 120  
 GCCAAAAGAC ATCCAGCTAG CACGCCGCAT ACGTGGAGAA CGTGCTTAAG AATCCACTAT 180  
 35 GATGGGAAAC ATTTCAATTCT CAAA 204

SEQ ID NO:1597

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS01812

SEQUENCE DESCRIPTION:

45 GATCATTATT ATATATAGGT ATTGATTGCT ACCCTGACCA CAGTGCTTTG GACTATGAGA 60  
 AACTTCTTAG ATTTTATAT GTAAATNCTG TGGACCACTG GGAGCACAAT GCCCACATCA 120  
 TCTTAAGNNG AGTTTATGTG CAGCATTTAA ATCACTGTGT TTTCCTTGTT AACTAAAACA 180  
 GACATGGGCT TTGATTTTTT TCATACTATT AGACCATATC TCATAAAACC TTTTGAATTA 240  
 ATGAAA 246

50 SEQ ID NO:1598

55

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01813

SEQUENCE DESCRIPTION:

GATCACGCAC ACACAATAAG TCTTTCTCTC CGAAACCGGA AGTAAATCTA TATCTGTTAG 60  
 AAATAATGTA GCCAAAAGAA TGTAATTTG AGGATTTTTT TGCCAATAGT TTATAGAAAA 120  
 TATATGANCC AAAGTGATTT GAGTTTGTA AAATGTAAAA TAGTATGANC AAAATTTGCA 180  
 CTCTACCAGA TTTGAACATC TAGTGAGGTT CACATTCATA CTAAGTTTTC AACATTGTGT 240  
 TCTTTTGTGA TTCATTTTTT ACTTTTATTA ANGGNTCAAA CCCGN 285

SEQ ID NO:1599

SEQUENCE LENGTH:241

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01814

SEQUENCE DESCRIPTION:

GATCTAACTA TGTTTCCCC CTTTCAAGAA TAGAACTATT GGGGTGAGGA TAAGGGGTGG 60  
 GGGAGAAAAA ATCACTGTTT GTTTTAAAA AGCAAATCTT TCTGTAAACA GAATAAAAGT 120  
 NCCTCTCCCT TCCCTTCCCT CACCCCTGAC ATGTACCCCC TTNCCCTTC TGGCTGTTCC 180  
 CCTGCTCTGT TGCCTCTCTA AGGTAACATT TATAGAAGAN NTGGAATGAA TCTCCANGAA 240  
 A 241

SEQ ID NO:1600

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01815

SEQUENCE DESCRIPTION:

GATCCAGAAT ACCCTGACCT CGCCCCAGTT CCAGCAGATG TGGAAGCGTT TGCCAAAGCC 60  
 ATGCAGACA ACGCCAAGCC CGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA 120  
 GAGGAGGACA TGAGCCTGGA CTGAGCCACG CGCCGTCCTC CGAGGAACTG GGCCTTGCA 180  
 GTGCGTTGCA CACCCTCACC TCCCACCCAC TGATTATTAA TAAAGTCTTT TCTTTTAAA 239

SEQ ID NO:1601

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01816

SEQUENCE DESCRIPTION:

GATCCAAAGT AATATGTAGG TTCAATATTT TGTAGGTTTT ATAATCAAAT GTCTCCCTAA 60  
 AGAGATGACA TAGGGAAGAA AAGCCTAATG TATCATCTTA ATGGATTGAG TTTTATTAT 120  
 GCACAAATAA CTGGGCTTGT AACCTAGGAA TATGATTAGA GCGTGATGCT GGCTTAAAAA 180  
 ATAGGACTNG TGAATCACAG TTTGTNNNTA ATAACTACT GGTGGAAT ATTTAA 236

EP 0 679 716 A1

SEQ ID NO:1602

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01817

SEQUENCE DESCRIPTION:

GATCTCCCCG CCGCAGCCTC CTCAGAAGAC ATCGAGCGGT CCTGAGAGCC TCCTGGGCAC 60  
GTTTGTCTGT GTGCTGTAAC CTGAAGTCAA ACCTTAAGAT AATGGATAAT CTTCCGCCAA 120  
TTTATGCAGA GTCAGCCATT CCTGTTCTCT TTGCCTTGAT GTTGTGTTGT TATCATTTAA 180  
GATTTTTTTT TTTTGGNAAT NATTTTGAGT GGCAAANTAA NGATTAGCAN TTAAA 235

SEQ ID NO:1603

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01818

SEQUENCE DESCRIPTION:

GATCTGCCCC GGTGCGCCAG ACTTCCTAGC ACACGTGCGC GGGAGCAGCT GCTTTGAGTG 60  
CACACACTAC CAATCGTTCC TGGAATACAG GGAGGTGGTG GACGGCCTGG AGAAGGCCAT 120  
CTACAAGGGC CCAGGCAGCG AAGAGGGCCC TGACTGCCCC CCCC GGCCCC CCTCTCGGGC 180  
TCTCTACCC AGCCTGGTAC TGAAGGTGCC AGACGTGNTC CTGCTGACCT TCTGCGGCTC 240  
CGGGCTGTGT CCTAAATGCA AAGCACACCT CGGCCGAGGN CTGCGNCCTG ACANGGNNAC 300  
CTCTCTGAAC TGCAACACTT GGAN 324

SEQ ID NO:1604

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01819

SEQUENCE DESCRIPTION:

GATCAAAAAG CAAGCAGAAA TGAATCCACA TTCTAGTCCT TTATGCAGTA TACAAGGAGA 60  
ACTGTCCTGT AGGATATTCT CTTCTGATG GTGCAGAACC CAGAATTAGA AGTTTGTGGT 120  
TACAGCATAC TCTGTCCTTC AGAAAGGCGT GATTCTAGCT GTTGACCCCT TGCAGCTGTT 180  
GGAATCTCTG CAAGAACCTC TGTATTCTTC TAATAAATTC CCTCTTTTAT TTAAA 235

SEQ ID NO:1605

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01820

SEQUENCE DESCRIPTION:

GATCCCAACA ATGAAGCCAT TCGAAATGCT ATGGGCTCCC TGGCCTCCNA GGCCACCAAG 60  
GACGGCAAGA AGGACAAGAA GGAGGAAGAC AAGAAGTGAG ACTGGAGGGA AAGGGTAGCT 120  
GAGTCTGCTT AGGGGACTGC ATGGNAAGCA CGGAATATAG GGTTAGATGT GTGTNATCTG 180  
TAACCATTAC AGCCTAAATA AAGCTTGGA ACTTTTTTCC CTTTTTGTCT TCAA 235

SEQ ID NO:1606

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01821

SEQUENCE DESCRIPTION:

GATCAAAAAG AGAGTGGTTG TGGAACCTGT TGGCCCAGTT GGTTC AAGC CAGAGACATT 60  
 CAGAAAGTTT TTAGCTCTAT ATTTGCATGG TGCTGCGTGA NGGAGGACCC CTCTGAATCC 120  
 TGAAACCCCT CTTGCCTCTC TTCCACGGAA GAGGGCCTGG GCCCGTGGA GCCTCAGTGC 180  
 CCGTTTGGCC TGCTGCTCTC GCTGACAATA AAGAGCCCTT GCGTTGCACT GAAA 234

SEQ ID NO:1607

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01822

SEQUENCE DESCRIPTION:

GATCTGGAAC CTCAGCCTGG CCAGACACAG GCCCTCCCTG TTCCCCAGAG AAAGGGGAGC 60  
 CCACTGTCCT GGGCCTGCAG AATTTGGGTT CTGCCTGCCA GCTGCACTGA TGCTGCCCCCT 120  
 CATCTCTCTG CCCAACCCTT CCCTCACCTT GGCACCAGAC ACCCAGGACT TATTTAAACT 180  
 CTGTTGCAAG TGCAATAAAT CTGACCCAGT GCCCCCACTG ACCAGAACTA GAAA 234

SEQ ID NO:1608

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01823

SEQUENCE DESCRIPTION:

GATCACATAA AACAGATTG CATAAAATTA CCATGATTGC TTTATGTTTA TATTTAACTT 60  
 GTATTTTGT ACAACAAGA TTGTGTAAGA TATATTGAA GTTTCAGTGA TTTAACAGTC 120  
 TTTCCAACCT TTCATGATT TNATGAGCAC AGACTTCAA GAAAATACTT GAAAATAAAT 180  
 TACATTGCCT TTTGTCCATT AATCAGCAAA TAAACATGG CCTTAACAAA GTTGTGTTGTG 240  
 TTATTGTACA ATTTGAAAAT TATGTCGGGA CATACCCTAT AGAATTACTA ACCTTACTGC 300  
 CCCTTGTA GA ATATGTATTA ATCATTCTAC ATTAAAGAAA ATAATGGGTT CTTAAA 356

SEQ ID NO:1609

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01824

SEQUENCE DESCRIPTION:

GATCACCTAT GCCAAGAAAT AACATTTGGG ATAGTCGTCT TTAAGAGACT TGGTGTATT 60  
 TACAGTGTGTT GTTTTGATAA CATTTGGCTG GGTCAATTTA ATAGTTAGAG ATGAGGAGGA 120  
 GTAAAGTGA AATTTTGTG AAGGACTTAA ATTATCCAGT GTTCTTTAG CCTTGGTGAA 180

CTATGAAATA CGAAGNCCTT AATTTTGTAC AATAAACTTT TATTTGTAAA

230

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SEQ ID NO:1610

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01825

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SEQUENCE DESCRIPTION:

GATCTGTTGA ATATTTGCTA AAGACCAGTT CTTTAAGCTA AGACATGTAA AAAATCCCAA 60  
 ATGGCAGTAC CTCATTGTTT ACTTAGCTTT TGTACTTATA TTTTCAGAG GAAAAAACAC 120  
 TACTGTAAAT TGTGAATAGC CAATACATAA CTGTATTGTA TGCAAATCTG TGATTGTTGG 180  
 CAGTGTCTATC TCTGAGAAAC AGATAAATAA AGTTTATTTA CTATAAA 227

15

SEQ ID NO:1611

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS01826

SEQUENCE DESCRIPTION:

GATCTAGCCA AGGCTGGTCT GCAGTATCAG ATGTCCAAAC TCATCTACTA TTAGCCATAT 60  
 TTTGTGAGTC GTTGTCTAA ACTTTGTCAA AAATGCCTTT GCCATGATTT TGTTGCTATC 120  
 TGGATTTCOA ACATGGACAG TTAGGAAGAT GTGCATTGAA GTAGGAAAAT TTTGTTTCAGA 180  
 TTTGCTGTTA TTTATTTTTT AAATTAAAAA TGGAATGTA TTTTAAAGTT TAAA 234

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SEQ ID NO:1612

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01827

SEQUENCE DESCRIPTION:

GATCTGTTGG GTTCTCTATT AATTTATTTT ATACATTATA GATTCTGGGT TGATAAATTC 60  
 TGCTCAATTT GAAAAATTTT ATATTTTGTG TCAAATCTGT TACAATTTAT ATTGGTGGGN 120  
 GCAAAAGTAA TTGCGGTTTT TGCCGTAGAC AGTAATGGCA AAAACTGACA ATTGCTTTTG 180  
 CACCACCCTA ATAATATTAA NTATAATCAT GACTTTAAAC ATCAAA 226

40

SEQ ID NO:1613

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01828

SEQUENCE DESCRIPTION:

GATCGGGAAC TGGCTCCGTT GTGCTGAGGT CATCTTTGGT CATCAGCCTC CAGCATNTGG 60  
 AAACACCTCC AACGCAATGT GGCTTTTACA TTTCTTTCTT TCTTTCTTTT TTTTCCTGG 120  
 TACTGGGAAT ACACAACACC AGCTGTTTTA TTATTATTG GGGAGGGGGT TGTGATTTTA 180  
 TTATTNGTTT TTTTAAATG AAAAATAAAA NGTTATATAT TAAA 224

55



SEQ ID NO:1614

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01829

SEQUENCE DESCRIPTION:

GATCAGCAGA TACATGTCAG TGCAGAGGTT CTCTGCCCTC CAGAAGCCCT CGTCTGGGAA 60  
 TTCGAGAGAG GAGGAGGACC CAGGGCCAAA GGAATCCTCA AACTCCCTC CAAGGGAGAT 120  
 ATTGTAAGGG GAAAACAAAG TGTTTATTC CCCAAAACAA CCCAGCTCA CCCCATGTCC 180  
 CTTCTACACG CTTACTCACT GAGGGTGAGT GGAACGNTA AA 222

SEQ ID NO:1615

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01830

SEQUENCE DESCRIPTION:

GATCAGAATA TGTATGCAGT TCTTTCTTTA ACCCTTTTTT CTCCTATGTA CTGTGAACAT 60  
 TTA AAAAGTA CTTTAAATA TTCTTTGGAA ACTTAGCTTT TAGTAACTAC TTGGTTGTAT 120  
 CATAATTNAT TAACTANTGN NTTATTGGTA AACATTGGCT TGCCTCCCAT GACTTGCCAT 180  
 TATAATTAAA ACTGTGACTA CTATCTGTCT CCATTNCATA AA 222

SEQ ID NO:1616

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01831

SEQUENCE DESCRIPTION:

GATCCCN TTC CCACCTCTC TGTTGGCCTC AGAGTCACTC CTGCCCCCTC TCCCTGACTT 60  
 GGTGCTCACA TGCACCTCAC TAGGGTTTGT GACCAGGGTC TGGATGAGCT TGAATTTGAA 120  
 TGAATTGAGT TTGTATTNT AGAACCTGG GTTTTACAT GTTTGGTCTT TTTTNGTTTT 180  
 GGTTTGTAC CNTCGATAAA GGAAGTATAT TCATCCAAA 219

SEQ ID NO:1617

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01832

SEQUENCE DESCRIPTION:

GATCGCGGCG GANTNGGCC CGCCGCCTGG TACTCAAGCC CGCGGGGACA TTGGGAAGGG 60  
 GACCCCGGCC CCCTGCCCTC CCCTCTCTGC ACCGTACTGT GGAAAAGAAA CACGCACTTA 120  
 GTCTCTAAAG AGTTATTTT AAGACGTGTT TGTGTTTGTN TGTGTTTGTN CTTTNNATTG 180  
 AATCTATTTA AGTAAAAAAA AAAATTGGTT CTTTATTAAA 220

EP 0 679 716 A1

SEQ ID NO:1618

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01833

SEQUENCE DESCRIPTION:

GATCANGGCA CTTCAACTCA TTTGGAAAA NTGAACACTG ATGACATGGT ATAGGAGTGG 60  
 GNNGGGTGTT GAGCCACCCA TCANACCCTC TTTAGCTGTG CAAGATAAAA GCAGCCTGGG 120  
 TCACCCAGGG CCACAAGGCC ATGGTTAATT NTTANCGGCA AGGCAAATCC ATNGTTGNGA 180  
 AGTGCANTGG GCATAGTAAA NGTGCATGAT TTAAAN 216

SEQ ID NO:1619

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01834

SEQUENCE DESCRIPTION:

GATCATAGAA AATAAATAGA AGAGACAGTG AAGCAAGTAA AAAGAAAAGC ATTGTTTTAA 60  
 TTTGTTTGCA TTAATTTTTT TCATTTGTCA AAATGCTTCT TTTGTTGCCA CAGTAAAGAA 120  
 CAGTTTTTAT TGTTTTGTA GTAAAATTAC GTAGCTGATT TTGTATGTAA AGATTAATTT 180  
 CCATAATAAA AATTATTGTA TGTTTACTGT GAAA 214

SEQ ID NO:1620

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01835

SEQUENCE DESCRIPTION:

GATCAGAGTG GCCCACAGAC ATTGCTTTCT TATCACCTAT CATGTGAATT CTACCTGTAT 60  
 TCCTGGGCTG GACCACTTGA TAACTTCCAG TGTCTGGCA GCTTTTGGA TNACAGCAGT 120  
 GGTATGGGGT TTATNATGCT ATAAAACAAT GTCTGAAAAG TTGCCTAGAA TATATTTTGT 180  
 TACAACTTG AAATAAACCA AATTTGATGT TAAA 214

SEQ ID NO:1621

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01836

SEQUENCE DESCRIPTION:

GATCTGTGTC ATAAGTGACT CCGGATGCAT CAGTGTCAC CAGTTGGAAG CAATGACAAG 60  
 GATGGCTGGC TGGTGTTTTT CAGCCTCCG GTTTATAGAC TGTATTTATC TAGTGGATTC 120  
 CTGCAGGCC CATACTGAGC CTGGACTGAA AGTATCCACT CGGACCATCT GTTATCTCTC 180  
 TACACTGAAA ATAAAACCTC TTCCACCCAA A 211

SEQ ID NO:1622

# EP 0 679 716 A1

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01837

SEQUENCE DESCRIPTION:

GATCTGAGAT GGAAGAGTTT CATCCCCAAA CCATCTCCCC CTGACCCCCA GTCCATGGAA 60  
AAATTGTCTT CCACAAAACC GGTCCCTGGT GCCAAAAAGG TTGGGGAAC TGTGGTCGGT 120  
ACAAAAGTAA TTGTGGTTTT TGCACNGTTG GAATTTGTCA TNTGATATTG GAATACATTC 180  
TTAAATAAAT GTGGTTATGT TATACATCAA A 211

SEQ ID NO:1623

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01838

SEQUENCE DESCRIPTION:

GATCAGCGAG GTTCTCCAGG ACCTTAGGTT TGATGCGGAA TCTGCCGAGT GATGGCGGCT 60  
CCCCAGGGAT GCCGCCGAGG GAGATGGGAA ACGGGGCGGA TGGCGCCCAG CCCAGCCCTA 120  
ACTGCCAGCT GGCTGGGGTC GCGCCCCACT GCGCTGCTGA CCTTCCTGCA GTTCCAGACA 180  
CCTCCCACAA TAAAGAGCTC CTCCTCTGTA AA 212

SEQ ID NO:1624

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01839

SEQUENCE DESCRIPTION:

GATCTATGAC AATGTATAGT CAATAAATGA TAGCAATTAT TTTAATTAT CAAAATAAAT 60  
TGTTAGAGAT TCAAGTTAGC ATACAAAATG GAAATACATT GACAATCTAA AACTATACT 120  
AAAACATAAA CTCAAGACTT TATTCCTCTT CCTGTTCTAT CAAAATTGTG CCAAGTAAA 180  
AANTAAAANT TGTCTTTTT ATTTCAA 208

SEQ ID NO:1625

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01840

SEQUENCE DESCRIPTION:

GATCTAGATG GCAGATAGGA ACTTNTTGT CACAAAAATA CTGGAGGAAA ATNTTGTA 60  
AATAGACTTT TGGACACACA GCTGTTGGGG CTGCACTGAG CTGCAATTTT TAACATGGAT 120  
TTATAACTTA ATGTTTCTGT TTATAAATA CTAATGATTT GCAATGTATT TTACTGGCCA 180  
ATTAAAACAG ATGTTTTATT CTTTCTGAAA 210

SEQ ID NO:1626

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01841

5 SEQUENCE DESCRIPTION:

GATCCAGGAT TCTGGGAGGC TTCAGTTACC GCTGGCCGAG CTGAAGAACT GGGTATGAGG 60  
 CTGGGNCGGG GCTGGAGGTG GCGCCCCCTG GTGGGACAAC AAAGAGGACA CCATTTTTTCC 120  
 AGAGCTGCAG AGAGCACCTG GTGGGGAGGA AGAAGTGTA CTCACCAGCC TCTGCTCTTA 180  
 TCTTTGTAAT AAATGTTAAA GCCAGAAA 208

SEQ ID NO:1627

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01842

SEQUENCE DESCRIPTION:

GATCTCAGC CCACGAATTT AGAACTTCCT CCTATAGCAT TTTCTATCTT TTTTATGGCA 60  
 TTTATTTTAT TCTATCTTGT TATGATTACA TAATCTGTTT AATCCCAAT TATATATTGT 120  
 AAATACCTTG AAGGAAAGGA GTCTTTATTA TCTTTGGTGC CTGGTGTTTA GTTTTAATAT 180  
 TTTATTAAAT ACATCCAAGG AAA 203

SEQ ID NO:1628

25 SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01843

SEQUENCE DESCRIPTION:

GATCCACTGT TCAATCTGCA CAAGATTNGG GNNCCAGACA TGGGAGACTT CAGCTGCCTC 60  
 AGAGGACCGT GGACAGGGAA GGCAGCCTCG CATCCCTCTG TCCATGCCTG GNNTGACTTT 120  
 AATAACCAAG AGTTTTATTT TTGAATTGT AGCTGTCGTT CACTTTTTAC CCACCCATTC 180  
 AATAAACCTT ACAGAATTGC AAA 203

SEQ ID NO:1629

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS01844

SEQUENCE DESCRIPTION:

GATCCAAGTA ACAGTGACTG CAGTTAGGGT CGAGAGCTTC TCCGAAGCAG CGGTCATGCA 60  
 GGCTTTTGTG TGGCTGACGC TTCCCTTTT CACAACAGTA AAAAGCTATC AATGGGAAAT 120  
 TGTGGACTTT TCCACCAGG GACTCAATGG GGAATCAATG TGCAATATTC AGTCAACATA 180  
 AAACCTCTTA AGAACTCCAA A 201

SEQ ID NO:1630

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS01845

SEQUENCE DESCRIPTION:

5 GATCACAGAC CACGAGTGCC TTTCCCGGAC CTGGACGTTG CCTCCAGAGC AGGCACCANC 60  
 TCTTTCCCTC TCTAGACAGA AATATTTTGT TAAGGTTCTG GGCAGGGAG GGAGCATGAA 120  
 GTACGAGGAA AACTTGAATT CCAGATTTTN AATGCAAAGT ATTTATCATT TCTACCAGAA 180  
 ATAAACGTTT TAAGTTTAA A 201

10

SEQ ID NO:1631

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS01846

SEQUENCE DESCRIPTION:

20 GATCTTGAGG TCACTTCGTT TAGGTCATTN TCTCAACCCA ACCTCCCCAA ACTCTGGTTT 60  
 GAGCCAATAT GTGTTCTATT GTTCTCAGAG CACCAGCCGA CTGTACAACA ATTGTTATAA 120  
 AAATGTTTAT TGTTTACCAA AACCAGTGGA CCTCTTATCA AATGCTGCTT GGTAACAAAA 180  
 TCTATCACAG TTTTAATAAA AAGAAAAAA AAGGAAA 217

25

SEQ ID NO:1632

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01847

SEQUENCE DESCRIPTION:

30 GATCTGTTTT NNTTAAACAC TAACAGAATA ATTCTTTATA AATAGGTAAG CCTTACACTT 60  
 GTTAAAGAAA TTACCTCTA ATTTCACTCT CACTAATGTA AAATACTGGG ACTTAAGTAT 120  
 ACAATTCAGT CACTAACTGT ACAGTTTTAT GTGGGGAACA ATTCATGCAG GCTACTGGAA 180  
 AATTAAATCT TATTACCAA 200

35

SEQ ID NO:1633

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01848

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SEQUENCE DESCRIPTION:

45 GATCCNGGGC ATTTNCTCTG GGGAGACAGG CCTGAGGCCA GCTCGGNAGC CAAGCAGATT 60  
 CCAAACCACT ACAACCCTG CCAAACACAG CCCACTCCAT TTANACCGC CTTCTGAGG 120  
 AGAAAATGCA GACTCAGGGT TCCAGTAACC AGTGATGGAT TCACCCCATC TCCCAAATAA 180  
 TGGTTTACTT GTTTTACAAA 200

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SEQ ID NO:1634

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

CLONE:HUMGS01849

SEQUENCE DESCRIPTION:

5 GATCTTCTAA GAATTTTGCA AAATTCTAAA CAAATATAGA GATGGTATAT AGAATTCATA 60  
 TCTAGAAAAC TTGATTTTA ATGTGAGCTT ATCAAATTTG TNCTGGCTTT TTTGGCACTA 120  
 AGGCAAAAAC ATGTTAACCA GAAATAATTT ATTCTTCATG TATGTAAAAT ATTTGAGAAT 180  
 GTTTAGCCTT TTATTAGAAT TTTATTGGA AAATATTTAT CTTTCTACAC ATTTTACACT 240  
 TATGTNCCTT TGCTTATAAC CCAATTTCTT AACTTTTTTG TTAATAAGC AAATATCAAT 300  
 10 NATGTTTTAT TATCTAATAA AGTGAAGAT TCN 333

SEQ ID NO:1635

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01850

SEQUENCE DESCRIPTION:

20 GATCGAATGG CTTTTGCGAG CTAACACTA TGTGTAGACA GGTTTTATAT TATAAAGTAT 60  
 GCATTCTTAT CACCTAGTAT ATAGTTAGTT TGTAGAGTGA TTTCCCCCA GTTTCTTGAA 120  
 CATGGTATCT TCACATCTTG GACCTTGGTC AGTTGTGCTA TTCATTATTA AACACTAAAA 180  
 CTTTGGCGGT TCTTGCAAA 199

SEQ ID NO:1636

25 SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01851

SEQUENCE DESCRIPTION:

30 GATCTGGATG TTGAAAAGAG TCTGGCACCT CCTCCNTCTC TCTTGCTCAC ACTCTCACCA 60  
 CGTGATATGC TGCCTCCTCC TGTGCCTTCC ACCATGAGTA NAAGCTTCCT TANNCTCTTN 120  
 TNAGAAGCAG ATGCTGGCAG CATGATTCTT GTACAGTCTG CAGAACAGTG AGCCAAATAA 180  
 35 ACCTCTTTTC TCTAAA 196

SEQ ID NO:1637

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01852

SEQUENCE DESCRIPTION:

40 GATCCAAGTA TTTCTNCATC AAGCAGTTTT TAAAAGGAAA ACGATAATAA TCAGTAGGCT 60  
 CCATGGAAGC CTTTNCCTTA ATAGCTATGT GCCAAATACT TTNATCTNGT GTGACAGTCA 120  
 45 TGTCAGAGTG AAATCTCTCA GGAAAAGTGT AACTAGTAGT TACAAAGTAA ATAAAGGATT 180  
 TCATTTTAAG GTGAAA 196

SEQ ID NO:1638

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS01853

SEQUENCE DESCRIPTION:

GATCCTCCTG CAGGGCTAGG CGGATTGTTC TGGATTTCCT TTTGTTTTTC CTTTATAGTTT 60  
TCCATCTTTT CCCTCCCTGG TGCTCATTGG AATCTGAGTA GAGTCTGGGG GAGGGTCCCC 120  
ACCTTCCTGT ACCTCCTCCC CACAGCTTGC TTTGTTGTA CCGTCTTTCA ATAAAAAGAA 180  
GCTGTTTGGT CTAAA 195

SEQ ID NO:1639

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01854

SEQUENCE DESCRIPTION:

GATCTTAGCT TTGATAAATG ACTGANGCTG GAGAAGCCGT GGTGAAGTC AGCCTACACT 60  
ACAGTGACACA GTTGAGGAGC CAGAGACTTC TTAAATCATC CTTAGAACCG TGACCATAGC 120  
AGTATATATT TCCCTCTTGG AACAAAAAAC TATTTTCCT GTATTTTAC CATATAAAGT 180  
ATTTAAAAAA CAAA 194

SEQ ID NO:1640

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01855

SEQUENCE DESCRIPTION:

GATCTGAGTA ATTAGCAGGT ATGATGCTGG GACTGGAAAA TAGAAAGTAA TAACTAAAGG 60  
GTAAATGTGC AACGTTATTT TTTGGCCTTG TTCATAATTT TATGTTTTCA GTGGCNTGTG 120  
TACATATAGA ATTGTTAAAG TTGTCATTTT CAATATTTAT ATTAGAAAAA TTATTAGAT 180  
ACTTTATAAT TTAAACCGGC ATTTTAAATA ATGACACTTG CATTTATTGT ATTGTAATAA 240  
ATTTCACTTT TAACTTTAAA AGTTTAAA 268

SEQ ID NO:1641

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01856

SEQUENCE DESCRIPTION:

GATCTCTGCT CAGAGAAGTG CAGGGGGAGC CTTCCAGCTC ACTCTCCCTG AGGACTGGCT 60  
TGACAGGGGC TATGGGTTTG CTTTGGTGTT GTTTTAAAA AAAGAAAATA TATTTTTTTG 120  
AAAAAACGAC TGCCCATCCC GGGTCCTTTC CCTGATGGGT TGGGGCAGTT ACCTGGTTGC 180  
TGTTTTAATT AAA 193

SEQ ID NO:1642

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01857

SEQUENCE DESCRIPTION:

GATCACATCA CTCCACCCCT GCCAGGCCCC AGGTTAGGAA TAGTGGTGGG AGGAAGGGGA 60  
AAGGGCTGGG CCTCACCCT CCCAGCAACT GAAAGGACAA CACTATCTGG AGCCACCCAC 120  
TGAAAGGGCT GCAGGCATGG GCTGTACCCA AGCTGATTTC TCATCTGGTC AATAAAGCTG 180  
TTTAGACCAG AAA 193

SEQ ID NO:1643

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01858

SEQUENCE DESCRIPTION:

GATCCTTAGT ACAACATGTG AAAGAAGATA TGTGTCTTT ACTCACAGTG GAGGCATTTT 60  
TCTAGCTGTG TTTGATTGG CTTCCCTATA GATTCAGGAC CCATAACTCT TGTTCTCACT 120  
CATCTGCTAT GCTGCTGATA AGGACTTTCA GGTCAACAGC TGTAAGTCT AAATGAAGTT 180  
AATACTCTGG AAA 193

SEQ ID NO:1644

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01859

SEQUENCE DESCRIPTION:

GATCTAGGCA AACCTTTATA AAGTTGCAGT ACCTAATCTG TTATTCACAC TTCTCTGTTA 60  
TTTTTGTGTG TCTTTTAA TATATAATAT ATATCAAGAT TTTCAAATTA TTTAGAAGCA 120  
GATTNCTG TAGAAAACT AATTTNCTG CCTTTTACCA AAAATAAACT CTTGGGGGAA 180  
GAAAAGTGGA AA 192

SEQ ID NO:1645

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01860

SEQUENCE DESCRIPTION:

GATCTGTCTG TTGCTGTTT AATATATTTT TTTTATGACA TTAATTAAAG TTTAAAAGGG 60  
TTTTNTATCC ACTGTCAATT TCAATTGGAT AACATTTTGT CAAGNTTTT TTTTCCTGAT 120  
TATTTGATGC TAGCTGGAAT TCAAGAAATG GCATTGACCT TATTCAAATA AAGAAATATT 180  
TTAGTAAA 188

SEQ ID NO:1646

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



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CLONE:HUMGS01861

SEQUENCE DESCRIPTION:

5 GATCAAAAAC TAATTTGGGA TATGTATGGG TAGGGTAAAT CAGTAAGAGG TGTTATTTGG 60  
AACCTTGTTT TGGACAGTTT ACCAGTTGCC TTTTATCCCA AAGTTGTTGT AACCTGCTGT 120  
GATACGATGC TTCAAGAGAA AATGCGGTTA TAAAAAATGG TTCAGAATTA AACTTTTAAT 180  
TCATTGAAAA 190

SEQ ID NO:1647

10 SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01862

15 SEQUENCE DESCRIPTION:

GATCAGTTGG GTGCTATGTG CTCAGCTTTC CTACTGCAGC TTCATTTAAT GCAGAGTGGT 60  
GTTTGAATTT GGCTTAGATG GGCTGGCAGG CATGATTTTA AAAAATGTAA TCATCAGTAA 120  
GAAGTACTTC CATGTTAAAG ATGCAAAAAA AAAAGTCTTC ATTAAAATTN CTATTTAANG 180  
AAA 183

SEQ ID NO:1648

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS01863

SEQUENCE DESCRIPTION:

30 GATCCAAACA AATACACATT CTGTNTTTTA GCTCAGTGTT TTCTAAAAAA AGAAACTGCC 60  
ACACAGCAAA AAATTGTTTA CTTTGTTGGA CAAACCAAAT CAGTTCTCAA AAAATNACCG 120  
GTGCTTATAA AAAGTTATAA ATATCGAGTA GCTCTAAAAC AAACCACCTG ACCAAGAGGG 180  
AAGTGAGCTT GTGCTTAGTA TTTACATTGG ATGCCAGTTT TGTAATCACT GACTTATGTG 240  
CAAACTGGTG CAGAAATTCT ATAACTCTT TGCTGTTTTT GATACCTGCT TTTNGTTTCA 300  
TTTTGTTTTG TTTTGTAATA ATGGTAAANC TTCAGAAAAT AAAATGTCAG TGTGNNTAA 360  
A 361

SEQ ID NO:1649

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS01864

SEQUENCE DESCRIPTION:

45 GATCAGGACC TGGGGGCCTA CAGTTCTGCC AGGAAGTGCC TGGCCAAACA GAGGCAGAGG 60  
ATGCTGCAAG AGAGAAAAGC TGCAAAANAG GCCGCCGCTG CCACCTCCTG AGGCAGNTGT 120  
GGGTGCCCCCT GCTGTGTGGC TCTGTATGAC TGTGCTGAA ATATAAGCC CTGCAACCTG 180  
AAA 183

SEQ ID NO:1650

50 SEQUENCE LENGTH:178

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01865

SEQUENCE DESCRIPTION:

GATCTCAGCA CAAGCAGGGG AGCAGCTGGG GGAACACAGC TTTATGTAAT TACCTCTGTT 60  
CAATATTTAG CAAGTTGCAT TGTAACATTG TAACTGTTT TTTCTCCTTG GATGATGAGC 120  
TACCCCAAG AAGGGGTCAT ATCAGATTGG GTCTCATTAA AATGTCTGAT GAATGAAA 178

SEQ ID NO:1651

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01866

SEQUENCE DESCRIPTION:

GATCTATGGC TTAATAAATT TGTTTCTGTG ACAATNTTTG TAAATCTAGC CAATAGAGTC 60  
ATTTACAGAA GAAAAATNAG CATGTAATAA TACAAGAACT GTTCCCCCT CAAAACCTGA 120  
ACCTGAATTA TTTGTAAAA CTGAAATTTA ATGATTAAAG AGAAGCCAGA ATTGTAAA 178

SEQ ID NO:1652

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01867

SEQUENCE DESCRIPTION:

GATCTGGAGC TAATAATGAC TGAGATGGAG ATATCTCGAG CAGCAGCAGA ACGCAGTTTG 60  
CGGGAACACA TGGGCAACGT GGTAGAGGCG CTTATTGCCC TAACCAACTG ATGCGTGCTT 120  
TCTCAAATAT ACCTACTGGA TTAATTTATG GCAATAAAAT TTTTTTTTGT CTTTTTCAGT 180  
TTTATCAAA 189

SEQ ID NO:1653

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01868

SEQUENCE DESCRIPTION:

GATCTCTGCT CTGCCCTCTC CCAGATTGGT GGGGAGGGAG GGCAGGAGGT AGATATAGGC 60  
CTGTCCTTTT TAGCAATGTG ATTCTTGTTG TTGATTCTCT CTCTGGAGTT CATGTGCTGC 120  
CTCANNNGAC TCTGATTTTA TATTTNAGAA AAATAAAGGC GTTCAATCTG CAAA 174

SEQ ID NO:1654

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01869

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCAGGCTC ATCTCATCTG CACCAACTGC TCTACCTGTT AGATGGAGAC CTTGCNTCAT 60  
GAATTTCTCG AAATGCTCCT GGAACCTTATT TATATGCCTC AAAATCCTCT AAATCATT 120  
ATAGTAACCC ATAGTTTAA TTTTATAAAT AAACGTATTT ATTAATCTT AAA 173

SEQ ID NO:1655

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01870

SEQUENCE DESCRIPTION:

GATCTCTAAT TTAAAGAAAC AGTTTTTATA TACCTAGAAT GAAGATTCTG TTTAAAGCGG 60  
TTTTGGTTAA CTTGGTTCTT GACATTTGCC TAAAATNTN TTGGATTGGG ACTAAAATGT 120  
NCTATTAGCC AATGAATAAC GTCCAAGTAA ATTTNTGTTT TATTTGGGA AA 172

SEQ ID NO:1656

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01871

SEQUENCE DESCRIPTION:

GATCTCAAAG GAGTCTGAAA TATCATATTT CTGTGTGTGT CTCTCTCAGC CCCTGCCAG 60  
GCTAGAGGGA AACAGCTACT GATAATCGAA AACTGCTGTT TGTGGCAGGA ACCCCTGGCT 120  
GTGCAAATAA ATGGGGCTGA GGCCCCTGTG TGATATTGAA AGGGTAAGAA A 171

SEQ ID NO:1657

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01872

SEQUENCE DESCRIPTION:

GATCGNCATT ATCCCCAGNA AAAAGCTCCG CAACAAGATA GCAGNTAATG TCACGCATCT 60  
GATGAAAGCGA ATTCAGAGAG GCCCAGTAAG AGGTATCTCC ATCAAGCTGA NCGAGGAGGA 120  
GAGAGAAAGG AGAGACAATT ATGTTCTCTGA GGTCTCAGCC TTGGNNCCNN N 171

SEQ ID NO:1658

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01873

SEQUENCE DESCRIPTION:

GATCAAAGAC ATCCTCATCC AGTATGACCG GACCNCTGG TAGCTGACCC TCGTCGNTGC 60  
GAGTCCAAAA AGTTNGGAGT CCTGTGCCCG AGTTCGTACC AGAATCCACC GTAAGCCATC 120  
GGNCTAAAC TTAATTNATA ATAACAGTTT TGAGGGATT AAAAGTTCAA A 171

SEQ ID NO:1659

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01874

SEQUENCE DESCRIPTION:

GATCAAAAAT CCAAGGAGAA TGGTGCCAGT GTATGATAAA ATCCATGTAG TGATGAGGAA 60  
TGGTGTAAAA TAATGTAATA TATAANANTC ATGATATANG ANTGTTTGAA GGTGATGCAT 120  
GTTTGATTTT NGTAGTATAA NTGTATTNA GTTCAAATGA TGTATAANGN 170

SEQ ID NO:1660

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01875

SEQUENCE DESCRIPTION:

GATCCTCGCT CCGTTGCACG GGCGCCNTAA GTTATTGGAC TATCTAATAT CTATGTATTT 60  
ATNTCGCTGG TTCTTTGTAG TCACATATTT AATAGTCTTA ATATCTTGTT TTTGCATCAC 120  
TGTGCCCATG GCAAATAAAT CACTTGGCCA GTTTGCTTTT CTACAAA 167

SEQ ID NO:1661

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01876

SEQUENCE DESCRIPTION:

GATCTGGGCG ATTCTGAAGC CATGCCATTT TTAACCTTAT GTCTGCTAGA AAGTGTGTA 60  
GTTGATTGAC CAAACCAAGT CATAAGGGGA ATTTTTTTTA AAAACAACA AAAAAAAC 120  
CATCCAAGGN NGGGTTTNTG ATTAAATTTT GTGGNGTTAC CAGTAAA 167

SEQ ID NO:1662

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01877

SEQUENCE DESCRIPTION:

GATCTTCCCC AAGAGGGACT GGGGTTTCTG GGTCCATTC TCTGAGTCAG TGGTTATTTG 60  
AAAATTTGAT TTTGATTTTA TTTTCTCT GTAACTTCC AAGCTGGCTT TTCCCATTTT 120  
AATCCTGTG ATTTATGCCA ATAAAGTTTG CCCATGATTT TCAAA 165

SEQ ID NO:1663

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01878

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCCCTNCC TTGGTGGGCA GTTCTGCCTT CCAAGGAAGA AGGGGAAGAA AAGGACCTGT 60  
GGGTGGGCTCA GGNCNAAGCA GACCCCGGGC TCCACCCAG CCCCNCAG GNTGCTGCCA 120  
GTNCACACTT TTACAAATTT AATATAAAGC AAGTCCAGTN TAAA 165

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SEQ ID NO:1664  
SEQUENCE LENGTH:161  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS01880

SEQUENCE DESCRIPTION:

GATCAGGCTG CTGAGGGAAT AAATTTAATC AAGGTCTTTG CAAAAACAGA AGCACAGAAG 60  
GGAGCCTATA TAGAACTAAC ACTGCAGACT TATCAAGAAG CACTCAGTCG CCATTCTGCA 120  
GCTTCCTAAA AATATTTTAA AAATACATTT ATTTTACTAA A 161

15

SEQ ID NO:1665  
SEQUENCE LENGTH:158  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS01881

SEQUENCE DESCRIPTION:

GATCAGTCCA TCCCAGAGGG ACCGGAGTTA TGACAAGCTT TCCAAATATT TTGCTTTATC 60  
AGCCGATATC AACACTTGTA TCTGGCCTCT GTGCCCCAGC AGTGCCTTGT GCAATGTGAA 120  
TGTGCGCGTC TCTGCTAAAC CACCATTTTA TTTGGAAA 158

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SEQ ID NO:1666  
SEQUENCE LENGTH:158  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS01882

SEQUENCE DESCRIPTION:

GATCGTGTAT TGAGATTCTT TAAATAATGC TTCAGATATT ATTGCTTTAT TGCTTTTTTG 60  
TATTGGTTAA AACTGTACAT TAAAAATTGC TATGTTACTA TTTTNTACAA TTAATAGTTT 120  
GTCTATTTTA AAATAAATTA GTTGTTAAGA GTCTTAAA 158

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SEQ ID NO:1667  
SEQUENCE LENGTH:155  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS01883

SEQUENCE DESCRIPTION:

GATCTTTGTT AGTTGCATAT TATATTTTCTG TGTATCTT CTTGGTGAAT TGACCTTTT 60  
ATCATTATGT AATCCCTTA TATTTATATC TTTATATTTA ANATAGGTTT CCTTAACATT 120  
TGAGAAGTAA AANTAAAATA AAATGTAATA GCAAA 155

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SEQ ID NO:1668

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# EP 0 679 716 A1

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01884

SEQUENCE DESCRIPTION:

GATCACTCTG GGCTCACTTG CCTGCCTAAT GGTCATCTCC CCAGTAGACT GTAAGCTCCT 60  
TGAGGGCAAG GATTGTGTTG GAATTTTGT ATTAACAGTG CCTGGCTTGG TGCCTGGCAC 120  
CTAGAAAGCA CTCAATAAAT GTTTGTTTAA TGAAA 155

SEQ ID NO:1669

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01885

SEQUENCE DESCRIPTION:

GATCAGATGC TTGAAATTTA ACACTTTCA CTTGGTTCTT ATACTGAATG CCGACTCTGC 60  
TCTGTGTTAG AGATATGAAA TGGTGTGTTGA TACTGTTTGA GACATTATGG AGAGATTTAA 120  
TTATTTGTAA TAAANGNTT GCTGCAGTCT GAAAACTGAA A 161

SEQ ID NO:1670

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01886

SEQUENCE DESCRIPTION:

GATCTATTGT AATGTGTTAT TTNGGCTGAN GTATGTNAAG AAAATACTAC CTTACAAAGN 60  
TATGTATTNT CAAAAGGAAA TACATATCAG AAAGTTTAA AGGGCCAGTG GGTGATACTG 120  
AAGTTGTCGG GATGGATGGT GTCTATCTGG NNN 153

SEQ ID NO:1671

SEQUENCE LENGTH:444

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01887

SEQUENCE DESCRIPTION:

GATCTAGAAG TTTTACTTTT ATAAAGATGG TGTCCGGAAG ATGTTGCTAA TGTATTTTAC 60  
TTCAACATAG GGAACAACT TTTTAAGTAT ATTAATAAAC CTGTATGGTT AGTTTTTAAC 120  
AGTTTTTTAA AATAAACTAT GGATATGACA AATATTCTGT GTTTTACTAA GTGCTTGGAT 180  
AGGCTTTCTA ATTTNGTATA CGTGCTAGAG TTAATTATTG ANCATTTTAA TCCAAATTTA 240  
GTTGTAACCTC TGTTTATACT ACTGATTGCT CATTCGTTTA AATGATATTN TNNNGTAAAA 300  
GTCATAACCA ACATATGANC AGACAGATTT ATGTCTTTAA ACACAGATTG TNAGCTATAG 360  
GTTTAATCTG ATACCAGTTG CTGGAAGGTT GCCATTTGGT TTTTCTNAAA ACCTATACCN 420  
CTAAAACTTT CTTTNAAGGT TAAA 444

SEQ ID NO:1672

# EP 0 679 716 A1

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01888

SEQUENCE DESCRIPTION:

GATCAGCAGC CCTCGCAATG TGCTCAGCGA GTACCAGCAG AGGCCGCAGC GGCTGGTGAG 60

CTACTTCATC AAGAAGAACT GAGCAAGGCC TGAGCGCTGC CTGAACTCCG AAGNCCTGTG 120

TGATGCTTTC CATTAAAAAN NATTGTCCAA A 151

SEQ ID NO:1673

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01889

SEQUENCE DESCRIPTION:

GATCCAGATG ATAAACCAGT GAACTATGTC AAAAGCACTC TCAATATTAC ATTTGACAAA 60

AAGTTTTGTA CTTTNCACAT AGCTTGTTGC CCCGTAAAAG GGTTAACAGC ACAATTTTTT 120

AAAAATAAAT TAAGANGTAT TTATNGGAAA 150

SEQ ID NO:1674

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01890

SEQUENCE DESCRIPTION:

GATCCGNCCG TCTCTGCCTT CCAAAGTGCT GGGATTACAG GCGTGAGCAC ATCTGCCCGG 60

CTTATTTTTC TTTATGTTTT TNCTTCGTAA GAGGTTCTGT TGAGCAGTGA TTTGCAACTC 120

TTGCTGACGT TGCTGGGGAA GCTTTAAA 148

SEQ ID NO:1675

SEQUENCE LENGTH:568

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01891

SEQUENCE DESCRIPTION:

GATCTACCCC AGGGAGAATC TGAGACATCT TGCCTACTTT TCTTTATTAG CTTTCTCCTC 60

ATTCAATTTCT TTTATACCTT TCCTTTTTGG GGAGTTGTTA TGCCATGATT TTTGGTATTT 120

ATGTAAAAGG ATTATTACTA ATTCTATTTC TCTATGTTTA TTCTAGTTAA GGAAATGTTG 180

AGGGCAAGCC ACCAAATTAC CTAGGCTGAG GTTAGAGAGA TTGGCCAGCA AAAACTGTGG 240

GAAGATGAAC TTTGTCATTA TGATTTTCATT ATCACATGAT TATAGAAGGC TGTCTTAGTG 300

CAAAAAACAT ACTTACATTT CAGACATATC CAAAGGGAAT ACTCACATTT TGTTAAGAAG 360

TTGAACTATG ACTGGAGTAA ACCATGTATT CCCTTATCTT TTAATTTTTT TCTGTGACAT 420

TTATGGTCTC ATGTAATTTG CATTACTCTG GTGGATTGTN CTAGTACTGT ATGGGGCTTC 480

TCGGTAATAG GTTATTTCCA TATACTATAA TTGGNAATAT TTTTGTACCA ATGGTTATAA 540

CNCTAGGGGT NTAAAAACCA GGTTCTGN 568

SEQ ID NO:1676

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01892

SEQUENCE DESCRIPTION:

GATCTCTAAG GTATTATGTT TGCCTTCTCT TAGTTATTTC TGGGTTGTCA CAAAGCTCAG 60  
TATCATGGTT TGACAGAAGC AGTTATGTGA ACTTTTATGT TAGGACATTA CTAAATAAAG 120  
AATTCCTAG CTGCTTATAA AGTAAA 146

SEQ ID NO:1677

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01893

SEQUENCE DESCRIPTION:

GATCCATTCT CCNTTTANTT CCCCCACCCT CCTCTCTNGG ATATGGTTGG NTTTGGCTCA 60  
TTTCACAATC AGCCCAAGGC TGGGAAAGCT GGAATGGGAT GGAACCCCT CCGCCGTGCA 120  
TCTNAATTTN AGGGGTCATG CNCN 144

SEQ ID NO:1678

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01895

SEQUENCE DESCRIPTION:

GATCGAGATG AGCTTTAAAA ACTTGAAAAA CAGTTTGTA GCTTTCAAC AGCAGCATCA 60  
ACCTACGTGG TGGAAATAGT AAACCTATAT TTTCATAATT CTATGTGTAT TTTTATTTTG 120  
AATAACAGA AAGAAATTTT GGGTTTTTAA A 151

SEQ ID NO:1679

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01896

SEQUENCE DESCRIPTION:

GATCTTGATG GTCGCTGCAG AGTAACTTCA GCGCTGAGTT CGTTTGAAAC CTCGGTTTG 60  
TTAAGATTCA GAATAACCAA TTGCTTTGTC TGTTAAATCT CCCGATTCT GTTAGGAAAA 120  
TAAAAGCCTC ATTTCTTAAA 140

SEQ ID NO:1680

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



CLONE:HUMGS01897

SEQUENCE DESCRIPTION:

5 GATCACTATG TAGGCAATGC TGGATACTGG NCTGTTATTT ACACATTTGT ATCACCTTTT 60  
 ATTTTCATAAG ATAGCATTGT CAGANTAATT TAGTATTTCA ACATAATCAA CAAGTAAAAT 120  
 AAAATTAATG AGAATGAAA 139

SEQ ID NO:1681

SEQUENCE LENGTH:139

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01898

SEQUENCE DESCRIPTION:

15 GATCTCCACA TTCAGGTTTC CTGATGCACT TTNCGACTCT TTGGGCAACC TCTGGACTCC 60  
 TTGTNCCCAG GGTCCACATT TAGTTTTATC TTTACTGCAT TGCTTTTATG AAAAAGAATA 120  
 AAATTGGATG AAACAGAAA 139

SEQ ID NO:1682

SEQUENCE LENGTH:143

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01899

SEQUENCE DESCRIPTION:

25 GATCAGTTAA TTTGTATGTA GCAGTGTATG CTCTCATATA CAATNACTGA CCTATGCTCT 60  
 AAAACATGAA TGCTTTGTGA CAGACCCAAG CTGTCCATTT CTGTGATGGG TTTTGAATAA 120  
 AGTATTCCCT GTCTTAAATG AAA 143

SEQ ID NO:1683

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01900

SEQUENCE DESCRIPTION:

35 GATCGAATCA CCTGAATGTT CTATGTANTG TAAAATATTC TTTCTTGCT TTCTTGTGTT 60  
 AAGGTATATA TTCTATTTGT ATGGAATTCT TATTCAAATA CAGTTCTATT AAAGAGTATA 120  
 CTCCTATTGG ATGAAA 136

SEQ ID NO:1684

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01901

SEQUENCE DESCRIPTION:

45 GATCTCAGCG GCATTAAGCT GTGCCTGAGC GAGTTTGTAG TGA CTCACTG CACAGCACCN 60  
 CCAGACTAGC ATGTGGTTCT ATATTTGTAA AGTTATTGGG ATAAGAAACA ATTAAACAGT 120  
 TTGTAGTAAA CACAAA 136

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EP 0 679 716 A1

SEQ ID NO:1685

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01902

SEQUENCE DESCRIPTION:

GATCTTCTAC TTCCCTNTGG GGAGGGGAGT GACAGGTCCA CACACCACAC TGGGTCACCC 60  
TGTCTGGAT GCCTCTGAAG AGAGGGACAG ACCGTCAGAA ACTGGAGAGT TTCTATTAA 120  
GGTCATTAA ACCAAA 136

SEQ ID NO:1686

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01903

SEQUENCE DESCRIPTION:

GATCTTTAAA AAAATTTTCC ATATGTCAAA GTGTAGAGAT GTTTCTAGCA GCATTTATCT 60  
TGTCATCTAT AGATTGAACA AAAAGTGGTA GCTGTNAAAT TGTGATTAT AATAAATACA 120  
TATTTGGTCT TCAAA 135

SEQ ID NO:1687

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01904

SEQUENCE DESCRIPTION:

GATCAGCAGT TCCAGCCCCT ACGCTNGCTG GGGGCGCAAC CACCCCTTCC TTAGGTTGAT 60  
GTGCTTGGNA AAGCTCCCTC CCCCTCCTC CCCAAGAGAG GAAATAAAAG CCACCTTCGC 120  
CCTAGGGCCA AGAAA 135

SEQ ID NO:1688

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01905

SEQUENCE DESCRIPTION:

GATCTTCATC TGTAGCCAAG AAGAGAGCAT TAAACCCAAG ANCATTGTGG AGAAGATTGA 60  
CTTTGACAGT GTGTCCAGCA TCATGGCCTC CTCCAGTAA CTTCAGGTGT TTAATAAAGA 120  
TGTGTTGACT CAGAAA 136

SEQ ID NO:1689

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS01906

SEQUENCE DESCRIPTION:

GATCTTAATG TTTCAAAGGA GTGCAGCCCT TCACAGCCAT CAGATATGAG GGCAGTGTTC 60  
TGTCTGGTGT TGTAGCCATC TCAAGAACAA ATCAACAGCA ACAAAGAGA AAGAATAAAT 120  
TTTTAAATT TAAA 134

SEQ ID NO:1690

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01907

SEQUENCE DESCRIPTION:

GATCTGTGAC CCTGGGCGCT GAAAATGGGA CCCAGGAATC CCCCCGTCA ATATCTTGGC 60  
CTCAGATGGC TCCCCAAGGT CATTATATC TCGGTTTGAG CTCATATCTT ATAATAACAC 120  
AAAGTAGCCA CAAA 134

SEQ ID NO:1691

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01908

SEQUENCE DESCRIPTION:

GATCTCTACT ACCACAAGGA AAATAGTTTA GGAGAAACCA GCTTTTACTG TTTTNAAAA 60  
ATTACAGCTT CACCCTGTCA AGTTAACAAG GAATGCCTGT GCCAATAAAA GGTTCCTCCA 120  
ACTTGAAGTC TAAA 134

SEQ ID NO:1692

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01909

SEQUENCE DESCRIPTION:

GATCAGTGTG GAGGACCCGC CCCAGCGCAC GGCCGGCGTC AAGGTGGAGA CCACTGAGGA 60  
CCTGGTGGCC AAGCTGAAGG AGATTGGGCG GATTGAGCC CCTCCAGAG ATGGCAATAA 120  
AACTGACTCT CAACATCAAA 140

SEQ ID NO:1693

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01910

SEQUENCE DESCRIPTION:

GATCTAACCT TTGANGCTTT AAAAAAGGAG AAAGAGGGTA GGGGTGGGAA ACTGGCATAAC 60  
TGTGTGTATA GCACTGCCGA TTGGCTAGGC CACTGTGTCT CTGCTACAAA TTAAAGAAAT 120  
CCTAAAAGTT AAA 133

# EP 0 679 716 A1

5 SEQ ID NO:1694  
 SEQUENCE LENGTH:133  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01911  
 SEQUENCE DESCRIPTION:  
 10 GATCGCGAAT AAAAATCAAC AAATGTGAAA GCCCAGAAAA ATATATTCGT ATTTCTGGTT 60  
 TTGCTGGATT TTTACATTTT TATATAATAA AAATGNTATT TTGAAATAAA GATTATGCTG 120  
 ACTCAAATGC AAA 133

15 SEQ ID NO:1695  
 SEQUENCE LENGTH:131  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01912  
 SEQUENCE DESCRIPTION:  
 20 GATCTATTGC AGATATTTGA TGTAAGTTTC TCTTTTAAAT TAATCAGAAA CCCCACTTCC 60  
 ATGTGATTGT CTGACACATG CTCTCAATAT ATAATAAATG GGAAATGTCG ATTTTCAATA 120  
 ATAGACTTAA A 131

25 SEQ ID NO:1696  
 SEQUENCE LENGTH:130  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01913  
 SEQUENCE DESCRIPTION:  
 30 GATCCGCCCCG GCTCAGCAGA ATTCACGCTC CTGTATGCCT CAGCCCCTCG ATATAACTCC 60  
 ATCGGATTCT AGCAGCCTGG TATTCTAGCA ATAAACCCA AGGCCTGAGA AACAGGGGCC 120  
 ATCCTGCAAA 130

35 SEQ ID NO:1697  
 SEQUENCE LENGTH:130  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS01914  
 SEQUENCE DESCRIPTION:  
 40 GATCAGACTG TCACTTTATA GTTTTTCTAT ATAAAGATTA TATAGTTGCA AACAAAGGTT 60  
 GTGAAATTC CCTTTGTTG TTTTNACTT TTAATTAATA AAAGTACATT GTTTTCATAG 120  
 CAAACTTAAA 130

45 SEQ ID NO:1698  
 SEQUENCE LENGTH:130  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
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CLONE:HUMGS01915

SEQUENCE DESCRIPTION:

GATCGAAGCT ACCGTAATGT GTTCTTGAGG TCAACATGTT TTGTGGAAGT CACTGTATTT 60  
 GCCCCNTTAT GTCAATTACC TATTATAAAC CGAGAGAAAT GGGAAAATTA AAAACCTGTT 120  
 TTGAATTAAA 130

SEQ ID NO:1699

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01916

SEQUENCE DESCRIPTION:

GATCCCTTGT AAACATGAAA TCATTCCATG GATGGCTGCC TTATAATTTT GTCTCTTTCC 60  
 ACTTTAATTG TGAATGGTTA AAAAAATGCT GTTTTCTGAT ATTAAATTTT TATTAGTGCA 120  
 TACCTTAAA 129

SEQ ID NO:1700

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01917

SEQUENCE DESCRIPTION:

GATCTGTACC TAGTACCCCT CCCATCTACT GATTGTGTTG TTTTGTAAC CAAACACATT 60  
 TTCAGATAGA AGGAGCCTTA AA 82

SEQ ID NO:1701

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01918

SEQUENCE DESCRIPTION:

GATCCCCTAT TCCCTCCACA ATAACAGAAA CACTCCCAGG GACTCTGGGG AGAGGCTGAG 60  
 GACAAATACC TGCTGTCACT CCAGAGGACA TTTTTTTAG CAATAAAATT GAGTGTCAAC 120  
 TATTTAAA 128

SEQ ID NO:1702

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01919

SEQUENCE DESCRIPTION:

GATCTACAAT NAAGCCCTCA AGGGCTGAAA ATAAATAGGG AAGATGGAGA CACCCTCTGG 60  
 GGGTCCTCTC TGAGTCAAAT CCAGTGGTGG GTAATTGTAC AATAAATTTT TTTTGGTCAA 120  
 ATTTAAAAAA AAATAAA 137

EP 0 679 716 A1

SEQ ID NO:1703

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01920

SEQUENCE DESCRIPTION:

GATCTGAGGA GGAAATGTGA CGCCGGACGC TTCNTGTNT TTGACCTTTT NAAAGGANGA 60  
GGAAGTTCAC CGACANTACC CATCACCCAC AAAAGTCTCA CTTCTTGAA GATTGTGTT 120  
AGGCTGNN 128

SEQ ID NO:1704

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01921

SEQUENCE DESCRIPTION:

GATCTGGCGT NCTACTATGA GGCTTCTTTT GACCTCATTN NTGTGGTNGC CGGCGTAGCC 60  
AGACCATCCT ATACTGTGAC TACTTCTACT NGTACATTAC AAAAGTACTC AAGGGAAAGA 120  
AGCTCNN 127

SEQ ID NO:1705

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01922

SEQUENCE DESCRIPTION:

GATCATAGCT ACACTGTATG TTTAGGTGGT GTGAAATNAT TTATAATCAC AGCTTGAAC 60  
GTGTTTGCTT GGTACTGTCA TAGTGATTAC AAATTTTCATG GAATGCGAAG AGCAACAATA 120  
AATAAAAAAT ACCACTCACC CTCAAA 146

SEQ ID NO:1706

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01923

SEQUENCE DESCRIPTION:

GATCAAAAAG GACTGAACCC CCACTATCAT AATCCATACA TTCATTTCCA TGTTGTTTGA 60  
CTAGCAGTGC ATATATGAAT GAATATGGTA ATTAATCTTA CCTATAAGAA CCAAATACTT 120  
TAATTATATT AAGATAGTGA ATAAAGATGT ATAATATTTT NATTAATACC TTGAATATAT 180  
TCAGTGGATT GAATGTGACT TCATAACTGT ACTACGATTG TATTAAAATA TTTCTGGAAA 240

SEQ ID NO:1707

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01924

SEQUENCE DESCRIPTION:

5 GATCTTATGA AGGAAGATTT GTGACCCTAC GTATATATAT ACACACACAT ACATATATAT 60  
 ATATATCCCG AACCAACANC GGGACTTTGT TTATATTGCA AATAAATATT ATTTTTCCTT 120  
 TAAA 124

SEQ ID NO:1708

SEQUENCE LENGTH:124

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01925

SEQUENCE DESCRIPTION:

15 GATCCCCTTT CTCTATGTCG GGACACTCAT TAGCAAGAAC TTNCTGCTC TACTNGAGGN 60  
 ACATGACATT TTTGTTCCAG AGGATGATGA TGATGATGAC TAACAGGAAT TACAGAANGN 120  
 NGAN 124

SEQ ID NO:1709

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01926

SEQUENCE DESCRIPTION:

25 GATCCGAGCA GTCCTCTGCC CGCCTCCCGT GAAGAAGAGG AAGAGAAAAT GCCTGCTGTT 60  
 GTAAATGTCT CAGCCCCTCG TTCTTGGTCC TGTCCCTTGG AACCTTTGTA CGCTTTGCTC 120  
 AAAAAAAAAAC AAAAAAAAAA AACAAA 146

SEQ ID NO:1710

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01927

SEQUENCE DESCRIPTION:

35 GATCCTGTGT AGAAGCTGTT CTCATTAAAC ACCAAACAGT TAAGTCCATT CTCTGGTACT 60  
 AGCTACAAAT TCGGTTTCAT ATTCTACTTA ACAATTTAAA TAAACTGAAA TATTTCTAAA 120

SEQ ID NO:1711

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01928

SEQUENCE DESCRIPTION:

45 GATCTGCGCC TCTCAGTGCC TTTTGAGGGG TTCCCATCAT CCCTCCCTGA TATTGTATTG 60  
 AAAATATTAT GCACACTGTT CATGCTTCTA CTAATCAATA AACGCTTTAT TTAAAGCCAA 120  
 A 121

# EP 0 679 716 A1

SEQ ID NO:1712

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01929

SEQUENCE DESCRIPTION:

GATCGGGGCA AGAGAAGGCT GAGTACGGAT GGGAAACTAT TGTGCACAAG TCTTTCCAGA 60  
GGAGTTTCTT AATNAGATAT TTGTATTAT TTCCAGACCA ATAAATTTGT AACTTTGCAG 120  
CGAAA 125

SEQ ID NO:1713

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01930

SEQUENCE DESCRIPTION:

GATCAGCCCA TCTCAGCTTG CTGTTTCAAT CACAATGGAA ACATATTTGC ATACGCTTCC 60  
AGCTACGACT GGTCAAAGGG ACATGAATTT NATAATCCCC AGAAAAAAN TTACATTTNC 120  
CTGCGTAATG CAGCCGAAGA GCTAAAGCCC AGGAATAAGA AGTAGTGGCT GGAGACTCTG 180  
GCTCAGCCAG AGTTGTTTCT CTCCANTCTG CCTCATCTCT GTACGANTTT GGGTCCCAGC 240  
CTTGTTGGGT TGTACGCCAT GGACATGGAT TTCAACCCCT GGAGAAAACG NTGTCATTGT 300  
TCAGCAGCTG AGNGCCCCAG GCGTCCGNGG CGNCTTTN 338

SEQ ID NO:1714

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01931

SEQUENCE DESCRIPTION:

GATCCCATAT CTATTACCGT GTCCATAGGA ATAATAGGTA AGGGCTCTGT CTCTGTCAAG 60  
CCATGTAACA AAGGACACTG TTAAA 85

SEQ ID NO:1715

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01932

SEQUENCE DESCRIPTION:

GATCCAGCCC TGGTTCTGGC TGTGGTCAGC AGATGCCAGT NAAGGGTTTT GTGTGTTTAG 60  
GCCTCATTTT TTTGTCTTTT TCCTACTCCG TTCCTGGCAT TTGCTGATTT CTAGTGTATA 120  
CTCTGTAGTC TCAGTTCGTG TTTGATTCCA TTCCATGGAA ATAAAAAGTA TGTGTACAT 180  
ACTGCCGAAG AATTGTCTTG CAAGTNAAGG CTTCCCCCTT TACTATAAGA CTATAAATAA 240  
AANCTTATTT NATCCNNAAA 260

SEQ ID NO:1716



SEQUENCE LENGTH:430

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01933

SEQUENCE DESCRIPTION:

GATCTTGTGC TGTGCTATCC GCAGAACCGC GAGATGGTCT AGAGTCAGCT TACATCCCTG 60  
AGCAGGAAAAG TTTACCCATG AAGATTGGTG GGATTTTTTG TTTGTTTGTT TTGNTTTGTT 120  
TGTTGTTTGT TGTTTGTTTT TTTGCCACTA ATTTTAGTAT TCATTCTGCA TTGCTAGATA 180  
AAAGCTGAAG TTACTTTATG TTTGTCTTTT AATGCTTCAT TCAATATTGA CATTTGTAGT 240  
TGAGCGGGGG GTTTGTTTTG CTTTGGTTTA TATTTTNCA GTTGTTTGTT TTTGCTGTGN 300  
ATATTAAGCA GAAATCCTGC AATGAAAGGT ACTATATTG CTAGACTCTA GACAAGATAT 360  
TGTACATAAA AGAATTTTTT TGNCTTTAAA TAGATACAAA TGTCTANCAC CTTAATCAA 420  
GTTGTACCTN 430

SEQ ID NO:1717

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01934

SEQUENCE DESCRIPTION:

GATCGAGCCA CTGCGCTCCG GCCTGGGTGA CAGGAGACTC CATCTCAAAA AATAAAATTA 60  
AAAAAAAAC TACTACAATA AATTATCACC TTGGACTGTA TAAACAACCT TTNAACTAG 120  
TCTTTTNAAG AAGTACACTT AAATAAAAT CTAANCATAA GNGANTGTAA A 171

SEQ ID NO:1718

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01935

SEQUENCE DESCRIPTION:

GATCGCTCAG AAAATGGGAA CCCAGGGCAA ATTGTATGTG CTCCTTACTG GGTATTATTAT 60  
AAGTGTACACA TGTTTTTTTAT AATAAAACAT AGGTGATTTC ACCTTAATGG ACAA 115

SEQ ID NO:1719

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01936

SEQUENCE DESCRIPTION:

GATCCTCCCA CCTCAGCCTC CTGAGTAGCT GGGACCATAG GCTCACAACA CCACACCTGG 60  
CAAAATTTGAT TTTTTTTTTT TTTCCAGAGA NGGGGTNTTG NANCATTGCC CAGNN 115

SEQ ID NO:1720

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS01937

SEQUENCE DESCRIPTION:

5 GATCTAGCAC TTTACAAAGT AAGTTTTTCT GTNACTTAGA GCTGAAAATA AAAGCAATGT 60  
AGAGTTACGC TTTTATAAGT ATTTNANGTT TCANAAATNA TGCATACAGC AATTN 115

SEQ ID NO:1721

10 SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01938

SEQUENCE DESCRIPTION:

15 GATCATTTAG TTCTATCTAT TTAGAAATAT GTAAACTGG ATTTTTTTTT AAGTAATATG 60  
TGACCAAAGT TAATTTTGTC CCAAAGGTCT AAATAAGAG CAGTTTCCA TAAA 114

SEQ ID NO:1722

20 SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01939

SEQUENCE DESCRIPTION:

25 GATCGCCACA GCCCTTCTTG GAAGAAAGGC GTCTGTGTTT CAGGTTCAC GCGAGTCACC 60  
TCTTTCGTCT TAATGTTTAC CGTCCACAGC TTTGGAATAA ACCATCCTGG GAAGTTAAA 119

SEQ ID NO:1723

30 SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01940

SEQUENCE DESCRIPTION:

35 GATCTTTGAC TGTATCATGC ATTGTACAAT TGATTTTATA TTTTATGAAA TGCCTTAATT 60  
TTCCTACTAT AACATAAAGA CAATGATGAA TAAAGTTTAT GTGTATGATT AAA 113

SEQ ID NO:1724

40 SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01941

SEQUENCE DESCRIPTION:

45 GATCAGAAAC ATACATACCC TNCCTAGGGA TTTAGAAAGT GGGTTGGCAG TCTTTCCTCA 60  
CGTCCATCAC GCANTTGGNA CCTACTNCAG TGTATTGTAA ACTTTTTTCT CNN 113

SEQ ID NO:1725

50 SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

55

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS01943

SEQUENCE DESCRIPTION:

5 GATCCCAGAG GTCANGACCA AANCCAATCA GTGAAAATTC AACTNTAGCT GTGAAAACAT 60  
TGCATAACA GGAGCTATCC AACAATGGAC CAGAATGTTG ACAATAAAGT N 111

SEQ ID NO:1726

SEQUENCE LENGTH:113

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01944

SEQUENCE DESCRIPTION:

15 GATCCCGCAG GTGGCAGTG ACAGCTAGGG TTCAAAACGT TCTCACCAA TCCAATGCTC 60  
CTCACATATT AATTTTATAA CCAGACAAAT AAATATTAGA GACAACCACC AAA 113

SEQ ID NO:1727

SEQUENCE LENGTH:109

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01945

SEQUENCE DESCRIPTION:

25 GATCTCAAAA TTCCAGAATT CCCTGTACAT CTNTCCACGT GCTTGTGCTC CAGGTGTGAC 60  
TTGTAAACTG TCTAGTGTTC GCNTTAAATA AAATGGCACC GAGCATAAA 109

SEQ ID NO:1728

SEQUENCE LENGTH:329

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01946

SEQUENCE DESCRIPTION:

35 GATCCGTATC GGTTTAAGAA GCGGACGGAG CTGTTTCATTG CCGCCGAGGG CATTACACG 60  
GGCCAGTTTG TGTATTGCGG CAAGAAGGCC CAGCTCAACA TTGGCAATTT GCTCCCTGTG 120  
GGCACCATGC CTGAGGGTAC AATCGTGTGC TGCCTGGAGG AGAAGCCTGG AGACCGTGGN 180  
AAGCTGGCCC GGGCATCAGG GAACTATGCC ACCGTTATCT CCNACAACCC TGAGACCANG 240  
ANGACCCGTG TGNAGNTGCC CTCCGANTCC AAGANGGTTA TNTCCTNAGN CATCAGNGCT 300  
40 GTGGTTGGTG TGGTGGCTGG NGNTNGNCN 329

SEQ ID NO:1729

SEQUENCE LENGTH:109

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01947

SEQUENCE DESCRIPTION:

50 GATCTGTCAA TTTCTTTGTN CAGAATGATT TGAAGTATTG TATTCAGTTT ACATGCATTA 60  
TTGGNTTATA ATNAATATCT AATGAAAATA CATGTTGTTA TATTGTAA 109

55

# EP 0 679 716 A1

SEQ ID NO:1730

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01948

SEQUENCE DESCRIPTION:

GATCAGCTGA TGGAGCTCCT GATTTGACAA AGGAGCTTNC CTCCTTTGAA TGACCTAGAG 60  
CACAGGGAGG AACTTGTCCA GTAGTTTGGA ATTGTGTTCT TCGTAAAGAC TGAGGCAAGC 120  
AAGTGCTGTG AAATAACATC ATCTTAGTCC CTTGGTGTGT GGGNNNTTGT TTTTTTTTTT 180  
ATATTTTGAG AATAAACTT CATATAAAAT TGAAA 215

SEQ ID NO:1731

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01949

SEQUENCE DESCRIPTION:

GATCGCACCG CCCCTCGCAG AGAGTGTATC ANCTGTTTTA TTTTGTAAA AACAAAGTGC 60  
TAAATAATAT TNATNACTTG GTTTGGTTNC AAAANCGGAT TAAATGN 107

SEQ ID NO:1732

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01950

SEQUENCE DESCRIPTION:

GATCACTGTG GTNTTCATAT TTCTAAAATA AATGAATTAA AAANTTTAAN GNCTTAGATG 60  
CTTATCTCTA TCATAGCTCA GAATGCAACT NCAATACCCC CATTCTN 107

SEQ ID NO:1733

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01951

SEQUENCE DESCRIPTION:

GATCAACTGT ACGCCTTTGG TATCTGACCA TAAAGTCTTT TGCTCCGCTG ACATTTGGGT 60  
GATGTCTTCA CATGAAATA TAATAAAAT AAAAATCTAG TTAAA 106

SEQ ID NO:1734

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01952

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCGAGGCT TCAGTGAGAT ATGGCTGAGA CACTGCTCTC AGCCTGGATG ACAGAGTGAG 60  
AACCTGTCTC AAACAAGAGA AAAAAATAAA TCAAANNCTA TTCAA 106

5 SEQ ID NO:1735  
SEQUENCE LENGTH:151  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS01953  
SEQUENCE DESCRIPTION:  
GATCTGAGGA GGCTTCGTGG GCTTTTGGGT CCTCTAACTA GGACTCCCTC ATTCCTAGAA 60  
ATTTAACCTT AATGAAATCC CTAATAAAAC TCAGTGCTGT GTTATTTGTG CCTCATTTC 120  
CCAGGAATAG TCACTGCCTT GAGGAACCAA A 151

15 SEQ ID NO:1736  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS01954  
SEQUENCE DESCRIPTION:  
GATCCACCCA CCTNAGGCCT CCCAAAGTGC TGGGANNACA GNCGTGANAA CCACGGCTTC 60  
GCCAACAATG GATTTTAAA TTATTTCCAC GCTCACAAAA AACCTN 106

25 SEQ ID NO:1737  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS01955  
SEQUENCE DESCRIPTION:  
GATCNANCCT CAACACCTAG TGCAATTCTT TTTACACATT AGGNACTTAG TAATTNGGGT 60  
TGAATTGTGT TGAACCTAAC TGGCGGTATA GGCAAAANTT GGAAGN 106

35 SEQ ID NO:1738  
SEQUENCE LENGTH:105  
SEQUENCE TYPE:nucleic acid  
40 TOPOLOGY:linear  
CLONE:HUMGS01956  
SEQUENCE DESCRIPTION:  
GATCTCCCAT TTCTAGGAAC CCCAGTCCTG CTTCTCCGCA ATGGCACATG CTTCCACTCC 60  
ATCCATACTG GCATCCTCAA ATAAACAGAT ATGTATACAT ATAAA 105

45 SEQ ID NO:1739  
SEQUENCE LENGTH:105  
SEQUENCE TYPE:nucleic acid  
50 TOPOLOGY:linear  
CLONE:HUMGS01957

55

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCAAGAG ATATATTTGG CAACTTTTTC TAGAAAAGGC ACATTGGGTA TAATTCATTA 60  
CATTCTTGAG TTTTGTGGG TTTTGTGTTT TTTTGTGNG NNANN 105

5

SEQ ID NO:1740  
SEQUENCE LENGTH:107  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01958

10

## SEQUENCE DESCRIPTION:

GATCCAGCTG GAAAGCTGAA GTATTTTCAT AACTGAATT GAGAAATACT TCTTCAAGTT 60  
ATGATGCTTG AAAGTTCTCA ATAAAGTTCA CGGTTTCATT ACCNAAA 107

15

SEQ ID NO:1741  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01959

20

## SEQUENCE DESCRIPTION:

GATCTTAAGG TATCAGTATT TCAGAATCCT GCGACGATTT TATTTCTAAA TTCATGTACT 60  
GTATGTCCAT AAGTGAAAAT AAAATNTCAT ATTCTTTTCT ATNATTGGTA TCATTCAAA 119

25

SEQ ID NO:1742  
SEQUENCE LENGTH:114  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01960

30

## SEQUENCE DESCRIPTION:

GATCCTTAGC TCTTTGCTCT ATGGCCCTTC CTCATCAGGG GACCGTTTCC CCCCTCTTCC 60  
TTCACAGTAT TTAAGAAATA AAAGTCGGAT TTNCTGGCT GCTTTCTCTC TAAA 114

35

SEQ ID NO:1743  
SEQUENCE LENGTH:102  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01961

40

## SEQUENCE DESCRIPTION:

GATCGCCCCA TTGCACTNCA ANCTGGACAG CAAGAGCAAA ACTCCGTNTC AAAAAACAAA 60  
AACAAAANCA AACAAAAAAN TTCCCCTGAG AGAAAACCTA TN 102

45

SEQ ID NO:1744  
SEQUENCE LENGTH:101  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS01962

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55

## SEQUENCE DESCRIPTION:

GATCACACAC TAAGAGAACG TTGATTGCCT CGGCTATTGT GCTGGCTGGA CACTTTGGTC 60  
ACTTTTGAAG CATGTTAATA AATGTCACTG ATTAATAACAA A 101

SEQ ID NO:1745

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01963

## SEQUENCE DESCRIPTION:

GATCCAAGTT TGAATAACAT TTTAGGCTAC TAGATATGAA CAACATCTTG ATTATGTAGT 60  
TGAAGGAAAT TAAAGATGAA TGGTTTAATT AAAAAATTA 100

SEQ ID NO:1746

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01964

## SEQUENCE DESCRIPTION:

GATCAAAATTA AATAATTCAA GCCCTGCCTT CAAAATGAAA TTTTTTTTTT AGTATTATTT 60  
AGCAAAANCA ATAAAACCCA AATTTTTTTA ACCATCAAA 99

SEQ ID NO:1747

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01965

## SEQUENCE DESCRIPTION:

GATCACTTCA AGCAAGCCCC CATGATGGTT CTCAGTCCTG CTTCTCTGTG GGTACGTGCC 60  
CCTCTGTTTA AAAATAAACT GAATATGGAT GTTTAAA 97

SEQ ID NO:1748

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01966

## SEQUENCE DESCRIPTION:

GATCAAAATG AAAACCTGTT GATGTGAATT CAGTTATTGA ACTTGTTACT TGTTTTGGC 60  
AGAAATGTTA TTAATAAATG TCAATGTGGG AGATAATAAA 100

SEQ ID NO:1749

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01967

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCTGATGT TCCTTTTATT TATAACAATG TTAAATGCAA TTGTCTTGTA CCTTGAGTTG 60  
AGTATTACAC ATTAAAGTAA AGTACAAGCT GTAAA 95

SEQ ID NO:1750

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01968

## SEQUENCE DESCRIPTION:

GATCCAGAAG TAAATGTATC TNCAAGCTGA TTAAATTGT AGATTTNNTC TTCATTGCAT 60  
ATTTNCTGAT GTTGAATAAA GTCTGAGTAT TAAA 94

SEQ ID NO:1751

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01969

## SEQUENCE DESCRIPTION:

GATCCAAAGT ATATTTTAC TGAGAATATA TCTGAAAAA TTTGAATTGA GATTAAATT 60  
TTAAATGAAA TATATTTACT TTTTAAAA 89

SEQ ID NO:1752

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01970

## SEQUENCE DESCRIPTION:

GATCCTGGCC CCTCAACCTC CTGTGGAACC CAGCAGTTCT GTTATATCCC CTGCTACCCT 60  
AGATGAATTA AGACGGTTAA ATACTGAAA 89

SEQ ID NO:1753

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01972

## SEQUENCE DESCRIPTION:

GATCTGTCTT GCTTATTGTT GCCCCTGCG NCTAGACAA TTCTGACACA CAATTGGAAC 60  
TTACTAAAAA TTTNTTTTA CTGTTTAA 89

SEQ ID NO:1754

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01973



## SEQUENCE DESCRIPTION:

GATCATATGG TAGTTTTGTT TTACTAATCT AAGGGTACTA GCATCTACAA TNATATAGAC 60  
 AAAATAAAAT ATTTCTTTAA TGGCAAA 87

5

SEQ ID NO:1755

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS01974

SEQUENCE DESCRIPTION:

GATCTGTTTT CTCTAAAATC TTACCATATT GTCTGTATAT GGTGTGAAAT NCAATGGAA 60  
 AGTAAAACGT TTTGGCCCTG ATAAA 85

15

SEQ ID NO:1756

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS01975

SEQUENCE DESCRIPTION:

GATCCTGCTG GAAACCACGG CAACCTGTAT CCACTATTAG GAGGTAAAAA TCAATAAAAT 60  
 GGCCCATTC A TTTGTGTTGT AGCTCAAA 88

25

SEQ ID NO:1757

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS01976

SEQUENCE DESCRIPTION:

GATCTACAAC ATATAAAATT GTGTATTTTC NTTGGTTGT CCCTATTAAC AAAAAAGTAT 60  
 TTNAATAAAA ANTTGAAATG NAAA 84

35

SEQ ID NO:1758

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS01977

SEQUENCE DESCRIPTION:

GATCCCACTG TAAATTGGA AATGGGCAGT TCTGAATTTT CACGTTTGAA ATGTAAAATA 60  
 TAAACTTCAG TCAATATCCA AA 82

45

SEQ ID NO:1759

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50

CLONE:HUMGS01978

55

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCTGGACG TTCACGTGCA CTCTCTTCCT GTACAGTATT TATTGTTCTT GGCACCTTAT 60  
TTAAAGATAT TTGACCCTCA AA 82

SEQ ID NO:1760

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01979

SEQUENCE DESCRIPTION:

GATCCTTACT CCTGCATTGT TCTTTGCCAG NGNCCTATTT AAAAATTTTA AAATTCTCAT 60  
TAAAGTCAGC TTGGGTTTAA A 81

SEQ ID NO:1761

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01981

SEQUENCE DESCRIPTION:

GATCTAAAGA GAAAAGGGAG AAGAGGGAAA AAGGAAACAA AGGAGAAGAA AGAGGGAAAG 60  
GAAAAAAAAG AAAAAGAAA 79

SEQ ID NO:1762

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01982

SEQUENCE DESCRIPTION:

GATCATGAAA GGTGATAAGC TCTTCTATGA TAGGGGAAGT AGCGTCTTGT AGACCTACTT 60  
GCGCTGTTGT ACTCTGAAA 79

SEQ ID NO:1763

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01983

SEQUENCE DESCRIPTION:

GATCAAAATAT TTTGCCTTTN ACTNAAATCA GCCAGCCCAT NACCCCAAT AAAGGGCAGC 60  
TGCCTCTGCT CCCTCTGAAA 80

SEQ ID NO:1764

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01984

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCAAATTT CTAAAGCAA ACAACAAAAA TGTACATTTT TGTTTTTCCT TTAAATAAAC 60  
AGGTGTACTC TTTATCAAA 79

SEQ ID NO:1765

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01985

## SEQUENCE DESCRIPTION:

GATCTAGTGT CCTTTTGTG CACTAAACAG GTGAATGCTG ACTTTTTTCA TTCTCCAATA 60  
AATNTCACTG AACTGAAA 78

SEQ ID NO:1766

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01986

## SEQUENCE DESCRIPTION:

GATCTTTTGT TAGTTTCAAG TCTTTTATA ACTAAATCTG CTGGCATTAG ACAATAAATA 60  
CATTTTCAAA ATAAA 75

SEQ ID NO:1767

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01987

## SEQUENCE DESCRIPTION:

GATCATATAT ACTTGCATAA TATCATCCCT TCCCTTGATT TCTTTCAATC TAAAAATAAA 60  
TATGAGAAAA ACAA 75

SEQ ID NO:1768

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01988

## SEQUENCE DESCRIPTION:

GATCGATATT AATGTATCCA ATGAAATAAT CGACTTGTNC TTGATAGCCT CATTAAAGCA 60  
TTTGGTTTTN CACATAAA 78

SEQ ID NO:1769

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01989

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCTGAGCC CCCAAGATGG AGAATGGGGA GGAGCTTTTT ATGGCGGACT GATTAAAACT 60  
CTTAAGCATT TAAA 74

SEQ ID NO:1770

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01990

SEQUENCE DESCRIPTION:

GATCTGCTTG GCCTTGATAA GCTATGTTGT TGCACTTTAA ACATTTAAAT TATACAATCA 60  
TCAACCCCCA AA 72

SEQ ID NO:1771

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01991

SEQUENCE DESCRIPTION:

GATCCTCCCC TTCAAATGAC TGTAATTAAC AACACTTAAA AAAGTTGAAT AAAATATTGA 60  
AACCTCAAA 69

SEQ ID NO:1772

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01992

SEQUENCE DESCRIPTION:

GATCTATTCT GAAGCTGTTT ATTTTAAACA AATAAAATGT TACAGGTTTC ACATGATTGA 60  
TTCTCAAA 68

SEQ ID NO:1773

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01994

SEQUENCE DESCRIPTION:

GATCCGTAAC TNCGGGATAA GGATTGGCTC TAAGGGCTGG AGAAGGAATG AATAAAAAAA 60  
AAGAAA 66

SEQ ID NO:1774

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01995

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCCATGT CTCTGCCAGG ACCAAGGCNG ATGTTTCCCC ACTAATAAAG TGCCGGGTGT 60  
CAGCAAAA 67

5

SEQ ID NO:1775  
SEQUENCE LENGTH:65  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS01996  
SEQUENCE DESCRIPTION:  
GATCCTTTTT AATACCACAG CATTGTACT GTTCCTTTTT AATATACTGA AAATATAAAA 60  
GGAAA 65

15

SEQ ID NO:1776  
SEQUENCE LENGTH:71  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS01997  
SEQUENCE DESCRIPTION:  
GATCCGATTA TTTCTGCCAG TNTATTTTGG NCACTTTATA ATCATTAAAG CACTTTCTTG 60  
GCAGGCNCAA A 71

25

SEQ ID NO:1777  
SEQUENCE LENGTH:72  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS01998  
SEQUENCE DESCRIPTION:  
GATCTTACAA TAATGTTCCA CTCTGCAAAT TTTTAAGGTT CAAATAAAGT TTAATTGTTT 60  
GCAAACTGTA AA 72

35

SEQ ID NO:1778  
SEQUENCE LENGTH:65  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40

CLONE:HUMGS01999  
SEQUENCE DESCRIPTION:  
GATCATTGCA CCATGTCAGA CTTTGTATA TNCCTTGAAA ATAAATGAAA GTNAGAATCN 60  
TCAAA 65

45

SEQ ID NO:1779  
SEQUENCE LENGTH:62  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02000

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# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCTGTCC TGATTCTCAA AAATTATTTT CTCTGTATGA TTAAGTTT ATTCCATTTA 60  
AA 62

SEQ ID NO:1780

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02001

## SEQUENCE DESCRIPTION:

GATCCCTTCA TTTGAATATT AATGGCTTTT TCCATTAAAG AATAAAATAT TTTGGACAAT 60  
GCCAAA 66

SEQ ID NO:1781

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02002

## SEQUENCE DESCRIPTION:

GATCAAATTT ATAAGTTATT ATTTTAATT TTCTAAATTA AATAAAAGAA AGAATGCAAA 60  
CCAGGAAA 68

SEQ ID NO:1782

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02003

## SEQUENCE DESCRIPTION:

GATCAATAAA GAGTAATTC TTGCTAAATA AATAAAAGAA ACCTTGTTGA AAAACTAAA 59

SEQ ID NO:1783

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02005

## SEQUENCE DESCRIPTION:

GATCTGAATN ATGCACCCCA CCCCCACCCC AATAAGAAA TAACAGAAAA CCCTCGAAA 59

SEQ ID NO:1784

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02006

## SEQUENCE DESCRIPTION:

GATCTTCATT TTTTTTTTA AACTTGGCGT TTTTGAATA AAAACCTTTT GTCTTAAA 58

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5 SEQ ID NO:1785  
 SEQUENCE LENGTH:59  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02007  
 SEQUENCE DESCRIPTION:  
 GATCTCAGTT GTAAATAGAA AAATCTAATT CAATAAACTC TGTATCAGCC CCCAACAAA 59

10 SEQ ID NO:1786  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 15 CLONE:HUMGS02010  
 SEQUENCE DESCRIPTION:  
 GATCCAAAGT CATGTGTCCA CACATTCATA AATAAAAATT TTACCTATGA AA 52

20 SEQ ID NO:1787  
 SEQUENCE LENGTH:51  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02011  
 25 SEQUENCE DESCRIPTION:  
 GATCCAGTGA AGCCAGAAGC CAAATAAACT CAAAAGCTGT CTCCCCACAA A 51

30 SEQ ID NO:1788  
 SEQUENCE LENGTH:54  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02012  
 SEQUENCE DESCRIPTION:  
 35 GATCCTAATT TATGCCTATG CAAAAAATAA ATAACGCCCA AGAGCTGTGG GAAA 54

40 SEQ ID NO:1789  
 SEQUENCE LENGTH:53  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02013  
 SEQUENCE DESCRIPTION:  
 45 GATCGCCTAG TATGTTCTGT GAACACAAAT AAAATTGATT TACTGTCTGC AAA 53

50 SEQ ID NO:1790  
 SEQUENCE LENGTH:58  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

55

CLONE:HUMGS02025

SEQUENCE DESCRIPTION:

GATCCG TAGT AATAAATTCT CAGAGGACTC AGCCTTTCCT GCGGGTCTGG AGCTCAA 58

5

SEQ ID NO:1791

SEQUENCE LENGTH:597

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS02039

SEQUENCE DESCRIPTION:

GATCAGAGTC TCTGGGCAT TTTATATTTT GCATTCTGAT GTACCTAGGA GTTTTGTAA 60  
 ACAGATGATG TATGTNAGTA TTTATCCCAT TTTATGCAAT TAACCAAATC AACCAAAAAA 120  
 AGTGACCATG AAGTCCTGTA TTTGTNTTTT TACTACATGT AGGAACTCTC ATGTGAATGA 180  
 GTACTGTAGT AATCCATTCT ATGGGAGCCT TATTTCAGAA ATATTTCAAA CTGGTGCAA 240  
 TGGAAAAGAC TTTCTCTTTT CCTTTAAAGC TAAAGACAAG AATATCATGC TATACAGGTG 300  
 CAACTCAATC CCCGTTAATA AAAACCAATG TAGGTATAGG CATTCTACCC TTTGAAATAG 360  
 CTGTGTCCCA ACCTGTTGCC ATTGATTTTT TGGGAATGGC TTTAGGAAAT ATCCAAGTTG 420  
 TCCTTGGAAT TGTCTAACCA TGGNCATAAA CAGTTGTCTC CCTTCTACTT GTGTAGAATA 480  
 CTTTGGNCTT AATTTTCCTN CCAGATACAG GGGGGTACCT GCCTGTTTTT CNAAGGGTTT 540  
 ATTACTGGNG GTACCATTG GTAGGATTGT TTAAATAAA AAAACCTGGT TTTTAAA 597

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SEQ ID NO:1792

SEQUENCE LENGTH:518

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02040

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SEQUENCE DESCRIPTION:

GATCCAAAAC TGGACCCTTG GAGCCGTCGA CTCACAGATG GATGACATGG ACATGGACTT 60  
 AGACAAGGAA AAAANNCAGG ACTTGAAGGA GCTCAAGGTG CTAGTGGCTG ACAAGGACCT 120  
 TCTGGACCTG CACAAGAGCC TGGTGTGCAC TGCTCTCCGG GGAAAGCTGG GCGTCTTCTC 180  
 TGAGATGGAA GCCAACTTCA AGAACCTGTC CCGGGGGCTG GTGAACGTGG CCGCCAAGCT 240  
 GACCCACAAT AANGATGTCA GAGACCTGTT TGTGGACCTC GTGGAGAAGT TTGTGGAACC 300  
 CTGCCGCTCC GACCACTGGC CACTCAGCGA CGTGCGGTTC TTCCTGAATC AGTATTGAGC 360  
 GTCTGTCCAC TCCCTCGATG GCTTCCGACA ACAAGGCCCT CTGGGACCGC TACATGGGCA 420  
 CCNTTCCGNG GCTGNCTNCT GCGGCCTGTN ATCATGACTG AGGTGGCCTN CCAAANGTTN 480  
 CGCCCAAGGT TGACAATAAA GTTGCTCTGA GTTTGAAA 518

40

SEQ ID NO:1793

SEQUENCE LENGTH:513

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02041

SEQUENCE DESCRIPTION:

GATCTGTAAT TTTAATTTTC ACCCTCTGTA CCCCATGACC TTATCCTTCC TCTCCTTCCT 60  
 TGTTACCCAT GAAAACTGG CAACATTCCA AGAATAGCAT CTGTACAAAG GGGAAAGAAC 120

50

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ATAAAGGTAA AACAAAACAA AACAACATTT TGAGAACAAA GATGACCATA ACCACTGAAG 180  
GGAATCACAT CTTTTAAGAC AAATTCATAT TCTTTTATTT GTTATGGCAG ATGACAAGAT 240  
GGTACAACCT TTATTCTTTT NCAAAATAAA ACAAAGGGCA CAGCATCTGT AGTCAGCCGA 300  
CAACTATTNC GGCCTTTTGG GGGTNGGTCT NGCCGTACTT GTGATTTTCA TGGTACGTGA 360  
CCNTNTTCTG GAAGGCTTGC CCCNTTGCCC GTGTACATAG GTGCATTGGT TNCTNTGGGA 420  
GGGGCCCAAG NACTTTTNGG CNANNGTTGT ACTGGTATTG TNATGAAATT TNCGGTTGGN 480  
CCTCTTGNN NTTTTTTNTG CANGAANGNN GGN 513

SEQ ID NO:1794  
SEQUENCE LENGTH:499  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02042

SEQUENCE DESCRIPTION:  
GATCTCTTAA GAGATGATGG ACTCATGTAT GTCACCCGAC TTCGCAACAC TGGGGTTCAG 60  
GTGACTCATA ACCATGTTGA GGATGGATTC CATGGAGCAT TTTCATTTCT GGGACTTAAA 120  
ATTAGTCACA GACTTATAAA TCAGTATATT GAGTGGCTAA AGGAAAATCT ATAGTAAAAC 180  
ATGTAGCTAT AACATATTTT AAAAAATAAA TCTGAAAACC TCAGAAAATT TGCATTAGAA 240  
ATTGGTCTTT CTTAGAATGG TCTAGTTAAG TTCCACATGT AGCATAATTC TTAATAGGC 300  
ACTTTTCTGT TTTTTTTTNC TNACTGTGGG ATTTTCATNNC AATTTTCTAC ATTGTCTATC 360  
TGCTTTTNC TNGATTTTCC NCTTACACTG TTAATCTNAT TTTAAAAAAA TGTACATNCC 420  
NNGNANACNT TAANTTTGGG GAGTTNGGCT ACNANTTNAC GGTGGCCAGG GGGNTTAAAT 480  
GGTGGGGCCA ATTTTAAAA 499

SEQ ID NO:1795  
SEQUENCE LENGTH:483  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02043

SEQUENCE DESCRIPTION:  
GATCAAAGCG CCACTGCCCT GCACTTCCTG GGCCGCGTGG CAACCCGCTG NGCACAGCAT 60  
GAGGCCAGGG NCCCAGAACA CAGTGCCTGG CAAGGCCTCT GCCCNTGGCC TTTGAAANAA 120  
AGGCCAGCAG CAGATAACAA CCCCAGGACAA ATCAGCGATG TGTCACCCCC AGTCTCCAC 180  
CTTTTCTTCT AATGAGTCGA CTTTNGCTG GAAAGCAGCC GTTCTCCTT GGTCTAAGTG 240  
TGCTGCATGG AGTGAGCAGT AGAAGCCTGC AGCGGCACAA ATGCACCTCC CAGTTTGCTG 300  
GGGTATTTT AGAGAATGGG GGTGGGGAGG CAAAGAACCA GTGTTTAGCG CGGGACTACT 360  
GTTCCAAAAA GANTTNCAAC CGNCCAGNTT GTTTGTGAAA CAAAAAAGTG TTNCCTTTTT 420  
CAAGTTTGAG AACAAAAATT GGGGTTTTAA AATTAAAGTA TACCATTTTT TGCATTTGNC 480  
AAA 483

SEQ ID NO:1796  
SEQUENCE LENGTH:481  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02044

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

5 GATCCAAAAC GCTTCGAGGC ACCCCAAATT ACCTGCCCAT TCGTCAGGAC ACCCACCAC 60  
 CCAGTGTAT ATTCTGCCTC GCCGGAGTGG GTGTTCCCGG GGGCACTTGC CGACCAGCCC 120  
 CTTGCGTCCC CAGGTNNNNA GCTCTCCCT GGGCCACTAA CCATCCTGGC CCGGGCTGCC 180  
 TNGTCTGACC TCCGTGCCTA GTCGTGGCTC TCCATCTTGT CTCCTCCCGG TGTCCCAAT 240  
 GTCTTCAGTG GGGGGCCCC TCTTGGGTCC CNTCCTCTGN CATCANCTGA AGACCCCCAC 300  
 GGCAAACACT GAATGTCACC TGTGNCTGCN GNCTCGGTCC ACCTTGCGGG CCGTGTTTGA 360  
 10 CTAACCTTNA ACTTCTTTA ACGGTAATAT TTCCGGCAA AATCCAATGG TTTGGGTTTT 420  
 GGTCTTTTAA CNTTGTAAC GGTGCGAAAT CCAAATAAAA GCAATTAAAA AGTCAATGAA 480  
 A 481

SEQ ID NO:1797

15 SEQUENCE LENGTH:462  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02045

## SEQUENCE DESCRIPTION:

20 GATCTAAAAG GGTTTTCTTA GAAAGGGCAA TATTGTCCAA TGAAGTAAGC AGAAGGACTC 60  
 TGGGTTAGAA GCATCTGCAC AAAAAGTGGT GAGACCTACT CTCCACTGCT CTGCAGCTGG 120  
 ATGGCTGATG GCAGGCTGAG CAGTGGGGAA GCAGGTTTTA ACAACAGGA GTCCTTCCAG 180  
 GTCCTGTAT ATTGNGAAGA AACATAAAAC TATTGTCTGT TACATTCCGA GGTGAGCCTT 240  
 25 CTNCTTAACG TTTTATAATA TGCAAATNCC AGCTTCTGGA AAGCANGTAT CATCATGTAC 300  
 CAAATGCTTT ATACACCATC ACATTCATGA NTTTTNAGC ATGGTCAGAN CTTGTGTAAA 360  
 TATGTCTCTT AGGATGATTT TGGGGGAGGA TGTGATTTAT TTTCCATAAT TTCAAANTN 420  
 GCATTTTCCA TTTCAAATA AGGNTAATCT NTGGGGCCA AA 462

SEQ ID NO:1798

30 SEQUENCE LENGTH:448  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 35 CLONE:HUMGS02046

## SEQUENCE DESCRIPTION:

40 GATCAGCCTG CAGCCATCCC CCGACCCTGC TGCTAGGCCA CGGTCTGCGC CCTGGGGCCT 60  
 CATCTCCCC AGCCCACTTG TTTTCCCCC TTTTATTCCC TAGGCCCTT TCAGACTCCT 120  
 GGGCCCTTGG NNNCTCTTCT CCCATCTCCC TTCACAGGAT GACACCCTCC CATACCCCAT 180  
 AGCTGGGGCC AGCAGGTCT GCTGAGGGTG GGGCTGGTGT AGGGACCCCC AAGAGACCCC 240  
 TGTCTGTCC CTTCAACAGT CCTGGGGAGG CTGGGACTCC CCCTGCCACA AGCCTGGGCC 300  
 ACAGTTCACA TTCCACTGCT GGGAGAAGAA ACAGGCCGAG GCCCAANAGT GGCCTGCCCC 360  
 CGGGAGCCAA AGACCCNAGT GGCCACANTG GGATTAGGT NGGGGAGGNT TGGNAGCGCT 420  
 45 NTTTTTATAA ATATTATACA TAAGGAAA 448

SEQ ID NO:1799

50 SEQUENCE LENGTH:448  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS02047

SEQUENCE DESCRIPTION:

5 GATCTGGTTG GTGGATGAAC AAGTGTACAG CTGGCCATCT CAATGGNGTT TATTACCAAG 60  
GTGGCACTTA CTCAAAAGCA TCTACTCCTA ATGGTTATGA TAATGGCATT ATTTGGGCCA 120  
CTTGGAAGAAC CCGGTGGTAT TCCATGAAGA AAACCACTAT GAAGATAATC CCATTCANCA 180  
GACTCACAAT TGGAGAAGGA CAGCAACACC ACCTGGGGGG AGCCAAACAG GCTGGAGACG 240  
TTTAAAGAC CGTTTCAAAA GAGATTTACT TTTTAAAGG ACTTTATCTG AACAGAGAGA 300  
10 TATAATATTT TTCCTATTGG ACAATGGACT TGCAAAGCTT CACTTCATTT NNNNGAGCAA 360  
AAGACCCCAT GTTGGAAAAC TCCATACCAG TTTTATGCTG ATTGATAATT TATCTACATG 420  
CATTTCATA AACCTTTTGT TTCCTAAA 448

SEQ ID NO:1800

15 SEQUENCE LENGTH:432  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02048

SEQUENCE DESCRIPTION:

20 GATCTGAATT ATCTGGCACC CTCCTGAATG GAACCCAGAG GTACCTCCTG TGTGGAAGGG 60  
TCCTGGATTT TCCCTAACAC CCACCTCTC CCCCTTCAGC CATGCTGATG GCAGAGAAGA 120  
TAAGAACTTG GAGCCCATTT CTCCTGGAG AGGAAACTT GTCATCTGGC TTTGCGGAGA 180  
AGGTTCACAC TTACGCTCGT AGTACATTAT CTTTACTATG TGCTAGGATA TCATATTTAA 240  
25 AAGGACAAAA AAATGTAAAA TACTTGAATG AGCTTGATT ATANCATTAA TATTATNNNG 300  
NGTATCTGCT TTCCAGGCTG AAGTGATTCA TTCATTATTC TAGTCCTGCT TTAGTCCTTT 360  
GTAATTTGTG GTAATTATGC TTTTCTTTT AATACAAAAA AATGTATAAA ATTAACACT 420  
TGAAAAGGCA AA 432

30 SEQ ID NO:1801

SEQUENCE LENGTH:430  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02049

SEQUENCE DESCRIPTION:

35 GATCCGNGCG AGGGCAACAG CGGNTCACCT ACAGCGCACT GTCGATGGCT GCACGAGTCA 60  
CACCAGAGCC TGGGGCAAGA CAGTGATTGA ATACAAAACC ACCAAGACCT CCCGCTGCC 120  
CATCATCGAT GTGGCCCCCT TGGACGTTGG TGCCCCAGAC CAGGAATTCG GCTTCGACGT 180  
40 TGGCCCTGTC TGCTTCCTGT AAACCTCCCTC CATCCCAACC TGGCTCCCTN CNACCCAACC 240  
AACTTTNCCC CCAACNNGG AAACAGACAA GCAACCCAAA CTGAACNNN TCAAAAGCCA 300  
AAAANTNGGG AGACAATTTC ACATGGACTT TGGAAAAATA TTNTTTTCTT TTGCATTCAT 360  
NTNTCAANCT TAGTNTNTA TCTTTGANCA ACCGGANCAT GGCCAAAAAN CAAAAGGTGC 420  
45 ATTCANCTN 430

SEQ ID NO:1802

50 SEQUENCE LENGTH:428  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS02050

SEQUENCE DESCRIPTION:

5 GATCCCAAGG GAAAGATGAT TTGTATGTTA AAGTGACTGC ACAAGTAAAA GTCCAATGTT 60  
GTGTGCATGA AAAGGATTCC TTGGTTATGT GCAGGGAATC ATCTCACATG CTGTTTTTCC 120  
TATTTGGTTT GAGAAACAGG CTGACACTAT TCTCTTTGAT TAGAAAAATA ACTCATAAAA 180  
CTCATAATGT TGATATAATC AAGATGTAAC CACTATAAAT ATGTAGAAGA GGNCGTTT 240  
AAAGACCTTA AGCTGGCATT GTGAAGGAAC ACCATGGTAG ACTCTTTTTG TAAATGTATT 300  
10 TTGTATTTAA TGAAATGCAG TATAAAGGTT GGTGANGTGT AATATANTTG TGAAACAAA 360  
TCCTGTTAAT AGAGAGATGT ACAGAATCGT TTTTGGTACT GTATCTTGA AACCTTTGTG 420  
AAAAAAN 428

SEQ ID NO:1803

15 SEQUENCE LENGTH:401

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02051

20 SEQUENCE DESCRIPTION:

GATCAAAACC AAAGTGTCA ATGTGACAGT CTGAAAATTA TATACTCTAC TTCATTCATG 60  
TTACTACTTT TTCTACTCCT TACCTGCTTT TACTAATGCA TTTATCCCCA AGAAAAATC 120  
CAACAATATG GGAATAATTT GGAACAATAT CCAGCAATTG GTATTTAAAT AATTACTGG 180  
TTACAAAACA ATATTATGAC CAGACTCCAT TTTAGAAAAA ATTAAATCTG CATCGAAAAG 240  
25 GGCCTTAAAA AATAGATTTC TAAAATCAAA ATCATGGTTG GCTCATGGGT GGGATTATTA 300  
GTGTTCTTA TAGTAGTTG TCTGGATGTA CTTTCTGATT CTCCTGTAAT AAGCATGCAT 360  
TGCTTTTGTA ATGNGGGAAT AATANACCA TAAAAAGGAA A 401

30 SEQ ID NO:1804

SEQUENCE LENGTH:396

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02052

35 SEQUENCE DESCRIPTION:

GATCCGGCTG CAAAATTCAT ACCAACCAAC AAATAAAGGA AGATACAAAG TCTTATAGAC 60  
ATCCGAAAAA AAGATTTTCTA CCTGTGCTGG TCTATGATGT ATGTGGCAGT TGCTGTCTGC 120  
AGTTTACAAT GTATTGTAAA TGAAGATTTT TTAAATCTA TCTTGCTGNT TNNNTNNAA 180  
40 ATATAAGAAA CTGGTACTTG GTAAAGAAAT CTGTCCGTAA GTACCCAC AATCAGTCAA 240  
ACTATATTTA AAGCCAGCCT GTTTTCAGAG TATGATGTCC TTTAATGTAA ACTCAAATAT 300  
CAATATTTTA AATGTCCGGA TAATATTCTA GAGGTTTAAA AAATGGAAAT ATTTGANCTT 360  
TCTATTGAAG ACAATAAAGG TACACAAGTC GTTAAA 396

45 SEQ ID NO:1805

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02053

50 SEQUENCE DESCRIPTION:

55

GATCAAGAGC AGTGCTTCTC CATTTGTTTT GCAGAGAAAT GTTTTTCATT TCCCGTGTGT 60  
 TTCCATTTC TTCTGAAATT CTGATTTTAT CCATTTTTTT AAGGCTCCTC CCCATCTCCT 120  
 TTCTTAAGGC ACTGTTGCTA TGGCACTTTT CTATAACCTT TTCATTCTGT TGTACAGTAG 180  
 CTTAAAATTG CAGTGATTGA GCATAACCTA CTTGTTTGTA TAAATTATTG AAATCCATTT 240  
 GCACCCTGTA AGAATGGACT TAAAAGTACT GCTGGACAGG CATGTGTGCT CAAAGTACAT 300  
 TGATTGCTCA AATATAAGGA AATGGCCCAA TGAACGTGGT TGTGGGAGGG GAAAGAGGAA 360  
 ACAGAGCTAG TCAGATGTGA ATTGTATCTG TN 392

SEQ ID NO:1806  
 SEQUENCE LENGTH:389  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02054

SEQUENCE DESCRIPTION:  
 GATCCTATTT GGTATGTTTT TGTCCACTGT TATGATTCAT CATGTATCTT ACAAGAGCCA 60  
 CTCAAGCAAG ACTCTGCTTC TATGTATGGT GAGGCCTTGT TGTTCAGGC TAGAATAAAC 120  
 TCTTTGTATG CCTCAGTGAA TATGCCAGGT AAAATATATG CAGTCAAGAA TGAATTATTT 180  
 TTCTGACTAA AGTGTGTAGC AGTAAGTTCA AAATNGTGCC CTTGTTTTAA CAGTTTCTGT 240  
 CAACATCTTC TCATTTTTCC CTACAAAAAC ACCAGGGTGT ATTATAAGTA CTGCCTGTGA 300  
 GAATTTGCAC TTTATGTATT TGTGTGTGGG ATTTCTTGTG GTTTtagcca AATGAAGTGT 360  
 TATCNNTAAT AACCAGGTCT CTTCATAAA 389

SEQ ID NO:1807  
 SEQUENCE LENGTH:388  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02055

SEQUENCE DESCRIPTION:  
 GATCCAATTG ATGTATATGT TTATATACTG GGTTCCTGTT TTATATACCT GGCTTTTACT 60  
 TTATTAATAT GAGTTACTGA AGGTGATGGA GGTATTTGAA AATTTTACTT CCATAGGACA 120  
 TACTGCATGT AAGCCAAGTC ATGGAGAATC TGCTGCATAG CTCTATTTTA AAGTAAAAGT 180  
 CTACCACCGA ATCCCTAGTC CCCCTGTTTT CTGTTTCTTC TTGTGATTGC TGCCATAATT 240  
 CTAAGTTATT TACTTTTACC ACTATTTAAG TTATCAACTT TAGCTAGTAT CTTCAAACCT 300  
 TCACTTTGAA AAATGAGAAT TTTATATTCT AAGCCAGTTT TCATTTTGGT TTTGTGGTTT 360  
 TGGGTTAATA AAACAATACT CAAATAAA 388

SEQ ID NO:1808  
 SEQUENCE LENGTH:379  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02056

SEQUENCE DESCRIPTION:  
 GATCTTTTCC ACCAGCACCC AGAGTGTCTT CTTTCTGGGC AAGGTCGTCG ACCCCACGAA 60  
 ACCATAGCCC TCCCAGGGCT GTCATCTGT TCCAAGCAGG AGGATGTGGC AGGGGAGGGC 120  
 TGGGAGTGAG TAGCTCTGTG TTAGAGTTG GGGACAAGGA TGACACCGAA GTCCAGGAGT 180

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CCAGGACAGC AGGTGCTGGC CGGTGGGGAG CGGGGAGGGG CACTGAGATG GGCAGGGCCT 240  
 GGACATTCCA CACCCTGGTG CTGTGCAGCC TCTGGCAGAG CATCCGACCT CTTGGAGCAA 300  
 GTTTCTGCCT CTGGAAGGG GGCAGGGCCT TTTCACAACA GGCTGGTTTG TACCGAGTAA 360  
 ACAACACGNT GCCATGAAA 379

SEQ ID NO:1809  
 SEQUENCE LENGTH:379  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02057

SEQUENCE DESCRIPTION:  
 GATCCTAGGG GGTGTTGTTT GGTGTTTNAAT TGTGAGGAAT AAAAAATNTT CTGCCCACAC 60  
 TGGCATTTTA AGGTGACTGA GGTCAAACGT TGTTTCCTTA GGTTGAAATA GCAGCCAAAA 120  
 CATTCTTNAC GCAGGGGCTT GGGATATGGC TGCTGGCAAC ACATTTTGTT GTGGGCTCCT 180  
 TAATTTAATG ATAAATTTA AGCTAAACAC AAGCCAAAAA TGAATAGGTT TTTTNAATTT 240  
 TNATTTTTC CTAACAGGC AATTGAAATA CATGGTACAA AAATAAGTGG TAAGATAATT 300  
 GTAAATGGA AATGGGCAGA NTATTCAATT TTCCATCTAT GNAAATTTTC NCATTAAAAAC 360  
 TCATAGNTTT CTTTGNAAA 379

SEQ ID NO:1810  
 SEQUENCE LENGTH:358  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02058

SEQUENCE DESCRIPTION:  
 GATCNGTTCA GCCCTGAAAA GTCCAACTC CCAGGTATTG TTGCAGAAGG NCGAGATGAC 60  
 CTCTATAAAT CAGATGCATT CCATAAGGCA TTTNTTGAGG TAAATGAAGA AGGCAGTGAA 120  
 GCAGCTGCAA GTACCGCTGT TGTGATTGCT GGCCGTTTCGC TAAACCCCAA CAGGGTGACT 180  
 TTCAAGGCCN CCNGGCTTNA AAAAGTTTTT ATAAGAGAAG TTCCTCTGAA CACTATTATC 240  
 TTCATGGGCA GAGTAGCCAA CCCTTGTTGT AAGTAAATG TTCTTATTCT TTGCACCTCT 300  
 TCCTATTTTN GGTGTTGTGAA CAGAAGTAAA AATAAATACA AACTNNTNNC ATCTCAA 358

SEQ ID NO:1811  
 SEQUENCE LENGTH:358  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02059

SEQUENCE DESCRIPTION:  
 GATCGTTTCT NATCTCNAAG TNCCTCATTG AGNTCGGTGC ATCTGGCCAN TGAGTCTGCT 60  
 GAGACTCTTG ACAGCACCTC CAGCTCTGCT GCTTCAACA ACAGTGACTT GCTCTCCAAT 120  
 GGTATCCAGT GATTCGTTGA AGAGGAGGTG CTCTGTAGCA GAAACTGAGC TCCGGGTGGC 180  
 TGGTTCTCAG TGGTTGTCTC ATGTCTCTTT TTCTGTCTTA GGTGTTTCA TTAAATGCAG 240  
 CACTTGGTTA GCAGATGTTT AATTTTTTTT TTAACAACAT TAACTTGTGG CCTCTTTCTA 300  
 CACCTGGAAA TTTACTCTTN GAATAAATAA AAACCTGTTT GNCTTTGNCT TCTGCAA 358

SEQ ID NO:1812  
 SEQUENCE LENGTH:344  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS02060

SEQUENCE DESCRIPTION:

GATCTATACT AGATAATCCT AGATGAAATG TTAGAGATGC TATATGATAC AACTGTGGCC 60  
 ATGACTGAGG AAAGGAGCTC ACGCCCAGAG ACTGGGCTGC TCTCCCGGAG GCCAAACCCA 120  
 AGAAGGTCTG GCAGNNNTCA GGCTCAGGGA GACTCTGCCC TGCTGCAGAC CTCGGTGTGG 180  
 ACACACGCTG CATAGAGCTC TCCTTGAAAA CAGAGGGGTC TCAAGACATT CTGCCTACCT 240  
 ATTAGCTTTN CTTTATTTTT TTAACTTTTT GGGGGGAAAA GTATTTTAA GAAGTTTGTC 300  
 TTGCAATGTA TTTATAAATA GTAAATAAAG TTTTACCAT TAAA 344

SEQ ID NO:1813  
 SEQUENCE LENGTH:338  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS02062

SEQUENCE DESCRIPTION:

GATCCAGTAG TAGAGACATC ATCGGTCCAA AAGACTTTGC ATCTCATTAG TTGTCCATAG 60  
 TGACTACCAG GAGGTGGCTG GCATCTATAA CGTGTGGGAC GTTTTATGT AAAGAACTGC 120  
 CTGTGTTTTT TTTTNAACC AAAGACACTG NCCATAGATT GACTTATACT TTTATAAGTC 180  
 TAATTGAAAT ACTTGGGGTA CTATGAAAGG NCTGTNCCTT GNGTGGCTAC GATTAGAAAA 240  
 TCAGGNCTAA CAAACTTTTC TTTGTCTGGA NGCATATATA TTTGTGATAT AATTTNAATA 300  
 TGTATAATTT TGGTTTAATA AATCAAATCT ATGCCAAA 338

SEQ ID NO:1814  
 SEQUENCE LENGTH:336  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS02063

SEQUENCE DESCRIPTION:

GATCCATAGA ATGGATACTG GGAGACAATT AGTAGACTTT GCTACAGGTA GCCAATAGCC 60  
 CAGCCTGCAG AGTCACGTCA GATATGAAAT CCCAAAGTTC CTCCTGACTA TTGGCAACAA 120  
 CAATCACTAA CTGCTACTAC AAAAAGGTAA AACAAAAATG AACTTACACT TTCAAAATAT 180  
 CATTGATGTA TATTAAACAA ATACTTCTTG AGTGTCTACC CAGTGCCAGA CAGTGGTCTA 240  
 GGTCTGTTGGA GGTACAGCAT CGTGGGCCAC ATGGTTAGAA GCTGAGTGTT CCTAACAAGG 300  
 AGGCTGATTT TGCTGCTCTA CTTTGCCTG GTTAAA 336

SEQ ID NO:1815  
 SEQUENCE LENGTH:335  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS02064

SEQUENCE DESCRIPTION:

GATCTGGATG TGGATGATGC GCCTGGAAAC AGTCAGCAGG CAACTCCGAA GACAACGAGA 60  
 TAAGCACCTT TCACAACCTC GGGAACGTTT ATTCCCCGCT GAAGCTTCTC ACCAGCATGG 120  
 CCATCTCGGT GGTGTGCTTC TTCTTCCTGG TGCCTGACT GCCTGGTGCC CAGCACATGT 180  
 GCTGCCCTAC AGCACCTGT GGTCTTCCTC GATAAAGGGA ACCACTTTCT TATTTTTTTC 240  
 TATTTTTTTT TTTTNGTAAN CCGGNANACC TCCTCCAGCC ATGAGGNNGG GGNNTANCCA 300  
 NGTGTNATGT TTNGGAAANN NAAATGGNAT CTTN 335

SEQ ID NO:1816  
 SEQUENCE LENGTH:335  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02065

## SEQUENCE DESCRIPTION:

GATCCATGTG TAATATCACA AGAAATTATG GAAAAATATA ACATAAAATT AAAGTGGACA 60  
 AACCAACAAA AGCTTTATTC AAGAACAGGT GACATAGTTG AATTTGTTT TAAATCTGGA 120  
 TATCATCCAA CAAAATCTCA TTCATTTCTG GCAATGTGTC AGAATGGGAA ACTGGTATAT 180  
 CCCAGTTGTG AAGAAAAATA GAATCAATGG CATTACTATT AGTAAATGC ACACCTTTTT 240  
 CTGAATTTAC TATTATATTT GTTTTCAATT TCATTTTCA AGTACTGTTT TACTCATTTT 300  
 TATTCATAAA TAAAGTTTGT TGTGATTGTG TGAAA 335

SEQ ID NO:1817  
 SEQUENCE LENGTH:334  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02066

## SEQUENCE DESCRIPTION:

GATCTTGATG CGGGACTTCA GTCCTAGTGG CATTTTCGGA GCGTTTCAAA GAGGTACTA 60  
 CCGNNACTAC AACAAGTACA TCAATGTGAA GAAGGGGAGC ATCTCGGGGA TTACCATGGT 120  
 GCTGGCATGC TACGTGCTCT TTAGCTACTC CTTTTCCTAC AAGCATCTCA AGCACGANC 180  
 GCTCCGCAAA TACCACTGAA GAGGACACAC TCTGCACCCC CCCACCCAC GACCTTGGCC 240  
 CGAGCCCTC CGGNNGGAAC ACAATCTCAA TCGTTGCTGA ATCCTTTCAT ATCCTAATAG 300  
 GAATTAACCT CCAAATAAAA CATGACTTGG TAAA 334

SEQ ID NO:1818  
 SEQUENCE LENGTH:328  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02067

## SEQUENCE DESCRIPTION:

GATCCAAACA TGAAAGCTGG AGCTACAAGT GAAGGCGTTC TGGCAAATTT CTTCAACAGT 60  
 TTGTTGAGTA AAAAGACTGG CTCTCCAGGA GGCCCTGGTG TGAGTGGTGG TAGCCCTGCA 120  
 GGTGGGGCTG GAGGTGGAAG CAGTGGTTTA CCACCATCCA CAAAAAGTC AGGCCAGAAG 180  
 CCTGTCTTAG ATGTTTCATGC AGAACTAGAC AGAATTACAC GAAAACCAGT TACAGTTTCT 240  
 CCCACAACAC CTACATCTCC TACGGAAGGA GAAGCTTCTT GAAGATACCA AATAAAGCCA 300  
 TTTATTCTGT TTTCTGGGNT AATGTAAA 328



SEQ ID NO:1819  
SEQUENCE LENGTH:328  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02068

SEQUENCE DESCRIPTION:

GATCGGGGCT GCTTATGCCT TTCGTTTATC CTTGGGGTTT GAGAGCGCTG TATTTGGGAG 60  
AGAGTTTAAA AATACATTAG GAGAGAGAAA CCATTAAAAG TTTCAGTGC AGAGATATTG 120  
TAGGTGCTAA TACTGGATTT CGTCTCANAT TTAATTTCTT TNATGGGTCT GTTAGTCATT 180  
CANCAAATCC CATAAGTATG TGTTAATATT TNAATTGTGT AAAACTCATT TGTTACTTTA 240  
CAGCCTGTAA TAGTGTGTCT GCATTTNCAA CCTGTTGCAA TAACTTTNCT GAAATATTAA 300  
CACATTAATA AAACCTTTCT TAAACAAA 328

SEQ ID NO:1820

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02069

SEQUENCE DESCRIPTION:

GATCAGAGAA GAGGCTACTG GGGGAGAATT CAGTGCCCCC TTCGCCCTCT AGGGNGCAGA 60  
CCTCCACTGC CATTGTCCTG TNAGCCGCCA AANACCCAC GGGGTGCCCG CATGTCCCTG 120  
TCTANNNGCA GCCCAGGGCC CCCACTCCTG GCTCCTNACA CTTGCCTCCC CTATGGCCGC 180  
TCTCCAGACC CTCCTCCTTT CTCTCCCCA CATCCGCACC TGCTGTTCCC ACTCTGGGGT 240  
TCTCAAGTCC ATGAACAGAT ATTGTTGCAT TTTCCACAAT GCTGATTAAA CATAATAAAC 300  
AATCCAGAAA AGCAGTTTGT CCCAGAAA 328

SEQ ID NO:1821

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02070

SEQUENCE DESCRIPTION:

GATCCAAAAG CCAGTCTCAG GAGTTTACCC CTGGGATGGG GGATGCATCT NCACCTGACT 60  
TTGGGGCCAC GTGCCCTGTG GCACCCAGC TCACTGGGAG TCTCAGGAGG GATAACCGGA 120  
TTTNTGCTCT TTCCCCTGTC ACTCCACAT CACACAGAAA AATGGCATTCT CTCTCTGTCT 180  
CTCCCTGGCA TGGAGAGGGC AGACTGTGCA CATTTCACTA GGGTCCAAAT ACAGAAGGGC 240  
CCAGGGCCCA GGGGCTTGCA GCTTCGTGAG GGGTCTCTGG CCCAGTTTCC AATGAATAAA 300  
GTTCTCTTGA CAGCTCAA 319

SEQ ID NO:1822

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02071

## SEQUENCE DESCRIPTION:

GATCATCAGA TGGTCGAGTA CTCTTGGAAT GTCTCTTTGC TGTTTACTGT GGCCTCTTTA 60  
 CAATGGTGAG ACTTATTTCT ACCCTCTACT TTCCACTATT ATTNTTTTCC CCTATTGGAT 120  
 AATACTAGTC TGAGCAGCCC TAATACTAGA TGTACCTAAA CAGAGATACA AGCCAAGTCA 180  
 TTGTTCACTG TAGTCATTTT TTAGTATCTG TTTATATTTT GTCACACATC AGAATGTATA 240  
 TTTTATAGAG CATGTGTTTG TCTACTNGTT TGTCTACTAT AATATGTCTT TAATAAAGCT 300  
 AAAANCATTC TGAAA 315

SEQ ID NO:1823

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02072

## SEQUENCE DESCRIPTION:

GATCGCTTTT TTGCCGCTCA TATTGAATG CATTGGGTTT CCTGGACCAG CTATTTGCAC 60  
 AAGACTAGGG GGAGGTTGAG GGTGGCATA GCAGGCAGGG GCTGGGATAG ACATTCAACC 120  
 TAGCTNNNT TCATGCTCTT AAGGCTTTAT TTTTCTAGAA TGCCAAGAAA CCAACTTTCT 180  
 TTAAACATGA CTCATCTCTT CGATTTTCTT GTATAGGTCT TCCTCCCACC CCAAATCTAC 240  
 ACTTGTTAGA AACAGAATAA TTACCTTTGC TTAATCCATT ATCAACACTT GGAGATAGAG 300  
 ACTTTACACT TCAGN 315

SEQ ID NO:1824

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02073

## SEQUENCE DESCRIPTION:

GATCGAAAAG GGACCCTGCT TCCAATTTCC CTCTTCCATT CCTCGAGCTA CTCCAGGGCT 60  
 TAGAAGAATG CTCTTGCTCT GTGGGTCCAG TGTGTCTGT CATCCATTTA AGTGTTCCTA 120  
 CTTTCAAGTG ACAATCCTCT CTTGGCCCT GCCATAGGGC AGAGCATGTN TGGCATAGCA 180  
 GCCTGACTTT NATGCCCTAA TCTTGAGTTG AGGAAATATA TGCACAGGAG TCAAAGAGAT 240  
 GTCTTTATAT CTGACTGTAT ATAAATGAAG TTTTNGTT TTTTNGTT TCCTTTTGG 300  
 TGCAATAAAG TTTGTTTGG CAGAAGGAGA AA 332

SEQ ID NO:1825

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02074

## SEQUENCE DESCRIPTION:

GATCAAGGCG CGGACGCTAT CTACGACCAC ATCAACGAGG GGAAGCTGTG GAAACACATC 60  
 AAGCACAAGT ATGAGAACAA GTAGTTCCTT GGAGGCCCC ATCCAGGCCA GAAGGACCAG 120  
 GTCCACCCAG CAGCTGTTTG CCCAGAGCTG GAGCCTCAGC TTGAAGATGA TGCTCAAGGT 180  
 ACTCTTCATG GACCACCATT CGCTGTTGGC AAGAAACGGC TTTACTTACA AAACAGACTC 240  
 TTTACCTTCT GCTGTGTTTG AAGTATGTTT AGTCAGCATG CTCAGGAAAT AAATGTGAAT 300

TGCCCTTGAA A

311

SEQ ID NO:1826

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02075

SEQUENCE DESCRIPTION:

GATCTAGTGT TTGGAACGGA CGTTACCTGC TGGTTTGTGC ACAACAGTGG AAAAGGATTC 60  
ATTGACGGGC ATTACAAGGA TTACTTCGTG CCTNAGCTCT ACAGCTTTCT CAAACGGCCT 120  
TAAAGGTTTA TAGTTTGGGA AATTATATAT TATTATACAT CTTCCCCCTG TCACTTTTCG 180  
AGATATTCTT CGGTNCCNAT AATTAAAAATG AACCAGATAT CAGGGTGGTT AATTAAAAATG 240  
AACCAGATAT CAGGGTGGTT TATAAAGCCT GTAAACACAC CTNAGAAAAT ANACATTTTA 300  
CANATGAAA 309

SEQ ID NO:1827

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02076

SEQUENCE DESCRIPTION:

GATCATGAAT AACTGATTAG TAAGTCTTGC CTATATTTTC CTGATAGCAT ATGACAAATG 60  
TTTCTAAGGT AACAAGATGA GAACAGATAA AGATTGTGTG GTGTTTGGGA TTTGGAGAGA 120  
AATATTTTAA TTTTAAATG CAGTTACAAA TTATAATGTA TTCATATTG TACTTTCTGT 180  
TAAAATGCAT GATTGCAGAA TTGTTTAGAT TTTGTGTTTA TTCTTGATGA AAAGCTTTGT 240  
TTGTTCTTGT TTTTAAGTTT GCACTCAAAT CTTAAGAAAT AAATCCACCC ATGTTATCAA 300  
A 301

SEQ ID NO:1828

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02077

SEQUENCE DESCRIPTION:

GATCAGTGAA CTCTGGTTTT AAGATAATCT GAAACAAGGT CCTTGGGAGT AATAAAATTG 60  
GTCACATTCT GTAAAGCACA TTCTGTTTAG GAATCAACTT ATCTCAAATA GTAACTCGGG 120  
GCCTAACTAT ATGAGATGGC TGAAAAAATA CCACATCGTC TGTTTTCCT AGGTGATGCC 180  
AAAAATTTTT GCTTTATGTA TATTACAGTT CTTTTTAAAA CACTGGAAGA CTCATGTAA 240  
ACTCTAATTG TGAAGGCAGA ATCTNTGCTA ATTTTTCAGA TTAATTTCT CTTTGAAA 298

SEQ ID NO:1829

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02078

## SEQUENCE DESCRIPTION:

GATCCCTTAT CCAACATGGT TCTAACCTTC AGTACTAAAG AAGATGCAGT TTCCTTTGCA 60  
 GAAAAAATG GATGGAGCTA TGNCATTGAA GAGAGGAAGG TTCCAAAACC CAAGTCCAAG 120  
 TCTTATGGTG CAAACTTTTC TTGGAACAAA AGAACAAGAG TATCCACAAA ATAGGTTGGC 180  
 ACTGACTATA TCTCTGCTTG ACTGTGAATA AAGTCAGCTG TNCAGTATTT ATAGTCCATG 240  
 TATAATAAAT ACATCTCTTA ATCTCCTAAT AAATTGGACC TTAAACTAC AAA 293

SEQ ID NO:1830

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02079

## SEQUENCE DESCRIPTION:

GATCANNATT TGAAGAGGNT TTCTAGAAAT TNGGGGTAAG AAGTACTACC AAAATGTAAC 60  
 TNCTAATCAA GGGTGATGCA CAGCAAAAGC AATGGACCCC ATCCCTCTAA AGCCTGCCCT 120  
 CCTTTGCCCTT CAACTGTATA TGCTGGGTAT TTCATTTGTN TTTTATTTT GGAGAAAGCG 180  
 NTTTTAACTG CAACTTTCTA TAATGCCAAA NTGACACATC TGTGCAATAG AATGATGTCT 240  
 GCTCTAGGGA AACCTTCAA NGCANTAAAA ATGCTGTNTT GAAATGCCAA A 291

SEQ ID NO:1831

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02080

## SEQUENCE DESCRIPTION:

GATCTGGGCC TGAATAAGGG TTATCGAATG GTGGTGAATG AAGGTTTCTA TGGTGGACAG 60  
 TCTGTCTATC ACGTTCATCT CCATGTTCTN GGAGGTCGGC AAATGCATTG GCCTCCTGGT 120  
 TAAGCACGTT TTGGGGATAA TTTTCTCTTC TTTAGGCAAT GATTAAGTTA GGCAATTTCC 180  
 AGTATGTAA GTAACACACT TATTTTGGCC TGTNTATGGA GAGATTCAAG AAATAATTTT 240  
 AAAACCGCAT ACATAATAAA AGACATTGTT GCATGGCTTA TAGTCAA 288

SEQ ID NO:1832

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02081

## SEQUENCE DESCRIPTION:

GATCCAGCCT TAATNTTTT CTGACATCCT AGTAATAGCA GACCCTGCAC AAAGTGGATA 60  
 TCAGACTTAA TACTGTNAGG AGACAAAATA ATGAGAATAG TTTTACCAA GATAATNAAA 120  
 TCTCGCATCA TGTCTGCATT TTACCATAGA TTGGAGTGCA TCCTTAGGAA ACTGAATGTA 180  
 AAAAAACCC AGGACATTTT TGGAAATTGT ATGCTCTCTA GCAACTTTGT GTGAATTTT 240  
 ATACAAACAC TGTTCTATGA GTTATATAAA ATGTTATAAA ACTAGAAA 288

SEQ ID NO:1833

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02082

SEQUENCE DESCRIPTION:

GATCCTGAGA ACTTCAGGCT CCTGGGCAAC GTGCTGGTCT GTGTGCTGGC CNNNCACTTT 60  
GGCAAAGAAT TCACCCACCC AGTGCAGGCT GCCTATNAGA AAGTGGTGGC TGGTGTGGCT 120  
AATGCCCTGG CCCACAAGTA TCACTAAGCT CGCTTTCTTG CTGTCCAATT TCTATTAAAG 180  
GTTCCCTTGT TCCCTAAGTC CAACTACTAA ACTGGGGGAT ATTATGAAGG GCCTTGAGCA 240  
TCTGGATTCT GCCTAATAAA AAACATTAT TTTCATTGCA AGAAA 285

SEQ ID NO:1834

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02084

SEQUENCE DESCRIPTION:

GATCTCATGG GCTTTCCTTG GAGGAAAGGT TTTTGTGTT GTTTTTTTT NAAGAACTTG 60  
AAACTTGTA ACAAGAGATG TCTGTAGCTT TTTNCCCAT CTGTAGTGTA TGTNAAGATT 120  
NCAAAACCTG AGAGCACTTT TCCTTTGTTT AGAATTATGA GAAAGGCACT AGATGACTTN 180  
AGGATTNCA TTTNCCCTT TATTGCCTCA TTTCTGTGA CGCCTGTGTG GGGAGGGAAA 240  
TCTGTTTATT TTTNCTACA AATAAAAAGC TAAGATTCTA AA 282

SEQ ID NO:1835

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02085

SEQUENCE DESCRIPTION:

GATCTTAAGC TTTGATAAGA GCTGTGCTGT GGCTGAGTAT GGTGTGTATG TGAAGGTGAC 60  
TTCCATCCAG GACTGGGTTC AGAAGACCAT AGCTGAGAAC TAATGCAAGG CTGGCCGGAA 120  
GCCCTTGCTT GAAAGCAAGN CTTAGCCTG GAAGAGGGCA AAGTGGACGG GAGTGGACAG 180  
GAGTNGATGC GATAAGATNN GGTTTGAAGC TGATGGGTGC CAGCCCTGCA TTGCTGAGTC 240  
AATCAATAAA GAGCTTTCTT TTGACCCAAA AAAANTAAA 279

SEQ ID NO:1836

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02086

SEQUENCE DESCRIPTION:

GATCCATAGT GCTACCTGCA CCTCTGGATT CTGGATTCAC AGACCAAGTC CAAGCCCGTT 60  
CTTACGTCGC CATAAAGGCC CCCGAACGGC ATTCTCGGTA CTTCTGTTTG TTTTGTACA 120  
TTTNATTAGA AAGGACTGTA AAATAGCCAC TTAGACACTT TACCTCTTCA GTATGCAAAT 180  
GTAAATAAAT TGTAATATAG GAAATCTTTT GTTTTAATAT AAGAATGAGC CTGTCCAATT 240  
TCTGCTGTAC ATTATTAATA GTTTTATTTC AAAAA 275

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SEQ ID NO:1837

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02087

SEQUENCE DESCRIPTION:

GATCCGAAGA GGAACCTCTG GTCATCTTTA ACAAGAAAAT CAGCAAGAAC CCTACCTTTA 60  
 AGTTATTAAA GGACAAAGTC AAGCTTGTGA AATGAACATT TGTGTATTTA AAANTTGAAT 120  
 CCATTCTGCT GACTTCTTAC TTCTACTGCT GTTTATAAAA TGTGTAATGA ATTCTAACAA 180  
 CTCAAAATTT GCTTTTGTAC GCNGTATTTT TANGTTANGN AAATATATTT NTGGTATAAC 240  
 TTTTATGCGA NAAATAAAAT ATATTCTGN 269

SEQ ID NO:1838

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02088

SEQUENCE DESCRIPTION:

GATCTCATTG TTTATTAACC TGTATTCTGT TTACATGTCT TTAACACAGT GGTTCCTAAA 60  
 TTGTAAGCTC AGGTTCAAAG TGTTGGTAAT GCCTGATTCA CAACTTTGAG AAGGTAGCAC 120  
 TGGAGAGAAT TGGAATGGGT GGCGGTAATT GGTGATACTT CTTTGAATGT AGATTTCCAA 180  
 TCACATCTTT AGTGTCTGAA TATATCCAAA TGTTTATAGGA TGTATGTTAC TTCTTAGAGA 240  
 GAAATAAAGC ATTTTGGGA AGAATAAA 268

SEQ ID NO:1839

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02089

SEQUENCE DESCRIPTION:

GATCTATCTA AATATATTAA GTAAAATTAC ACCATTCACT TGTTGGGAAA ATAATCTTTG 60  
 GTTTGGAAGA TATTACATA ATGGGCATCT TAGAATCATA AATCACATGA AATGAGAGAC 120  
 AATGCAATAT TGTATAATTC CTGGATGATG CAATTGTTTT AATTGANNTT TCAAGTGCCA 180  
 TTATAAAGTT TTAATAATTA TCAATATGAG TTGGTGCCCTA ATTTTNNNTT TCCTAAAAAT 240  
 AAAATTTTTC CTTTTATGA GTAAA 265

SEQ ID NO:1840

SEQUENCE LENGTH:261

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02090

SEQUENCE DESCRIPTION:

GATCATAAAA CCTTCATTCC ATAGGTACCC TTTATCCTCA CAGATACAGA GACACCAAGA 60  
 AGAATCTGGA CAAATAGGAC TTGCTAAGTT CTCCACAGTT TATTACCATT AGATTATGTC 120

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CTTTTGTNCT CTGATTATAC TTCTGCATAA GACTGTACAT AAAANTACAC AAGTTTTCCT 180  
 ATTTNTTTTT TGTCTTCATT TCTGAAGATT CCTGTCATGT AAAACTTACA GTAAATAAAT 240  
 GTGTGTGCTT TTNTCAATAA A 261

SEQ ID NO:1841

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02091

SEQUENCE DESCRIPTION:

GATCAGGTTA GGGCGAGCGC TACCTCTCCA GCCTCAGCTC TCAGTTGCAG CCCTGCTNAT 60  
 GCCTGCTTGG ACTTGGCCCC TGCCACCTCC NGCCTCAGGT GTCCGCTATC CACCAAAAGG 120  
 GCTCCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT GGCCCTGCCA 180  
 TGCTCTCCAA ACCACTTTTT GCAGCTTTTT CTAGTTCAAG TTCACCAGAC TCTATAAATA 240  
 AAACCGACA GACCATGAAC AAA 263

SEQ ID NO:1842

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02092

SEQUENCE DESCRIPTION:

GATCAGAAAG AAACCTTTTG TAGCAATATC AAGAATCTAG TTTCATCTGA GAACTTCTGA 60  
 TTAGCTCTCA GTCTTCAGCT CTATTTATCT TAGGAGTTTA ATTTGCCCTT CTCTCCCAT 120  
 CTTCCCTCAG TTCCATAAAA ACCTTCATTA CACATAAAGA TACACGTGGG GGTCAGTGAA 180  
 TCTGCTTNAN NATCCTGAAA GTTTCTGGGG CTTAAGATTC CAGACTCTGA TTCATTAAAC 240  
 TATAGTCACC CGTGTCTGT GAAA 264

SEQ ID NO:1843

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02093

SEQUENCE DESCRIPTION:

GATCAAATGT CACACAGCAG TTTCCTTGCA ACACTTTCAG CTCCCCATGC TCCAGAATAC 60  
 CCACCAAGA AAATAATAGG CTTTAAACA ATATCGGCTC CTCATCCAAA GAACAACTGC 120  
 TGATTGAAAC ACCTCATTAG CTGAGTGTAG AGAAGTGCAT CTTATGAAAC AGTCTTAGCA 180  
 GTGGTAGGTT GGGAAGGAGA TAGCTGCAAC CAAAAAGAA ATANATATTC TATAACCTT 240  
 CAGAAA 246

SEQ ID NO:1844

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02094

## SEQUENCE DESCRIPTION:

GATCTGTGTG CATGNTGTG TTTGTGTATA TATACATATC TAGGGCTAGT ACTTAGTTTC 60  
 ACACCCGGGA GCTGGGAGAA AAAACCTGTA CAGTTGTCTT TCTCTNATTT TNAATAAAAT 120  
 AGAAAAATCG CGCACTTGCG GTCCCCCCCC CACCCCCTTT TTAAACAAG TGTTACTNNN 180  
 NCCGGGAAAA TTTNCTGTC TTTGTAATTT TAAAACTTA AAATAAATTG GAAAAGGGAG 240  
 AAA 243

SEQ ID NO:1845

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02095

## SEQUENCE DESCRIPTION:

GATCTAGTGA ACATTCGACC TCCATTACGG AGAGTTTCCT ATGTTTCACT GTGCAAATAT 60  
 ATCTGCTATT CTCCATACTC TGTAACAGTT GCATTGACTG TCACATAATG CTCATACTTA 120  
 TCTAATGTTG AGTTATTAAT ATGTTATTAT TAAATAGAGA AATATGATTT GTGTATTATA 180  
 ATTCAAAGGC ATTTCTTTTC TGCATGTTCT AAATAAAAAG CATTATTATT TGCTGAGAAA 240

SEQ ID NO:1846

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02096

## SEQUENCE DESCRIPTION:

GATCTAAGCA GCGTTCCAC AGCCCCCTCT AGATTCTTGG AGTTCCGCAG AGCTTACTAT 60  
 ACGCGGTCTG TCCTAATCTT TGTGGTGTTT GCTATCTCTT GTGTCAAATC TGGTGAACGC 120  
 TACGCTTACA TATATTGTCT TTGTGCTGCT GTNTGACAAA CGCAATGCAA AAACAATCCT 180  
 CTTTCTCTCT CTTAATGCAT GATACAGAAT AATAATAAGA NTTTCATCTT TAAATGAAA 239

SEQ ID NO:1847

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02097

## SEQUENCE DESCRIPTION:

GATCCATCCT CTCTCCTAGC TGAGTAAATC CGGGTCTCTA GGATGCCAGA GCAGCGCACA 60  
 CAAGCTGGGA AATCCTCAGG GCTCCTACCA GCAGGACTGC CTCGCTGCCC CACCTCCCGC 120  
 TCCTTGGCCT GTCCCCAGAT TCCTTCCCTG GTTGACTTGA CTCATGCTTG TTCACTTTT 180  
 ACATGGAATT TCCCAGTTAT GAAATTAATA AAAATCAATG GTTTCACAA A 231

SEQ ID NO:1848

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02098



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## SEQUENCE DESCRIPTION:

GATCCAAAAT GCTGACAGGT TCAAACAAAA TTGGAATTGA AAATCAGAGT GCGTTCAAGA 60  
 GTATCAAACA ATACTATCTT GTTACTTGCT TATTACCTTA GTAGACTGGA AGCAACACTT 120  
 CACACAAAAA AAGGGTTTGG ATGTAATTC GGATAAGAAG AGATGTTTCT GTAAAGTCTT 180  
 TCCTGAGANG CATATTATTT GAGAAAAACA CATATTTCTG TTTTAGTAA A 231

SEQ ID NO:1849

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02099

## SEQUENCE DESCRIPTION:

GATCTACCAT GTAAATGTT GTAGAGATAG AGCCATATAA CGTCACGTTT CAAAACACTAGC 60  
 TCTACAGTTT TGCTTCTCCT ATTAGCCATA TGATAATTGG GCTATGTAGT ATCAATATTT 120  
 ACTTTAATCA CAAAGGATGG TTTCTTGAAA TAATTTGTAT TGATTGAGGC CTATGAACTG 180  
 ACCTGAATTG GAAAGGATGT GATTAATATA AATAATAGCA GATATAAA 228

SEQ ID NO:1850

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02100

## SEQUENCE DESCRIPTION:

GATCTACCGG CCCCGCTGGG GTGCCCTTGG GGACTACCTC TCCTTCACCA TACCCCTGGG 60  
 CACCCCTGA CAACTTCTGC ACATACTGGG GCCCTGCTTA TTNTCCCAGG ACAGGCTCCT 120  
 TAAAGCAGAG GAGCCNGTNC TGGGAGCCCC TTCTCAAACCT CCTAAGACTT GTTTTCATGT 180  
 CCCACGTTCT CTGCTGACAT CCCCCAATAA AGGACCCTAA CTTTNGGNNN TNNAAG 236

SEQ ID NO:1851

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02101

## SEQUENCE DESCRIPTION:

GATCTATGGT TTCTGCCAC CCAGGATAGT CTTGTCTCTA GACAATGTAT TGATGATGCA 60  
 AATGTTCTGG AACTAAATAG TGGTGATGGT GGCACAACAC TGTGAATGTA CTAAATGTCA 120  
 CTGATTTGTA CGTATTTAAT ATGAATTAAG TGTAAAAATG GTGAATTATA TTTATGTATA 180  
 TTTNACCATA ATAAAAATAT GCATTGGAAG ATGCATTTTT TGTGAAA 227

SEQ ID NO:1852

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02102

## SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTTTGGA CCAGTTTCTA GCAAAGTTGT GTTTGAAAGA TACTCTATTA AAGAAGACTG 60  
 TGGAAATCTTT TTATCGGTGC CCATTATATC CTTAAGTTTG GATATTTAGC TGACCTTCGC 120  
 TTTAACATAG GTCTAATTTA TTTGCCGTGT CATTTTCCAT ACAAATCAGT TGATTAAAA 180  
 AAGTTCATTT CTCATACTGT GCATTAAAT AAAAATTTGA ACAATTAAA 229

SEQ ID NO:1853

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02103

SEQUENCE DESCRIPTION:

GATCTCCTGT TTTTTCAGG CTCCTAAAGT AACATCAGCC ATNTTNNAGA TTGGTTCTGT 60  
 TTTCGTACCT TCCCACTGGC CTCAAGTGAG CCAAGAAACA CTGCCTGCCC TCTGTCTGTC 120  
 TTCTCCTAAT TCTGCAGGTG GAGGTTGCTA GTCTAGTTTC CTTTTTGAGA TACTATTTTC 180  
 ATTTTGTGA GCCTCTTGT AATAAAATGG TACATTTCTA TAAA 224

SEQ ID NO:1854

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02104

SEQUENCE DESCRIPTION:

GATCAAGGCC GGACCCACT GCCCACTGC CCAACTGATA GCCACGCTGA NNGAATGGAA 60  
 GGAAAATTG CTTGGACCTG CAAGCCCCGC TGTACAAGAA AATAATTAAG AAACCTTTGG 120  
 AGAGTTAGCT ACTAGCTGCC TACGTGTGN CATTTGCTAT ATAGCATACT TCTTTTTTCC 180  
 AGTTTCAATC TAACTGTGAA AGAACTTCTG ATATTTTGTG TTN 223

SEQ ID NO:1855

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02105

SEQUENCE DESCRIPTION:

GATCCTAGTA ATTGCCTAGA AATATCTTTC TCTTACCTGT TATTTATCAA TTTTCCCAG 60  
 TATTTTATA CGGAAAAAT TGTATTGAAA AACTTAGTA TGCAGTTGAT AAGAGGAATT 120  
 TGGTATAATT ATGGTGGGTG ATTATTTTTT ATACTGTATG TGCCAAAGCT TTACTACTGT 180  
 GGAAAGACAA CTGTTTAAAT AAAAGATTGA CATTCCAAAA AAACAAA 227

SEQ ID NO:1856

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02106

SEQUENCE DESCRIPTION:

GATCTATACA AAGTCTTTGA GAGGTGTTAA ATATGGTTAT TTATGCACTG TGGGATGTGT 60

EP 0 679 716 A1

TCTTCTTTCT CTGTATTCCG ATACAAAGTG TTGTATCAAA GTGTGATATA CAANGTGTAC 120  
CAACATAAGT GTTGGTAGCA CNTAAGACTT ATACTTGCCT TCTGATAGTA TTCCTTTATA 180  
CACAGTGGAT TGATTATAAA TAAATAGATG TGTCTTAAA 219

SEQ ID NO:1857  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02107

SEQUENCE DESCRIPTION:  
GATCAAGAAA GACAAAAAGC CAGCCTGCAG CAAGCACTTT GGAGAGCAAA TCTGNAAAGA 60  
GAGTAACGCG GAGTGTCAAG AGGTGTGCAG AAAATCCAAA GAAGGCTGAG GACAATGTGT 120  
GTGTCAAGAA AATAAGAACC AGAAGTCATA GGGACAGTGA AGATATTTGA CAGAAAAATC 180  
GAACTGGGAA AAATATAATA AAGTTAGTTT TGTGATAAA 219

SEQ ID NO:1858  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02108

SEQUENCE DESCRIPTION:  
GATCTGTCGG AACCAGGACA CAAAAGCAGC AAGAAGCGGG GAGAGAGAGG GATAGAAAAC 60  
AAGCGCAGGA GAGCCTGCGA ACGCAAAANT GAATGAGGGC TTTTGTGGC TGGGGATGGG 120  
TTTTGGTTTT GGGGTTTTTT TTTTNAATT GTTTGACTT CGTACAGGGT ACTTTTTCCC 180  
AACCTCATCT NTCAGAAATC CATGTGGGNT TCCTGGAAA 219

SEQ ID NO:1859  
SEQUENCE LENGTH:217  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02110

SEQUENCE DESCRIPTION:  
GATCTGAAGA AATTACCAA CATTAAAATG AGANAAATTT GCGCTAATGA TGCAATTCCC 60  
AAGACGTGCA AGAGGAAAAC TATTATAACT GTAGACCAAG ATTTGGGGGA ATTGGAAC TA 120  
AACGATGAAT CAAGTGATTC AGATGAGGAA ATGACTGCAG TGGCCTAATT GTCTTCACTT 180  
GAATTGAAAA TAAATAATTT GAGAGCTTCA AATTAAA 217

SEQ ID NO:1860  
SEQUENCE LENGTH:216  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02111

SEQUENCE DESCRIPTION:  
GATCCATTTT TTTAAAATAC TGACATATAG AGTTGTACCT TATATAGAAT ATAGTTGTAT 60  
CTTGAAGTCA ACATATTAAA TTATTCTCAA AATTATGTAT TTNCAGATTG TACTTGTAAG 120

TTTCAAAAGAA AAATTACCGT CTTTTCATAT TGACCTGGAA ACTAAATAGG ATGTGATTCA 180  
GCTACATTAA TTTCTTAATA CAATCTAGGA AAGAAA 216

SEQ ID NO:1861  
SEQUENCE LENGTH:213  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02112

SEQUENCE DESCRIPTION:

GATCCTTTTC TTGAAAGAAT AACAGAAAAT GTGTCATCCA TTTTTCAGAA TATAACCACT 60  
CAAGCTACTG GCACATAGTG AAAGATTACT TCTGACATTC CATTNCTCTT CTTTGTGAAA 120  
TTAGTATNGT AATTAAATGT ACTTTTGTAA AATTAATAGA ATTATTTAAA TTACAGTATA 180  
TGTNGCAAAA TATATCACTT TTGATACAAT AAA 213

SEQ ID NO:1862  
SEQUENCE LENGTH:210  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02113

SEQUENCE DESCRIPTION:

GATCTATCTC ATCAAACAAC ACAATGAAGA TATTTTAGAG TACAAAAGAA GAAATGGGCT 60  
GGAATAAACT TTGAAACAC TAATGTAGTA TGCTCCGTAT AGTGATTGTA GCTGTTCCTC 120  
TGGATTACCC ATCTGTTGAG TTGTAAATGT GNGANAAAAA GTTATATGTG AATATATATC 180  
AAGCCAGCAT TTGTATTTTG CATCATTAAT 210

SEQ ID NO:1863  
SEQUENCE LENGTH:209  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02115

SEQUENCE DESCRIPTION:

GATCGGGGCT GCCAGAGGGN TAGAAGCGAG GGCACCAGCA GTTGTGGGTG GGGAGCAANG 60  
GAAGAGAGAA ACTCTTCAGC GAATCCTTCT AGTACTAGTG GAGAGTTTGA CTGTGAATTA 120  
ATTTTATGCC ATAAAAGACC AACCAGTTC TGTTTNNNNC TGTAGCATCT TGAAGAAGAA 180  
AATTATAATA AAGCCCCAAA ATTAAGAAA 209

SEQ ID NO:1864  
SEQUENCE LENGTH:208  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02116

SEQUENCE DESCRIPTION:

GATCTGGAGC AACAGCTAGG AAATATCATT AATTCTGCTC TTCAGAGATG TTAAAAATAA 60  
ATTACACGTG GGAGCTTTCC AAAGAAATGG AAATTGATGG GAAATTATTT GTCAAGCAAA 120  
TGTTTAAAAA CCAAATGAGA ACTAAATAAA GTGTTGAACA TCAACTGGGG AATTGAAGCC 180

AATAAACCTT CCTTCTTAAC CATTCAAA

208

SEQ ID NO:1865

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02117

SEQUENCE DESCRIPTION:

GATCTATACT TAGAATGCAA TGTNGACAGA GGGCAGTTAA AATATCCAAG ATGTATTCCA 60  
AGACAAAGCA AACAAACAAC TGGAAGTGGT AATCAATTCA ACAGGCCTTC TGAATTNTCT 120  
GAAGCNAAAG CAACGTTTGC CATNNGATAT TTGTGACACT TTGGCAAATG GAAAAATAAA 180  
CCAATTATA CGTGCAATAA A 201

SEQ ID NO:1866

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02118

SEQUENCE DESCRIPTION:

GATCATGAAG GTATCCACAC TTCCCTTGC ATTCCTTCT TAACTCTCTG TTACACGTCA 60  
TTGAAACTAC ACTTTTTTGG TCTGTTTTG TGCTAGACTG TAAGTTCCTT GGGGGCAGGG 120  
CCTTTGTCTG TCTCATCTCT GTATTCCCAA ATGCCTAACA GTACAGAGCC ATGACTCAAT 180  
AAATACATGT TAAATGGAAA 200

SEQ ID NO:1867

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02119

SEQUENCE DESCRIPTION:

GATCACATTT TGAAATGCCT AAAAGACTTT ATTGTTCTAA TTATCCAGAT GTACCTTTGT 60  
AAAATAGCTC TTTTATGAAT TAGCTGATAA GGCTGTATGT TTCTGGAACA AAATATTGGT 120  
CATCTAAAAN CTTTCTGTTT NCTGGGGTCT GGGAAAATAG AAAATAAGAT TTCAAATATT 180  
AAATAAGCTT AANGGCACCA AA 202

SEQ ID NO:1868

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02120

SEQUENCE DESCRIPTION:

GATCAGGCCC TTCTTCCCAC AGCAATAGTC CCCAATACGT AGATTTTTCG TCTTCTGTAT 60  
GTGACAACAT TTTTGTACAT TATGTTATTG GAATTNCTT TCATACATTA TATTCCTCTA 120  
AAACTCTCAA GCAGACGTGA GTGTGACTTT TTGAAAAAAG TATAGGATAA ATTACATTA 180  
AATAGCACAT GATTTTCAAA 200

SEQ ID NO:1869

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02121

SEQUENCE DESCRIPTION:

GATCTNTNTG TTCATTGTAT TCTTTTTNTC TCAAGAGTTC CATTTAATGG AAATAAAACG 60  
GTATAATTAA TAATTGTCTA GGGGGGAAAA ATGAAGCAAA TNTCATTGGA TATTTTTAAA 120  
GGTCTCCACA GAGTTTATGC CATATTGGAA TTTTGTGTA TAATTGTCAA ATAAATATTT 180  
TGGTGANGCA TAAA 194

SEQ ID NO:1870

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02122

SEQUENCE DESCRIPTION:

GATCCAATAC TATTAGTTT ATTATTGAAA TTGGAAGGAT TCATTGAGCA GCATAGAAGT 60  
TTGTTTACAT GTTACTTTGA GATGCTAGGT ATTTGTGGAA TTAAAAAGAA TCAGGCTCTT 120  
TTGTACTNAN TTTTAAATC TGTGATGCTT NTCAAATTA ATTCATAATA AATTGATGCA 180  
ATTCATAAA 190

SEQ ID NO:1871

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02123

SEQUENCE DESCRIPTION:

GATCGAACAG TTTTGAAGCT ACTGTGTGTG TGAATGAACA CTCTTGCTTT ATTCCAGAAT 60  
GCTGTACATC TATTTTGGAT TGTATATTGT GTTTGTGTAT TTACGCTTGG ATTCANNAGT 120  
AACTTCTTAT GGAATTNATT TGCATTGAAC ACAAACTGTA AATAAAAAGA AATGGCTGAA 180  
AGAGCAAA 188

SEQ ID NO:1872

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02124

SEQUENCE DESCRIPTION:

GATCCTATTT ATTTGTTTGG GCCATCTTTA ATTTCTTTCA GCAGTGTTTT GTAGTTTCCA 60  
TTAGAGATTT TCCATGTCNT TTGTTAAGTT TATTCCTAGG TATTTTATTT TTTATGGTAT 120  
TNTATTATAA TCCTNNGATG TCTATTATAT AGAAATATAA TTNATTTTNG TTATTGACTG 180  
NNNN 184

SEQ ID NO:1873

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02126

SEQUENCE DESCRIPTION:

GATCCAAGTN CTGACTTTTC CCCCTGACAG CTGTGTGACC TTCGTGAAGT CGCCAAACCT 60  
 CAAATGAGCC CCAGTCATTG CTAGTAAGAC CTGCCTTTGA GTTGGTATGA TGTTCAAGTT 120  
 AGATAACAAA ATGTTTATAC CCATTAGAAC AGAGAATAAA TAGAACTACA TTTCTTGCAA 180  
 A 181

SEQ ID NO:1874

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02127

SEQUENCE DESCRIPTION:

GATCTTAAAT TTTCTCATCT CAAAAAATA TGTAAGTGA TAGATATGTT AAATAGCTNN 60  
 TATGTATTTT GCAATGTGTA GTGTATATAT ATAAACATCA CACAGTACAC CATAAATATA 120  
 TTTAATTTTT GTCAATTACT CTTTAAACCT TAATAAAGTT GATAAAACAT TCTTTTTTAA 180  
 A 181

SEQ ID NO:1875

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02128

SEQUENCE DESCRIPTION:

GATCAGGTTA GCAAATGATG TAAAAGAAGC TTTATTGTCT AGTTGTTTTT TTTCCCCCAA 60  
 GACAAAGGCA AGTTCCCTA AGTTTGAGTT GATAGTTATT AAAAAGAAAA CAAAACAAAA 120  
 AAAAGGCAAG GCACAACAAA AAAATATCCT GGGCAATAAA AAAANTATTT TAAACCAA 179

SEQ ID NO:1876

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02129

SEQUENCE DESCRIPTION:

GATCCGGGAG CACACCGTTT CCTGATTGCT CAGGGACTCA TCTTCCCTC CTTGGTGATT 60  
 CCGCAGTGAG AGAGTGGCTG GGGCATGGAA GGCAAGATTG TGTCCTATC CCCCAGTGCG 120  
 GCCAGCTCCG CGCCAGGATG GCGANGGAAC TCAATAAAGT GCTTTGAAAA TGCTGAAA 178

SEQ ID NO:1877

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02130

SEQUENCE DESCRIPTION:

5 GATCATTCTC CGAAAGCAAC TCCTGACAAT TAAGCATTTT TTTCTCCAAA TACAAAGTAT 60  
ATTCTCTTTA TTGGAAAATA AATTAATAAA TATATTCTGT ATTTTNNCTC TCCGTGAAAA 120  
ACAAAAGAGC CTCTGACATT ACTGTCTCTC AGTGTGTTGGT CAGATTGAGG CTTN 175

SEQ ID NO:1878

10 SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02131

15 SEQUENCE DESCRIPTION:

GATCAATCCT TCTTATGTTT GCTTTAATGT GTATTGAAGA AAAGCACTTT TTAAAAAGTA 60  
CTCTTTAAGA GTGAAATAAT TAAAAACCAC TGAACATTG CTTTGTTTTT TAAAGTTGTT 120  
CACATATATG TAATTTAGCA GTCCAAAGAA CAAGAAATTG TTTCTTTTCA AA 172

20 SEQ ID NO:1879

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS02132

SEQUENCE DESCRIPTION:

30 GATCTGATTG TTAAAAAGTA CACAGCACCT CCCTCCCCAC TCTCTCTTGC TCCTGCTTTC 60  
ATCAAGTGAA AACTCCCTGA GGCCTCCTCA GAAGCTGAGT AGAGGCCAGC ACTATGCTTC 120  
CTGTACAGCC TGTGGAACCA TGAGGCAATT AAACCTCTTT TCTTTATAAA 170

SEQ ID NO:1880

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS02133

SEQUENCE DESCRIPTION:

40 GATCAGAAAA ATTCATCTTT TTTAACCCTG CCCTAATTTT TCTTGAGGAA TTAAATAGAG 60  
CAAACATTTT TCAGGTTATG CTTACAATAA AATATACTTA AGAAAAATGAC TGAAGATGTA 120  
TGTTTTTGAA TGTTTTGATT AAATAAATGT ACACATTTAG AACACAAA 168

SEQ ID NO:1881

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02134

SEQUENCE DESCRIPTION:

50 GATCAGCCTC CCTGTAAGCC AGTTATCAGT ATCCAAGTGC TTAAACACAG GCTTCTCAGA 60  
AGAAATCATT TTTATTCCTA-CCATTATTTT-ATACCAAAGC ATCATTATGT GCTACAGTTC 120

55



CAATTTCTTA CACAAGAATG AAAAGGGTTA CCAATGCAGC AAGTTAAA 168

5 SEQ ID NO:1882  
SEQUENCE LENGTH:167  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02135  
10 SEQUENCE DESCRIPTION:  
GATCTTACTG TAAGTTGAAG GGAGTTTTC CCTAACTCAT GGATTGTGCA AGAATGAACT 60  
GCTGTTGGGT TTGACTGACT GTCGATGGAT TGTGGTGTGG TGTATCTNAA GGCTATTGAA 120  
TGCAACTTAC AATGCTTAGG TAAAAATCTT TATNCTTTTA GTATAAA 167

15 SEQ ID NO:1883  
SEQUENCE LENGTH:165  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS02136  
SEQUENCE DESCRIPTION:  
GATCCTTGAT GAGCCAACAT TGCAGTGTGG ATACATATCT ATGTTTACGC GCTATTAGAA 60  
CAGAAGGCGC TGTATATAGA AATGTTGCTT TGAAGCAATA TTGCAAAAC ACNCAGACTN 120  
25 CAGNATCTGT ATTTGGAAAA AATAAAACAG GTTCTTGTG CTAAA 165

SEQ ID NO:1884  
SEQUENCE LENGTH:168  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS02137  
SEQUENCE DESCRIPTION:  
GATCTGACCT CCACGGAGCC GCTGTCCCCG NCCCCCTTGC TTCCCGTCTG TCTGTCCTGT 60  
35 CTGATTCTNT TAGGTGTCAT GTTCTTTTTT CTGTCTTGTC TTCAACTTTT TTTAAAACTA 120  
GATTGCTTTG AAAACATGAC TCAATAAAAG TTTCTGNCC AATTTAAA 168

SEQ ID NO:1885  
SEQUENCE LENGTH:163  
40 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02138  
SEQUENCE DESCRIPTION:  
45 GATCACGATG GCTTCACAAG CCAGCTGTTG GGTTTGCTAT GTCAGTGTGG CTCAGTCACA 60  
TCCCTGCGTG TATACTGTCT GCGGGGCACA TATGTATCCA TTAGAGCTA AAGGAATCAG 120  
TGTACACTAC AGCTAATCCT AATAAATCCG ATGTTTTTCGG AAA 163

50 SEQ ID NO:1886  
SEQUENCE LENGTH:159  
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS02139

SEQUENCE DESCRIPTION:

5 GATCTAGCAG CATGCAAACA CATCACCTAA ACTACAAAAG AAAGGTCCTC ACTGTCTCTA 60  
 AAAAATAAAC TCATTAACTT TGAGTTATTT GCAGACAGCC AAATCACCCA GGGCAACTTT 120  
 AAAGAGTCAG AAAATAAAAC TTTCCCGTTG TATGACAAA 159

SEQ ID NO:1887

10 SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02140

15 SEQUENCE DESCRIPTION:

GATCATGGAG GAAAAAGGTA CTGGATAAAA GTAAACTTCA AACCTTAGGG CGGGANACTA 60  
 AAACCAAAAT ACATGTATTA TTTATAGAAA ATATTTTCTG TTTTAATCTT TTCTNTTTAA 120  
 ACAAGGACTC ATACTTAAAA AAATGTTTAG CAAA 154

20 SEQ ID NO:1888

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS02141

SEQUENCE DESCRIPTION:

30 GATCTCTGAT GACCTAACCT AAGCAAAACC ACTGAGCTTC TGGGAAGACA ACTAGGATAC 60  
 TTTCTACTTT TTCTAGCTAC AATATCTTCA TACAATGACA AGTATGATGA TTTGCTATCA 120  
 AAATAAATTG AAATATAATG CAAACCATAA A 151

SEQ ID NO:1889

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS02142

SEQUENCE DESCRIPTION:

40 GATCTATATT CTTCTTAATT TTTATGGCTA TATTTAATGT TTTCCATCAT TGTGCCTTTA 60  
 AAAAGTATAT GTACATGTAT GCATAAATTT ATGTGAAGTT ATATATANGN NTCCGTTATT 120  
 CCAGATTAAA GTTTATCTTT AGTAATCAAA 150

SEQ ID NO:1890

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02143

SEQUENCE DESCRIPTION:

50 GATCAAAAAT ATGTGACCTT AATGAGATTT TTATGATTTT TAAAGTAACA ATAAAAGCAG 60  
 TTTTATAGAGT TGAGTTCCAG AGAGGGCAGG GCAATGGCAG TNACATGTTT GTCATTTTAA 120

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TAATAAATAA CATCTATTGA GTNCTTAAA 149

SEQ ID NO:1891

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02144

SEQUENCE DESCRIPTION:

GATCCGCGGG GACCCTGCCG AGGGGGCTGT CATGCGGTTT CCAAGGTGCA CATTNCCAC 60  
GGAAACAGAA CTCGATGCAC TGANCTGCTC CGCCAGGANA GTGAGCGTGT AGGTNCCTGA 120  
GGAATAAAAT GTTCCGATGA TGTGGAAA 148

SEQ ID NO:1892

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02145

SEQUENCE DESCRIPTION:

GATCCCCGTT CTTCAAGCTT CTCTGCTCAG TGTCTACTAA CGACCGACAT TTGCTAATGT 60  
AAATAATAGT AAATNATTGA GAATTCTAAT TCTTTTACAC AGTCTGTTTT TAATCTATTT 120  
TAATTAAATA AAATCTATGA CTCTAAA 147

SEQ ID NO:1893

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02146

SEQUENCE DESCRIPTION:

GATCTGGGAG TAAACTTAAC ATTCAGTGTG TCTCTGCTCT GCATCCGCCA TTTGTGTGTG 60  
TTTCTGGACT GTGGGCTGTG TGTACCTTGG TTGGTGACTC AGTGAGAAGA AGCAGGAATN 120  
CCAAAGATAC TGTGAATNTT CTGAAA 146

SEQ ID NO:1894

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02147

SEQUENCE DESCRIPTION:

GATCTAAATG TCTAGTTTGT TATTCTTTTG TGTGTGTTCA CTGTTTCTCA GTATTACCAC 60  
TTGAATAATT CTCTGTACAG GGGGGTTTGT GCTATACACT GGGATGTCTA ATTGCAGCAA 120  
TAAAGCCTTT CTTTAAAAAG GAAA 144

SEQ ID NO:1895

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02148

SEQUENCE DESCRIPTION:

GATCTTGGAA ATGCTTGAAG ACCACAAGGC TGAAAAGTGC TTTGCTGGAG TCCTGTTCTC 60  
AGAGCTCCAC AGAAGACACG TGTTTTGTGA TCTTTAAAGA CTTGATGAAT AAACACTTTT 120  
TCTGGTCAAT GTCAAANNAA A 141

SEQ ID NO:1896

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02149

SEQUENCE DESCRIPTION:

GATCCAGATA AACTTTCCTG TCATGTGTTA GAACTTTATT ATTATTAATA TTGTTAAACT 60  
TCTGTGCTGT TCCTGTGAAT CTCCAAATTT TGTACCTTGT TCTAAGCTAA TATATAGCAA 120  
TTAAAAAGAG AGAAAGAGGA AA 142

SEQ ID NO:1897

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02150

SEQUENCE DESCRIPTION:

GATCAAAGTG TGGGATGNGC TGCAAGACGT AGAACCTACC TGCCCTGCCC CCGTCCCCNC 60  
CCTTCCTTAT TTATTCCTGC TGCCCCAGAA CATAGGTCTT GGAATAAAAT GGCTGGTTCT 120  
TTTGTTTTCC AAA 133

SEQ ID NO:1898

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02151

SEQUENCE DESCRIPTION:

GATCTAAGTT GCATCTTTAA TCCTGGTGGT CTTGCCTTCT GATTTTAAAT TTGTATCCTT 60  
TTCTATTAAG ATATATTTGT CATTTTCTCT TGAATATGA TTAAAATATC CCAAGCAATC 120  
CAGTAACAAA 130

SEQ ID NO:1899

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02152

SEQUENCE DESCRIPTION:

GATCGAGGAG ATGCCCTCTG AACGCCTGTC CCGGAGCACC CGCCAGCGGG CAGCCTGTGC 60  
CCAGCTCAAC GACTTCCTCC AGGAGTATGG CACTCAGGGG TGCCAGGTCN TNAGGGCTGC 120

EP 0 679 716 A1

CCTCCCACNN CCGCTGGGAG GAACCTNAAC CTGGGAACCA TGAAGCTGGA AGCACTGCTG 180  
TGTCCGCTTT NATGAACACA GCCTGGGACC AGGGCATATN AAAGGCTTTT GGCAGCAAAG 240  
TGTCAAA 247

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SEQ ID NO:1900  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS02153

SEQUENCE DESCRIPTION:

GATCTTCTTG CTACCCTCTT GGATTCTAAG TGGTTCCAAG CTTAACTTGA GACCTTCCCT 60  
TCAAATCTAA AATTGGCAAA AAGTCACTTA AAATAGTGGA CTTCTGTAAT AAAGGTTGCC 120  
TAAAATAACA AA 132

15

SEQ ID NO:1901  
SEQUENCE LENGTH:128  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02154

20

SEQUENCE DESCRIPTION:

GATCTACAGG TTNCAATTCA ACCTGTTTCT AGGTTTTTTT GTAAATTTAG TTTTGATTAA 60  
GCATTATAAG CATTTGAGTC TATAAACTTT ATAGTAGCAT CTTTCAGAAT AAACATTTTT 120  
AATTGAAA 128

25

SEQ ID NO:1902  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02155

30

SEQUENCE DESCRIPTION:

GATCCATGAG TTTGCCCTGG TTTCCTGGC CCAAGTGGTT TGTGCTAACC ACGTCTGTCT 60  
TCACAGCTCT GTGTTGCCAT GTGTGCTGAA CAAAAAATAA AAATTATTAT TGATTTTATA 120  
TTTCAGGGGA AA 132

35

SEQ ID NO:1903  
SEQUENCE LENGTH:128  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02156

40

SEQUENCE DESCRIPTION:

GATCCAAGAC AGAATAATGA ATGGACTCAA ACTGCCTTGG CTTAGGGGA GTCCCGTCAG 60  
GNCGTTGAGG ACTTTTCGAC CAATTCAACC CTTTGCCCCA CCTTTATTAA AATCTTAAAC 120  
AACGGAAA 128

45

SEQ ID NO:1904

50

55

# EP 0 679 716 A1

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02157

SEQUENCE DESCRIPTION:

GATCCACAGG GGTGGTGTCA AATGCTATTG AAATTGTGTT GAATTGTATG CTTTTTCACT 60

TTTGATAAAT AACATGTAA AAATGTTTCA AAAAAATAAT AAAATAAATA AATATGAAAC 120

CTTAAA 126

SEQ ID NO:1905

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02158

SEQUENCE DESCRIPTION:

GATCTACAGA TGAATATTTA ACTCAATAGA AAAATTATTT TAGAACACAT TGTATTGGTA 60

TTACAACCAG ATTATATTCT TGACGTTGAC TTCATTAAAA TTATCTACAA TTTCCTAATA 120

AA 122

SEQ ID NO:1906

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02159

SEQUENCE DESCRIPTION:

GATCTCATGG ATACAAACAG GTGACCTTGC CAATTGGTGC TTTTGTGTG TTAAAGAAAA 60

GAACAGTAGT AACCTTGCTC CCTGGNTACC AATAAAAAAT CTATTATTTT TTAAAAAGAA 120

A 121

SEQ ID NO:1907

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02160

SEQUENCE DESCRIPTION:

GATCTGACCC CTGTCAGATG NAAATGATTC ACAGCTCTGG CAGTTCCCAA GTCTGGGGAG 60

GGGTATAGGT TTGAAAGGCT GTTGAAAGA GGAATGTTTA ATAAAGGCTT TGATTTAAA 119

SEQ ID NO:1908

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02161

SEQUENCE DESCRIPTION:

GATCCCAGCT GGCCCTATG TTGTGTTCTG NGACTGAGGC CTTTGCTGTG AACTGCAGTG 60

TTTCATACGA ACCATCTTTC CTAGTGCATG AGAAATAAAG ATTATTTAAG TAATGAGGAA 120  
A 121

5 SEQ ID NO:1909  
SEQUENCE LENGTH:116  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02162  
10 SEQUENCE DESCRIPTION:  
GATCTCACTT TTCAGGAAAC TTAAATTTA CCCATTATTG GGAAGCTTAA ATGAATTGAA 60  
GCTATGCAAG TCTTTTATAT TATTAAATAT TTAAAGTAA ACCTGTACTA ATCAAA 116

15 SEQ ID NO:1910  
SEQUENCE LENGTH:116  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02163  
20 SEQUENCE DESCRIPTION:  
GATCGATATG CTCATAAAAG TGCTCAATTA TATTNCTGT ATTTGTATG NTGTATTTTC 60  
CAAGACGTAT ATTATTTTAC TATTAAAGAA AAAATCATT TTTTTCCTCC GAGAAA 116

25 SEQ ID NO:1911  
SEQUENCE LENGTH:124  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02164  
30 SEQUENCE DESCRIPTION:  
GATCCGGGCA TGGGAGACCC CACTTTAGAA AGGGTCGTCA CTCCTTTAAT CCTCTACTCA 60  
ACAATGTACT CTTTACTTT TATATTAAAA AAAATAAAAT AAATATGTGC CTAACCTC 120  
CAAA 124

35 SEQ ID NO:1912  
SEQUENCE LENGTH:115  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
40 CLONE:HUMGS02165  
SEQUENCE DESCRIPTION:  
GATCCACTTC TACTTAATGA GTAGTAAATA TATTTNCTTT TCCTTATGAT TTTCTTACTA 60  
TTNCTTTAG CTTGCTTTAT TATAAGANTA TAGCATATAA TATAAATAAA ATAAA 115

45 SEQ ID NO:1913  
SEQUENCE LENGTH:112  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
50 CLONE:HUMGS02166

55

## SEQUENCE DESCRIPTION:

GATCCAGAAA TTGTGAACAA TGTTTGATTT AGTAGCGTGA CTTGCCTTTC CCTTTAAAAA 60  
CATCTTTTAC AAATCTGTCT TGGAAATAAG TCTATTTTCT GCCTTTTGGA AA 112

SEQ ID NO:1914

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02167

## SEQUENCE DESCRIPTION:

GATCCTAATT GCCTAGAAAT ATCTTTCTCT TACCTGTTAT TTATCAATTT TNCCCAGTAT 60  
TTTATACGG AAAAAATTGT ATTGAAAACA CTTAGTATGC AGTTGANNNN GN 112

SEQ ID NO:1915

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02168

## SEQUENCE DESCRIPTION:

GATCAACCGT GAAGCGTAAC AAATTCTGTA TTTAGTTTTT TTTTCTGTTG TGGTGGTTTT 60  
TGTTTTGTTT TTTGTTTTTG TAAGATTCTA AATAAATNAA ATACGAGTCA AA 112

SEQ ID NO:1916

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02169

## SEQUENCE DESCRIPTION:

GATCAAGACT NCAGTTTGGG AATGCATGGA CACCGGATTT GTTCTTATT CCTTCACTTT 60  
TGGGGAAAAA CTCNCCNTNT TTAAAAAGTG ATAAATTGG TGTTAGGTCA AA 112

SEQ ID NO:1917

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02170

## SEQUENCE DESCRIPTION:

GATCAACGCG ACTGTATTTT GAAACATTCC AGGAAGGTTA CTTCTTGTC AACTTGCCTG 60  
GCAGTGTTTG TTCAAANCTT GTATTTAATA AATGANCATC TGACTTTACA AA 112

SEQ ID NO:1918

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02171



# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCTATCTT AAGAAGTGAC CAGGAAAGAG GTTCATTGAA ATAATCATGC ATGAAGCGCC 60  
 AAAGATGCAC CATGTAGAAT TTTCACTTTG TACTGGCAGG CTCGTTTTAC CTGATTCTAG 120  
 AATATTTAAG AATCTAAAAA TAAAGGGCAA CTCTGACTTA AA 162

SEQ ID NO:1919

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02172

## SEQUENCE DESCRIPTION:

GATCAGGGAA CTAAGCATT TGTGAATTCA CCAGCAAGAT GTACAGNACG CCTGTNTTTA 60  
 CATTGTTTT ATGGAAGTAG CAGAATAAAN CATCTATTTT AAAAATGCAA A 111

SEQ ID NO:1920

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02173

## SEQUENCE DESCRIPTION:

GATCTGCGAG GAAGCCGCCT ACTCCAACCC CAGCCTACCT NTGGTGCACA NATCCGTCCC 60  
 ATAGCAAAGC CCCTGCACAG ACTCCAGCCG AGCCACACACC TGGNTATNAG GTGGGCCAGC 120  
 GGAAGCGCCT CATCTCCTCG GTGGAGGACT TCACCGAGTT TNTNTGAGGC CGGGGCCCTC 180  
 CCTCTGCAC TGGCCTTGA CCGTATTGCC TGTCAAGTAA ATAAATAAAG TCCTGACCCT 240  
 AGTGACACAGA CATAGAGGCA CAGATTGCAG TCAAA 275

SEQ ID NO:1921

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02174

## SEQUENCE DESCRIPTION:

GATCAGGACA GAGACTTGGG GGCCATCCTG CCCCTCCAAC CCGGACATGT GTACCTCAGC 60  
 TTTTCCCTC ACGTTGCATC AATAAAGCTT CTGTGTTTGG AACAGNTAAA CAAA 114

SEQ ID NO:1922

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02175

## SEQUENCE DESCRIPTION:

GATCCCAAGC NTCCCGTCCC TTGGAAAGTN CAGCCAGAAT CTNCGTCCTG ACCCCCAGACA 60  
 GCCCAGCCTA GCCCACTTGT CATCCATAAA GCAAGCTCAA CCTTGAAG 108

SEQ ID NO:1923

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02176

SEQUENCE DESCRIPTION:

GATCCCCCAG GTTCAGACTG AGCTCCCCCT TCCCAGTAGC TCTTGCATCC TCCTCCCAAC 60  
 TCTAGCCTGA NTNCTTNCA ATAAAAATA CAATTCAAGT TGCTTCTCAT GGATGGCACT 120  
 GCTTTCCTGA GGA CTCAAGG TGCCAAGATG GAGGGGCTGA CTCAGTCCAG CCAACNTTTA 180  
 ATGAGNACCT ANNNGGTGTA TGGAGCTCTA ACCCATGGGT CCATGGGAAT AAAGCAGTGA 240  
 ATAGTAACAA TAAATAATTG TAACAGCANA AA 272

SEQ ID NO:1924

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02177

SEQUENCE DESCRIPTION:

GATCTGACGT TTTCTACGTA GCTTTTGTAT TTTTTTTTTT TAATTNNAAG GAACACTTAT 60  
 GAAGCCCTGC CATNCCCCTC CCGNGTCTAA TAAAACGTAT AATCACAAA 109

SEQ ID NO:1925

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02178

SEQUENCE DESCRIPTION:

GATCAACTTG TGCTTGCCAG AGGACGCCAA TGAAGTTTGA AACACCAACA ATCAGAGATT 60  
 TTGTTTCTGT TCCTCATTAA ATCATGAGCT TTTGTGCCGA GAAA 104

SEQ ID NO:1926

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02179

SEQUENCE DESCRIPTION:

GATCGTGTGT GTAGGTGGTG TTGTGTGGTT TTCCTTTGTG AAGGAGAGAG GGAAACTATN 60  
 TGTAGCTTGT TTTATAAAAA ATAAAAATG GGTAAATCTT GAAA 104

SEQ ID NO:1927

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02180

SEQUENCE DESCRIPTION:

GATCCTCCA CTCCACCTC CCAAGTAGCT GTGGCTACAG GTGTGTGCCA CCATGTCCAG 60

CTGATTTTNG TATTTTNAGT AGGGACAGTA TTTCTCCATG AAA

103

SEQ ID NO:1928

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02181

SEQUENCE DESCRIPTION:

GATCTAAATC TCATTTTATG CTGTATTTTA TATCTNAGTT GTNTTTGAAA ACGTTTGTAT 60  
 TTTTGGAAAC ACATCAAAAT AAATAATGGC GTTNTTTGTA TGCAAA 106

SEQ ID NO:1929

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02182

SEQUENCE DESCRIPTION:

GATCTGGACG AATGATACCA AACGTTTCTT TCTAACATTG TATTTTATAA CTCTGGCCTA 60  
 TGATTGTINTT GTGTCTTGCA TTAAAAA AAAATTTGAGA GTGGTAGAAT TACTTCTGTT 120  
 ATCTGAAATA CCTGAGATGC ACTTTAACT GTTGAAATGT AAGCNCTGAG GGCAGGGNCC 180  
 GTATCTNATT TACTGTAGT ATCCGTTGCA TCTAGTGTGG TGCACCTGGC ACACAGTAGG 240  
 CACTCAATAA ATATGTATTG ATTAANCA AA 272

SEQ ID NO:1930

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02183

SEQUENCE DESCRIPTION:

GATCTACAGC TCCTGGATAA TTGCTTGATT CTCGCCAGAG ACTGTCAATA TTTNATTCAT 60  
 TGCCATTACC AATAAATCAT TGCTTTTGTT NAGATGGTAT CACTAGTGTT TCCATTGTAA 120  
 TCTTGACACA TGCAATTGTA AATAAAAGTC ACCACTTTTG CCAAGCTTAA A 171

SEQ ID NO:1931

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02184

SEQUENCE DESCRIPTION:

GATCATACCA CTGCACTCTA GTCTGGGTGA CAGAGCGAGA CCCTGTCTTG AAAAAAATAA 60  
 AAAAAAATAA AAAAAATAA AACTGGCACT ACGTTTAAA 99

SEQ ID NO:1932

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS02185

SEQUENCE DESCRIPTION:

5 GATCTGTGTC TTAAAACTTA CTGGAATGGA AATCTATGAA TTATTGCAAA TTGTAATGCT 60  
GGAAACAAA AATAAATCCT TGGTTAAAGG GTTTGTAAA 99

SEQ ID NO:1933

SEQUENCE LENGTH:99

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02186

SEQUENCE DESCRIPTION:

15 GATCCTGACA CTCTANCACT CGACTCTGCT GCTCATGGGA AGAACAGAAT TNCTCCTGCA 60  
TGCAACTAAT TCAATAAAAC TGTCTTGTA GCTGATAAA 99

SEQ ID NO:1934

SEQUENCE LENGTH:90

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02187

SEQUENCE DESCRIPTION:

25 GATCTTGACT TATATTCTGT ACCACATACA CTTCTGTGGA CTTTtagcat TTGTGGGTAG 60  
ACTTAATAAA GCATGTATAA AAGTGGCAAA 90

SEQ ID NO:1935

SEQUENCE LENGTH:91

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02188

SEQUENCE DESCRIPTION:

35 GATCAGGNTG CGGATAGACT TGTAAGGGTG TTTGCTGCAT ACAGTGTAAG CATTGTGACC 60  
GCCAATAANC TTCAATGGTT TCTACTGNAA A 91

SEQ ID NO:1936

SEQUENCE LENGTH:91

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02189

SEQUENCE DESCRIPTION:

45 GATCTTTCGT NTTTCTAAGC GACTCTACTT TCATTGTTT CCAGCNTAGC TCGTTGCTGT 60  
TGCCCAATAA AGCTNGTGTA CGTNCTGCAA A 91

SEQ ID NO:1937

SEQUENCE LENGTH:86

50 SEQUENCE TYPE:nucleic acid

55

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS02191

SEQUENCE DESCRIPTION:

5 GATCTTACAT CTGCAGCTCT TTCTTCTTTG AATTCCTAT CTGTATGTCT GCCTAATTAA 60  
AAAAATATAT ATTGTATTAT GCTAAA 86

SEQ ID NO:1938

SEQUENCE LENGTH:86

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02192

SEQUENCE DESCRIPTION:

15 GATCATCAGT GTTCCTTTTT ACTTATAAAG TTGGATTCTT TTTTAGAATT TGTAATAAAAT 60  
AAAAACTGCT GCTTTACCAC TGTAAT 86

SEQ ID NO:1939

SEQUENCE LENGTH:91

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02193

SEQUENCE DESCRIPTION:

25 GATCTACCCT GCCTGTACTA CTCTAGGGAG TATGCTGGAG GCAGAGGGCA AGGGAGGGGT 60  
GGTATTAAAC AAGTCAATTC TGTGTNGTAA A 91

SEQ ID NO:1940

SEQUENCE LENGTH:84

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02194

SEQUENCE DESCRIPTION:

35 GATCATGAGT GACCCAGCTG TCTCAGTTG TTTATTCTGC GTCCCCTTCT CCAATAAAAC 60  
AAGCCAGTTG GCGTNGTTA TAAA 84

SEQ ID NO:1941

SEQUENCE LENGTH:79

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02195

SEQUENCE DESCRIPTION:

45 GATCCCCATG CCTAGCAGAG TGCTGGCACT TAGTAGGTCC TCAATAAATA TTTATTAAAT 60  
GATGAGATGA TGGAGCAAA 79

SEQ ID NO:1942

SEQUENCE LENGTH:78

50 SEQUENCE TYPE:nucleic acid

55

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS02196

SEQUENCE DESCRIPTION:

5 GATCCAATCC CATAGACAGC TCTGGGCCTC TTGCATTGGA GTTTTTTAGA ATTAAACTGC 60  
AGTATTTTGG AAAGCAAA 78

SEQ ID NO:1943

10 SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02197

SEQUENCE DESCRIPTION:

15 GATCCACTAA GGAAATGTTT TAACAGCTAG AGACCACTGC TTGCCTGAAA GGGCGTTCTT 60  
AAATTTGGTG CAGCAAA 77

SEQ ID NO:1944

20 SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02198

SEQUENCE DESCRIPTION:

25 GATCCACTTC AAGAATTGCT TGCTTTCAGG AAGAGAGATG TGTTTCAACA AGCCAACTAA 60  
AATATATTGC TGCAAA 76

SEQ ID NO:1945

30 SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02199

SEQUENCE DESCRIPTION:

35 GATCGACTTT GTGTCTCTGT TGTCTAAAAT AGGTTTTCCC TGTCTGGAC ATTTCAATATA 60  
AATGGAATCA CACAAA 76

SEQ ID NO:1946

40 SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02200

SEQUENCE DESCRIPTION:

45 GATCATAGAT TTCTGATTTT ATGTAAAATT TTGCCTAATA CATTAAAGCA GTCACTTTTC 60  
CTGTGCTGTT TCAAA 75

SEQ ID NO:1947

50 SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

55

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS02202

SEQUENCE DESCRIPTION:

5 GATCTGTCAA AGAAAACCTC CAAAAAGATT TATTAATTAA ACCAGACTCT GTTGCAATAA 60  
AAATCCTACA GAAA 74

SEQ ID NO:1948

SEQUENCE LENGTH:73

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02203

SEQUENCE DESCRIPTION:

15 GATCCACTTT AGCAAACCTT GCTGCAGAGG ACTGTAAAAA CAAATAACTA AAAATAAACT 60  
TAGAAAATAC AAA 73

SEQ ID NO:1949

SEQUENCE LENGTH:73

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02204

SEQUENCE DESCRIPTION:

25 GATCGTAATG TTTATCATGT TACTTCCCA CCCCTACATT TTTTGAATA AAATAAGGAA 60  
TTTTATTCTC AAA 73

SEQ ID NO:1950

SEQUENCE LENGTH:72

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02205

SEQUENCE DESCRIPTION:

35 GATCNCCTGCA ACTAAGNTTA AAGCAGTGTG ACTGTGTTGC TNAAATATCA AGTATTGTTT 60  
ATAACCACCA AA 72

SEQ ID NO:1951

SEQUENCE LENGTH:66

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02206

SEQUENCE DESCRIPTION:

45 GATCTCAGCT ATTAAGATGC AAGTCTGCCA ATGCTCCTGG CCAAATAAAC CTCTTCCTTC 60  
TTTAAA 66

SEQ ID NO:1952

SEQUENCE LENGTH:65

50 SEQUENCE TYPE:nucleic acid

55

# EP 0 679 716 A1

TOPOLOGY:linear  
 CLONE:HUMGS02207  
 SEQUENCE DESCRIPTION:  
 5 GATCCTCTTG TACTGGGAGA GGTGCCTTTT GTATCCCCAA TTAAAGGTAG AAAACCACCC 60  
 TGAAA 65

SEQ ID NO:1953  
 SEQUENCE LENGTH:62  
 10 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02208  
 SEQUENCE DESCRIPTION:  
 15 GATCTCGAAG AAAAAAGGGG GAGACCAAAG AATAAAGAA GGGTTTCCCC ACTAAAATGA 60  
 AA 62

SEQ ID NO:1954  
 SEQUENCE LENGTH:62  
 20 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02209  
 SEQUENCE DESCRIPTION:  
 25 GATCCAGCTG TNCTTAAGAG CCAGTAATGT CTTAATAAAC ATGTGGCAGC TTNNTTTGA 60  
 AA 62

SEQ ID NO:1955  
 SEQUENCE LENGTH:61  
 30 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02210  
 SEQUENCE DESCRIPTION:  
 35 GATCTCACAT TTCACCCAG GCTCAACTGA GGATGTGGCT TATTAAACAC GGAAGTGCAA 60  
 A 61

SEQ ID NO:1956  
 SEQUENCE LENGTH:59  
 40 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02211  
 SEQUENCE DESCRIPTION:  
 45 GATCAGCCAT GTNTATCTTT TAAAAAATA AACAGGTTGC TTTATTCTT AGCTTCAA 59

SEQ ID NO:1957  
 SEQUENCE LENGTH:59  
 SEQUENCE TYPE:nucleic acid  
 50 TOPOLOGY:linear

55



# EP 0 679 716 A1

CLONE:HUMGS02212

SEQUENCE DESCRIPTION:

GATCAGATGA GATTTAATGA AGACCCAGTG TAAAGAATAA ATGANTCTTA CTCCTTAAA 59

5

SEQ ID NO:1958

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS02213

SEQUENCE DESCRIPTION:

GATCTACACC TGGACTGCCC AGGTCTATAA GCCAATAAAG CCCCTGTTTA CTGAAA 57

15

SEQ ID NO:1959

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS02214

SEQUENCE DESCRIPTION:

GATCGAAGAA AAAGGGGNGN CAAAGAATAA AAGAAGGGTT TCCCACTAAA ATGAAA 56

25

SEQ ID NO:1960

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02215

30

SEQUENCE DESCRIPTION:

GATCAGAAAT GTTGANTGTG CATTGAGTAT TAAAAATTA GATGTATATT ATNCATTGTC 60  
CTTACTCAT GAGTACCTTA TAATANTANT ANTGTATTCT TTGTTAACAA A 111

35

SEQ ID NO:1961

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02216

40

SEQUENCE DESCRIPTION:

GATCTATTCC CCATCCCAAG GCAAGCATGA ATAAAATTAG GTTAAACGTA GCATGTGGCA 60  
TCGCAGTCTC TTAGAATTG TTTCATCTAT TTNATTTTAT TGAATACTGT CTGTATCTTT 120  
GGTTATCCTG TTTGAAGAAA AAGGACAAAT AAAACATGGC CAGCAA 167

45

SEQ ID NO:1962

SEQUENCE LENGTH:516

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02237

50

SEQUENCE DESCRIPTION:

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5 GATCCTCATT CTCACCCATT TGGCTAATCC AGGAATATTG TTATCCCTNA NCCATTATAT 60  
 TNAAGTTGAG AAATGTGACA GAGGCATTTA GAGTATGGAC TTTCTTTCC TTTNCTTTT 120  
 NCTTTTTTCC TTTTGTAGAT GGAGTCACAC TCTCCAGGCT GGAGTNCAGT GGCACAATCT 180  
 CGGCTCACTG CAATTNCCGT CTCCCAAGTT CAAGCGATTG TCCTGCTTTA GACTATGGAT 240  
 TTCTTTAAGG AATACTGGTT TGCAGTTTTG TTTTCTGGAC TATATCAGCA GATGGTAGAC 300  
 AGTGTTTATG TAGATGTGTT GTTGTTTTTA TCATTGGGAT TTTAACTTGG NCCGAGTNA 360  
 ATAATCAGGT TTTTGTCACT CACACTCTCC CCCAGTTTTT GGGAATAACT TTGGAAGGTA 420  
 10 AGGTTTCANTN CCCTAAGGCC GGTGGGGTTN CTGTTGGACC TATGGGGGGN CCACAAC TGN 480  
 ACTATTTAAT TCCNCCCAC TGTAAGGGGC AAAGGN 516

SEQ ID NO:1963

SEQUENCE LENGTH:483

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02238

SEQUENCE DESCRIPTION:

20 GATCTTTCCA GATGACTTGT CCAAGGTCAC ACAGGAGTCA GATGGCCTTT CCACTACCCC 60  
 ACAACACAGA TGCATAGTTA CTCTGTGGGC TAATACAATT CAGAATTCAG AGCTCTGCCC 120  
 ATGGTCACCG GTGGAATCCA CCAGCCATCT CCCTGACCTT GCTCTCCTCT GTTCTCCTCG 180  
 TCTCCAGGGT CCCATGATTG AGGGCGAGCT GGCTTCAGGA TGTGGGCAAG AGGGGTTTGA 240  
 GATGGAAGGG TTTTCCTCCA GGACAGAATG TTAAGCCAAG CCTGGACTTA ATTGTTCCAA 300  
 25 GATGTCGTTA GAATTGGTGG ACAATTTTTT TTAATGATT AGCAAAGGAC AAGGCTTTTG 360  
 GTGGTCATTA GTATTGTTCA TCAAATATTC CAGTTCTCCA CAATTCTGGG GTACCATGGT 420  
 ANGGATGAAC CTTCCCTGTC TTTTCAGGGT TAAGTTTAGC TCTNGTGATG TGCTTTTGTG 480  
 AAA 483

30 SEQ ID NO:1964

SEQUENCE LENGTH:452

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS02239

SEQUENCE DESCRIPTION:

40 GATCGCTGGA GCTGTGGTCG CTGCTGTGAT GTGGAGGAGG AAGAGCTCAG ATAGAAAAGG 60  
 AGGGAGCTAC TCTCAGGCTG CAAGCAGTGA CAGTGCCCAG GGCTCTGATA TGTCTCTCAC 120  
 AGCTTGTAAG GTGTGAGACA GCTGCCTTGT GTGGGACTGA GAGGCAAGAT TTGTTCTCTG 180  
 CCTTCCCTTT GTGACTTGAA GAACCCTGAC TTGTTTCTG CAAAGGCACC TGCATGTGTC 240  
 TGTGTTCTTG TAGGCATAAT GTGAGGAGGT GGGGNGACCA CCCCACCCNN ATGTCCACCA 300  
 TGACCCTCTT CCCACGNTGA CCTGTGCTCC CTCCCAATC ATCTNTCCTG TTCCAGAGAG 360  
 GTGGGGCTGA GGTGTCTCCA TCTCTGCCTC AACTTCATGG TGCACTGAGC TGTAACNTT 420  
 45 TCCTGNNTAT TAAAATAAGA CCTGAGTTTA AA 452

SEQ ID NO:1965

SEQUENCE LENGTH:433

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

CLONE:HUMGS02240

SEQUENCE DESCRIPTION:

5 GATCAGACAC CAGAGGGTTG GGCATTCTTG CAATACCTTA ACAGTGCTGA AATCTGCAGC 60  
ATGGTACTAA GGAAGTAAA GTTTGAATGT AACCACCTTA TTTAAAAGGT TTTTCTCTT 120  
AATTTAAATG AAATGGTGGT TGAAGTGAAC ATGATTTTGT TGACCATGTT CGTGAATTAC 180  
AGATGCAACA TGCATTGGTA GAATCGTGTG ATGGTCTTTT GTGATACTTA ATTTTACAT 240  
ATCCCACTCT CTGTATGTAT CTGCATAGAC AAAGAAAAAA CAAACTCCTG CTTTGCTTTT 300  
10 ATTGAANGGG TTTCCAGGAC TGCCTGTCTG CTCCTGAGCT CTGTTTAAAG TATGTGTATC 360  
CTTTGCTTGT ATTTTGTAA TAAAAAATA AGGAAAAGGA NGCCTTTATT TGTTGGNGCA 420  
TGTTGGCATT GTN 433

SEQ ID NO:1966

SEQUENCE LENGTH:424

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02241

SEQUENCE DESCRIPTION:

20 GATCTGCAAA GAAAGCTTTT CTNCGTCGC TGCCTCAGNC TCCTCCCTAT GCCTCTNGCA 60  
CCTGCGCAGA AGTGCTGGCT GTGCTGANGT CACCATCATC TTCCTCTCCC CCAGCCTCCC 120  
AGGCTGGATG GCATGGACTG TTTGCTGACC TCTGTTCTCT TAGGGCATGG GAGGTGGGAG 180  
GATATCAAA TCTNTAGCCC TTTCTCCTA TTCTCCAAG NAGAGAGNTT CCCATTTCTC 240  
25 CTCGGCCATT GTACCTAGCT CTTGTCCCTA GCTGCATTTC AGTGGACCAT GGATAGAGGG 300  
ACTGAGNGTT AGACGGGGAA GACTGGCAGN GAGGCACGCA GGTACTGTGA AAATCCTNNC 360  
CTTTGACCTC CNCCAGTGGG AGAGGGGNGT TGGGGTTTTT AATGTGAGAA CAGNAACAAA 420  
TAAN 424

SEQ ID NO:1967

SEQUENCE LENGTH:418

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02242

SEQUENCE DESCRIPTION:

35 GATCNCCTGC TCTCCAAGCA TGGCATCTAT GTGCAGGCCA TCAACTACCC AACTGTCCCC 60  
CGGGGTGAAG AGCTCCTGCG CTTGGCACCC TCCCCCACC ACAGCCCTCA GATGATGGAA 120  
GATTTTGTGG AGANGNTGCT GCTGGCTTGG ACTGCGGTGG GGCTGCCCCT CCAGGATGTG 180  
40 TCTGTGGCTG CCTGCAATTT CTGTCGCCGT CCTGTACACT TTGAGCTCAT GAGTGAGTNG 240  
GAACGTTCTT ACTTCGGGAA CATGGGGCCC CAGTATGTCA CCACCTATGC CTGAGAAGCC 300  
AGNTGCCTAG GATTCACACC CCACCTGCGN TTAACCTGGG TCCAGGCCTA CTCCTGTCTT 360  
CTGCTTTGTT GTGTGCCTCT AGCTGAATTG AGCCTAAAAA TAAAGNACAA ACCACAAA 418

SEQ ID NO:1968

SEQUENCE LENGTH:413

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02243

## SEQUENCE DESCRIPTION:

5 GATCATTGAA TAAAACGGGT GTAGAGTACA GGAATGGGGC AGACGCGATT CAGGTGAACA 60  
 GCACANGNAG AATATGAGGT GGTTCCTAGG AGCAACACTT TCGACCTCCA GTTCTCCNTG 120  
 ATGACAGTAG CTGTCTCCNN GNGAAAAATC CTCACTTATT AACTCTCTTT TCTTGCATCT 180  
 CATTTTTATA GAGCTACTCA TCCTTATTTG GAAAAACCAA CAACAAAAA GGCTTTTAGA 240  
 AAATGGTTGT AAATCTGACT TCTTTGCAAG TAACTATGTA TATTGTAAAT AGGATATAAA 300  
 AAGGCCTTTT TTCTAAATAA GGCCTTAACT GCCTGTAACA TGAAACTTCA AACTAAACCA 360  
 10 CTTAACTCAN TGNACTACCT TATGGGTTTG TCTGACATCC CTCAACTTAC CAN 413

SEQ ID NO:1969

SEQUENCE LENGTH:412

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS02244

## SEQUENCE DESCRIPTION:

20 GATCCCACCG AGAAGAACCA TGGGTGGACC CGAACTCCCC GGTGCTCTNA GAGGACCCAN 60  
 NNCTTTGTGC CTTGGCAAAA AAGCACAAGC GAACCCAGC CCTGATTGCC CTGCGCTACC 120  
 AGCTACAGCG TGGGGTTGTG GTCCTGGCCA AGAGCTACAA TNAGCAGCGC ATCAGACAGA 180  
 ACGTGCAGGT GTTTGAATTC CAGTTGACTT CAGAGGAGAT GAAAGCCATA GATGGCCTAA 240  
 ACAGAAATGT GCGATATTTG ACCCTTGNTA TTTTGTCTGG NCCCCCTAAT TATCCATTTT 300  
 CTGATGAATA TTAACATGGA GGGCATTGCA TNGGGGTCTA CCAGAAGNNC NTNGGGTNTT 360  
 25 GGANTGGTNG CANAAGNGGG TNGGTTCTTA TGGCTGGGGG NACTTGGGCA AN 412

SEQ ID NO:1970

SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS02245

## SEQUENCE DESCRIPTION:

35 GATCCAAAGT TCATACATTT TATGTACAAG ATACATTAGA CTTACAATAN AGTCTAATTA 60  
 TTAGACTTTT ATGTCAGTGG ATTGTGCTTG CAGAAATACA GAAGTAACAT ACTGACCCTA 120  
 GGTGAGGAGT TTCTTACATG GTTAACTGGA TTGACCCAAT TGGAGTAAAA GATTTTGTGCT 180  
 GTTACCTCGA TGCTCCTGCA GTTGTTACCT CAGCATGCCA CTGTAGTCCT TGACTCTCAC 240  
 ATTAAACTA ACTTTGGCTA GGTACTGGTG GCTCACACCT GTANGTAATC CCAGTACTTT 300  
 AGGAGGCTGA GACTGGAGGA TTACTTGAGT CCAGGAGTTG GAGACCAGCC TGGCCAATAT 360  
 40 AGACTGTCCC TACAAAGGAA AATAAANTTT GTTTCATCTT TCNAAA 406

SEQ ID NO:1971

SEQUENCE LENGTH:401

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS02246

## SEQUENCE DESCRIPTION:

50 GATCAAATAT GGCATCAACA ATATCCGGGA GCTGGTGGGC CACAAGGTGA ACCTGCAGAT 60  
 GGTGTATGAC AGTCCCCTGT NCCGCCTGGA TGCCGAGCCG AGGCCCCCTC CCACACAGGA 120

EP 0 679 716 A1

GGCTGCGTGA CATGGGCCAC TCTAGGACAG GTCATCCTCC CCGAGTCCCT GCTGCTGCGC 180  
 TCCTTTGCAT CCCTGGCCAG TNACCTTGTA TTTATGAGGC CTCTGTNAGG CAGCCCCCAC 240  
 CTTCTCTTT CCCACCTGTC CCAGGACCAG AATCCCAGGG ACAGAGGACT GGGTAGCAGG 300  
 TTCCTTCTGT TGTCTGTGT GGTGTGTCTA CTGTGAGGGT GGGCCCTGAG GAGACCTGTG 360  
 GGCCANCTAT TGTCTAATAA AGTGGGGCAG TTGCCCCCAA A 401

SEQ ID NO:1972

SEQUENCE LENGTH:384

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02247

SEQUENCE DESCRIPTION:

GATCTTTNAT GTTGTTNATT TTGGAGAGAA GCACAAGGAG TATTCTCTTT CTAGGGAAAAG 60  
 TTGTGAACCC AACGGAAGCG TAGTTGGGAA AAAGGCCATT GGCTAATTNC ACGTGTGTAT 120  
 TGCAATGGGA AATAAATAAA TAATATAGCC TGGTGTGATT GATGTGAGCT TGGNCTTGCA 180  
 TTCCCTTATG ATGGGATGAA GATTGACCCC TGGCTGACCT TTNTTGGCTG TGGAAGAGGN 240  
 CAATCCTATG GCAGAGCATT CAGAATGTCA ATGCGTAATT CATTATTATC CAAAGCATAG 300  
 GAAGGCTCTA TGTNTGTATA TNCCCTNTG TCGGAATACC CCCTTANCTC ATTTTCCNCT 360  
 TAATAAATTT CACTGGGTTG NAAA 384

SEQ ID NO:1973

SEQUENCE LENGTH:383

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02248

SEQUENCE DESCRIPTION:

GATCCTGCTT CTCCCCTGGG GTCTTCTTGG TTCCCTGAAG CCCCTCTTCC GGAGTCCCTG 60  
 CCCTCTATCG GCTCTGCCTC CTGCTTCTTT TCTGTATTGC CATGATTTT GCTAAGGATA 120  
 AAGGACAAC TCAATGGCTT CTTTGGGAAA CTTGCAATCT CCCCACACAG GCCCCTCTGA 180  
 GATTTCTCCT TTTGCCACCT TCGATATTT CTCCAGTTT CTTGATTCTT TTGATACGTC 240  
 CCCATTCAAG CCACTCTGGC CTTCCATCCA ACCTGCCAGA ACTTTTCCA CTTCAAGCACT 300  
 TCAGTCACTT AACATTAGG GCTCCCTGCC CTAAAGGGAC TCAAAATCCT GCAAAANCAA 360  
 CCACNNAAGG ATAAAAAAT AAA 383

SEQ ID NO:1974

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02249

SEQUENCE DESCRIPTION:

GATCAACAGG AAGAACATGG TGGTCTCCTT TGGAGATGGG GTTACCTTCG TGGTCGTCCT 60  
 ACACCAGGTG TGGAAGAAAC ATCCTGTCCA CCGTGACTTT CTAGGCTTCT ACGTGGTGGA 120  
 CAGTCACCGG ATGTCAGCAC AGACGCATGG GCTGNTGGGG CAATTCTTCC AACCTTTGA 180  
 CTTTAAAGTG TCTGACATCN GGCCAGGCTC TNACCCACA AAGCCAGATG CCACATTGGT 240  
 GGTGAAGAAC CATCANGNTG ATTNTNACCA GGGGCTCCCN GAAAGANTAC AGNAAAGGNA 300

TGCCANGCAT CGGCACGAAN GGTGTCTTC TTGGTTCGNN CACANCAACG GGGAATGTTG 360  
 TTGNTTGANT GGTGN 375

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SEQ ID NO:1975  
 SEQUENCE LENGTH:370  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS02250

SEQUENCE DESCRIPTION:

15

GATCTATGTG CACACACCCN CATCACATGG AATGGGCTGG TCTAGGCTGT GGCCTGNCAC 60  
 CTTCTTAGA GTGAATAGGG CGGACACTCC TCTCTTTTCC TGTAGCGTGT GGACCGGTCC 120  
 ACGCAATTCT TTATCCTGTG AACTCATCTG AGTGGGAGGT GGTGGACACT GGGGTTTCCT 180  
 TCCCTCTCTC CGTAGCATCC GTTGGTCTTT CTCTCCATCT CTGTTGGTTT GTCTGTCTCT 240  
 GTCTTCCTCC CAATCCCTAG GGAAGGGGG CATTGGCTA GGGGGTGCC CTGTGAGCCT 300  
 NGACCTGCC CCCTCGTCCN TCTCCCAGT GTTCCAGGA CCCCCAATA ACCTTGTCT 360  
 GTCAGTCAAA 370

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SEQ ID NO:1976  
 SEQUENCE LENGTH:367  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

25

CLONE:HUMGS02252

SEQUENCE DESCRIPTION:

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GATCGATACA GGGGAGGGGG GAGGTGGAAC CAAACAACAA AACTGTACAT TTTTTTTAAA 60  
 GTTTGTTGAA AAGAATATTG TCTTATTCTA TAAACATTT CAAACCTAGT TAGAGATTTG 120  
 TAATCAAAAA ACATTGCGC AGAAAGCAGC ACTTAGGGCT GCCTGTTCTA TACCCTACAG 180  
 TCAGACAGGA AAAGANCTGA AAATGGCACC CTTCTGACAT TCTGNGGCAG CTGGNCTNGC 240  
 AGCCANGTAA NGGNGAGTTT ATGAGGTGGT GTGGGGAGGG TGGGGGAGGC NGCGTGGGGG 300  
 NTTCTCTCCA CAGCAGGTGG GNGCAGGCAA GNNTTTGGNG GCCAGANGGN GNGCTTGTN 360  
 CNTGGGN 367

35

SEQ ID NO:1977  
 SEQUENCE LENGTH:353  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

40

CLONE:HUMGS02254

SEQUENCE DESCRIPTION:

45

GATCTCCAGC CTTACCGCGG CTCGAAATGG ACCCCAACCTG CTCCTGCACC ACTGGTGTCT 60  
 CCTGCGCCTG CACCGGCTCC TGCAAGTGCA AAGAGTGCAA ATGCACCTCC TGCAAGAAGA 120  
 GCTGCTGCTC CTGCTGCCCC GTGGGCTGTG CCAAGTGTGC CCACGGCTGT GTCTGCAAAG 180  
 GGACGTTGGA GAACTGCAGC TGCTGTGCCT GATGTGGGAA CAGCTCTTCT CCCAGATGTT 240  
 AATAGAACAA GCTGCACAAC CTGGATTTTT TTTTCAATAC GATACTGAGC CATTGTGNGC 300  
 ATTTCTTTTT ATGTTAAATA TGTGAGTGAC AATAAAACAA TTTTGACTTG AAA 353

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SEQ ID NO:1978

55

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02255

SEQUENCE DESCRIPTION:

GATCTNACCT GAGGTGCTGG GTGAGAAATC TTAGGGACCA GATGGAAGAG GGCCTGTNTA 60  
 TANNGACATT AGGAAGGAGG TTTGGGAAGG TTTGGGAGGG CAGCCTGACT TGTCTCCAGA 120  
 GAAAGTTAGA ACTGGTTGAC TTAGCAACCA AGGGNCACTG GGTCAAAGAC GAGGANTCAG 180  
 GACGTCGGTG CCTAGTGACT GAGCGCCANC CAGCCCATT CTNTACATTG CCATGGGCTA 240  
 AACCCAGTGT GCTGTAAACT CTTGCAGTTC CTTGNGGTTA TGGGATTTTG NTATCTTGNC 300  
 NGTGTTCCT CAANTAAAGG NNCTTGTTTG TAAAAATTGG GNAANAAGAA A 351

SEQ ID NO:1979

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02256

SEQUENCE DESCRIPTION:

GATCTGTTTC CTACAGACTT CAAATTTGAC ACCCCAGTGG ACAAACCTACC ACAGCTATAA 60  
 ATTGAGGCAG CTAACGTCAA ATTCTTGAAT ACAAACCTTT GCCTGTTGTA CATAGCCTAT 120  
 ACAAATGCT GGGTTGAGCC TTTCATGAGG AAAAAACAAA GACATGGTAC GCATTCCAGG 180  
 GCTGAATACT ATTGCTTGGC ATNNNGTATG TATATACTAG TGAAACATAT TTAATGATTT 240  
 AAATTTCTTA TCAAATTTCT TTTGTAGCAA TCTAGGAAAC TGTATTTTGG AAGATATTTG 300  
 AAATTATGTA ATTCTTGAAT AAAACATTTT TCAAACTCA AA 342

SEQ ID NO:1980

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02257

SEQUENCE DESCRIPTION:

GATCAGCATG ACCAGCACTC GTTGGNGGAA AGGTGTCTNT NAGGAGACGT CTGGAGCTTA 60  
 TGAGAAAACA GATACTGATG GGAAGTTTCT CTATCACAAA TCCAAATGGA ACATAACCAT 120  
 GGCCTCCTAT GTGGTCCACA CCAACTATGA TGAGTATGCC ATTTTCCTGA CCAAGAAATT 180  
 CAGCCGCCAT CATNGACCCA CCATTACTGC GGTGTCCCTG GTGATGGNGA TGAGGAGCTN 240  
 CTGCGCTTCT CCAACTGACA ACTGGCCGNT CTGCANGTCA GAGGATGGNC AGTGTCTGTC 300  
 CNGGGGTACT GTGGCAGNCA GCGACAAGCA ACCTGNGTCN 340

SEQ ID NO:1981

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02258

SEQUENCE DESCRIPTION:

GATCNTTCG NCTCTGAAGA AGACATGGTG ACTGTGGTGG AGGACTGGAT GANNTTCTAC 60

EP 0 679 716 A1

ATCAACTATT ACAGGCAGCA GGTGACAGGG GAGCCCCAAG AGCGAGACAA GGCTCTGCAG 120  
 GAGCTTCGGC AAGAGCTGAA CACTCTGGCC AACCCTTTCC TGGCCAAGTA CAGGGACTTC 180  
 CTGAAGTCTC ATGAGCTCCC GAGTCACCCA CCGCCCTCCT CCTAGCTCAG GGACCCAGCC 240  
 CCTCCTCTCT GAGAAACTCT GACCTTCATG TCCTTAGGCT GTGCTCCTGC CACTCTACCC 300  
 TGACACCTCA ATAAAGACCA GTGCTGGTTT TGTGGAAA 339

SEQ ID NO:1982

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02259

SEQUENCE DESCRIPTION:

GATCCTTNCG TGCTGAATAT CTGAAAAGAG AAATTTTTC TACAAAATCT CTTGGGTCAA 60  
 GAAAGTTCTA GAATTTNAAT TGATAACAT GGTGGGTTGG CTNAGGGNAA GAGTATATGA 120  
 GGAACCTTTT AAACGACAAC AATACTGCTA GCTTTCAGGA TGATTTTAA AAAATAGATT 180  
 CAAATGTGTT ATCCTCTCTC TGAAACGCTT CCTATACTC GAGTTTATAG GGGAAGAAAA 240  
 AGCTATTGTT TACAATTATA TCACCATTAA GGCAACTGCT ACACCCTGCT TTGTATTCTG 300  
 GGCTAAGATN CATTAAAAAC TAGCTGCNCT TAAA 334

SEQ ID NO:1983

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02260

SEQUENCE DESCRIPTION:

GATCTTGTC CAAGCTNAGG GTGTAGCGCT GCAAACGATG AAGCAAGAGT TTCTCATTAA 60  
 CCTTGTAAG CAAAAGCCAC AAATAACANA GGAACAACCT GAGGCTGTCA TTGCANATTT 120  
 CTCAGGCTNT TGGAGAAATG CTGCCAAGGC AGGACAGGAG TCTGCTTTGT GAGAGGGCAA 180  
 AAAGTGAAT CAAAACTCG CCTGCTTTGG GNTTTAAAT ACTTCAGGGN AGANAGCAAA 240  
 CAGNCTTTC ATTCGGTGTN ACTTTTCTCT NNAATTTTAA CTNNTTTAAC ACTTTTGTG 300  
 GATTAATGNA ATGATAAACG CTTTATCGC NN 332

SEQ ID NO:1984

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02261

SEQUENCE DESCRIPTION:

GATCCTGTGT GTGTGTACTA CCATAGAATG GGCCCCAAGA TGCATGATNA AGTGAGGAAA 60  
 AAAGCCCATG GTATCCTAAT GTTTGGAATG GAGAAAGTGT GTAGATGTAT GTGTGTGCAT 120  
 ATGTTTTTAC ACAGACGTAT ACACGTGTAT ATCATATGTC CACCTGCATA TGCCTAGGAT 180  
 GTCTCTGGGA GGATATCTAG CAGCCCGGCA GCCTGAATTG CCTCTGGGAA GAGGGGTGGG 240  
 AATGACTTTT CAATGTACAC CTTTTGTACC TTTTGAATTT TCGTACCATG TACATGTATT 300  
 ATCTATTAAA AAATAGTTCT TAATTTTAA A 331



EP 0 679 716 A1

SEQ ID NO:1985

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02262

SEQUENCE DESCRIPTION:

GATCACCCGG CAAGTTCAGG CTGAATTCTG AAGGCAAAC T GAGCAGACG GTCTCCATGG 60  
 CAACCCGAGC TTCAGAGGCC GAGGATGCCT CCCTTCTCAG CTTTCATGCAG GGCTACATGA 120  
 AGCACGCCAC CAAGACCGCC AAGGATGCAC TGAGCAGCGT GCAGGAGTCC CAGGTGGCCC 180  
 AGCAGGCCAG GGGCTGGGTG ACCGATGGCT TCAGTTCCT GAAAGACTAC TGGAGCACCG 240  
 TTAAGGACAA GTTCTCTGAG TTCTGGGATT TGGACCCTGA GGTGAGACCA ACTTCAGCCG 300  
 TGGCTGCCTG AGGACCTCAA TACCCN 326

SEQ ID NO:1986

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02263

SEQUENCE DESCRIPTION:

GATCCTTACA TCTGCATCTA GTTATCAGTA ATTTAGATAT TGAGCTATTT TGATTTATAT 60  
 TTAAGAAATT AATACATTAG CACTGAAAGT TAAATAGTGT GTTTAAGGTA GTTAATTTCA 120  
 GGTGGAATGG GTTTTTTTTA ATGAAGTGTA AATAATACCA ATGTATAAGN GTATATTATN 180  
 ATATTAAATA TTATAGTAAA AAGGAATGTG TGGTATTTNC TNCAGCAAAA CTATTTTTGT 240  
 GATNTTTTNA TTCTCANCTT TNTATTTAAA AAATGTTACA TCTGCAGAAA AGTTGAAAGT 300  
 ATAATAAACT CTTCAGTTAA A 321

SEQ ID NO:1987

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02264

SEQUENCE DESCRIPTION:

GATCTGCGCT GTGGCTGTCC CTGGACGTGC TGCAGCCCTC CTGTCCCTTC CCCCCAGTCA 60  
 GTATTACCCT GTGAAGCCCC TTCCCTCCTT TATTATTCAG GAGGGCTGGG GGGGCTCCCT 120  
 GGTTCNAGC ATCATCCTTT CCCCTCCCCT CTCTTCTCC CCTCTGCACT TTGTTTACTT 180  
 GTTTTGACA GACGTGGGCC TGGGCCTTCT CAGCAGCCGC CTTCTAGTTG GGGGCTAGTC 240  
 GCCGAATTCT ACAATCCCGC TGGGGCGGCC GGGGCGGGAG AGAAAGGTGG TGCTGCAGTG 300  
 GTGGCCCTGG GGGGCCATTC N 321

SEQ ID NO:1988

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02266

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCAAAAAT TTCTATCTGG AGAACCTCTG CGGACAAACC GAGTGCTTCC TGCAATTCCA 60  
 AGTCAACGAA GACACAGCAC AGCAGCAGAA GAGAGTGAAC ATTCTGCCAA CCCCACCAGT 120  
 GATGAAAATT AACTGTGGGC CACTCGCTGC AGAAATGTAG ATGAATATGT ATTTTCAACT 180  
 CTCAAAGGAC AAGATTACTC CAGTTTGTA GAACGAAGAC CAATTAGTA AGCTGCATTG 240  
 TATAAGCCAT CAGTTTATA ACTCGAAATT CTTTATTCCA AATAAAGATA CTCCCTAAAT 300  
 AAGCACTTAG ANAAA 315

SEQ ID NO:1989  
 SEQUENCE LENGTH:312  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS02268

SEQUENCE DESCRIPTION:

GATCAAAGCT GGGGCTGGAG GGTGGAGGTG TCAAGCCAGG CCAGGCAAAG GGAGATTGA 60  
 AGCCAGAGCA GGTGGGCGCA TCTCCAGGA AACCTGCAT CATTCTTCC TGGTGATTCT 120  
 TTCCTTCTTT GTTATGGTTC ACATGAGTCT ATGGAGTGCT CATTCTACAT TCTCCGTTCT 180  
 TATCTTCATC CTATGCAACT TTAGACCGCT ACTGTTTTTT AAAAGTGATT TGATTGNGG 240  
 CTGTAACCTT TTTTATTGT TGTTAGCTTT GACTTTGAAA TGTGTAATAA AGATTCAAGT 300  
 GAGCATTAGA AA 312

SEQ ID NO:1990

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02269

SEQUENCE DESCRIPTION:

GATCTTGGGG TCCCCGACG ACGTGCTCGA GTTCCTGAAG GTGTATGAGA AGCACTCNGC 60  
CCAGTGAGCA CCTGCCCTGC CTGCATCTGG AGAATTGCCT CTACCTGGAC CTTTTGTCTC 120  
ACACAGCAGT ACCCTGACCT GCTGTGCACC TTACATTCTT AGAGAGCAGA AATAAAAAGC 180  
ATGACTATTT CCACCATCAA ATGCTGTAGA ATGCTTGGCA CTCCCTAACC AAATGCTGTC 240  
TCCATAATGC CACTGGTGTT AAGATATATT TTGAGTGGAT GGAGGAGAAA TAAACTTATT 300  
CCTCCTTAAA 310

SEQ ID NO:1991

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02270

SEQUENCE DESCRIPTION:

GATCCGAGTG AATGCAGTAA ACCCCACAGT GGTGATGACG TCCATGGGCC AGGCCACCTG 60  
GAGTGACCCC CACAAGGCCA AGACTATGCT GAACCGAATC CCACTTGGCA AGTTTGCTGA 120  
GGTAGAGCAC GTGGTGAACG CCATCCTCTT TCTGCTGAGT GACCGAAGTG GCATGACCAC 180  
GGGTTCCACT TTGCCGNTGG AAGGGGGCTT CTGGGCCTGC TGAGCTCCCT CCACACACCT 240  
NAAGCCCCAT GGGCGTGCTC ATCCTACCCC CAATCCNTCC AATAAACCTG ATTCTGCTGG 300  
CCAAA 305

SEQ ID NO:1992

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02271

SEQUENCE DESCRIPTION:

GATCGAGACA CGTGATGGGA AGCTGGTGTC TGAGTCCTCT GACGTCCTGC CCAAGTGAAC 60  
AGCTGCGGCA GCCCTCCCAG CCTACCCCTC CTGCGCTGCC CCAGNNNCTG GGAAGGAGGC 120  
CGCTATGCAG GGTAGCACTG GGAACAGGAG ACCCACCTGA GGCTCAGCCC TAGCCCTCAG 180  
CCCACCTGGG GAGTTTACTA CCTGGGGACC CCCCTTGCCC ATGCNTCCAG CTACAAAACA 240  
ATTCAATTGC TTTTTTTTTT TGGTCCAAAN TAAACNTCA GTTAGCTNTG CCAATTTNAA 300  
A 301

SEQ ID NO:1993

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02272

## SEQUENCE DESCRIPTION:

GATCTGAACT CCAGCTGCCC TACAACTCC GTCACAGCTT TTNTTCTCAC TTCATGTGAA 60  
AACTACCCCA GTGGCTGACT GAATTGCTGA CCTTCAAGC TCTGTCCTTA TCCATTACCT 120  
TAAAGCAGTC ATTCCTTAGT AAAGTTTCCA ACAAATAGAA ATTAATGAAT AAATGTTGAC 180  
ACTTTGATAG CACTGATATG GAGATTATCC TTTCAATTGAG CCTTTTATCC TCTGGTCTTC 240  
TTTGAAGAAC CCCTCACTGT CACCTTCCTG AGAATACTCT AAGACCAATA AATACTTCAG 300  
TATTTAGAA A 311

SEQ ID NO:1994

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02274

## SEQUENCE DESCRIPTION:

GATCTAAAAC TNAAGAACAA ATTCTATTTA TTTATTATTG GAAAATNAAA AGCAACTCAA 60  
AACAACCTCA ACCTGGAGGT GCATTATATA TTCATTCTGC ATTTATTCTG TAAAAAGGTG 120  
ACTGTTTTAT AAATNCTTTT AATTTATGTT CAATATATAT AAAAAAGTGCA TCTNTTTTNT 180  
TTTTCCCTTT TTTCTCCATA ATTTTAAGAA ATGAATNNGN TTGTTGTCAA CACATTGTG 240  
AAGTCTTGTG CTATAAAGGG GAACTTCCCC TAATAAAAGG GCCTTGGAAA CCTCAAA 297

SEQ ID NO:1995

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02275

## SEQUENCE DESCRIPTION:

GATCTAGGAG AGGCGGCTCT GAACGATTAC CTGCGGGTCA AGACAGTNAC CTTCAATAC 60  
TGAAGAAAGG TCTTTTAAAG AAGAAAGTCC CTGCCCCCTC CTCGTGGCTG GGGCCCCCTC 120  
CCTNTTAAGC CTGGNTGCAC AGCACCTCCC ACCTGGGGGG CTAGTGGAAG CCCTCCTGCN 180  
TGCACACCAT GTTTGCNTCT TGGACGCCCT CTTTCCAGTN ANAAGCAGCC CTTGGNTGGN 240  
TNAGGTGTGC CCCTCCCAGG NAGAATAAAG CTTCTAAAGA NAGACCGTCC AAA 293

SEQ ID NO:1996

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02276

## SEQUENCE DESCRIPTION:

GATCAGGAGG AAGTGAGCAG TCGCCTGCCT GCAGCAGGNA GCTTTCTACT CCTGCCTCAT 60  
GCGTACGTCC CACAAATGCA GGTGTCCTGA GCACCACACC CAGTGGGAAG AGTGTGGGGG 120  
AGGCGCACAG TGTGAGCCCG CCCCCACGTC GTGGGTAAAC ATCTGTTATC AACTGCTGT 180  
CGTTGTTGTG GGTGTTGTCC TTGAACAAGA TGTGGGCCTT GCAAGATGGG AGAGTAAACC 240  
TTGAAGGGCT TTATTAAAGA AATAAAAAAG NACTTNTTGT ATCTTTTAAA 290

SEQ ID NO:1997

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02277

SEQUENCE DESCRIPTION:

GATCCTGAAG AGGATGGTGT GGGAAATGCAC TTTGAGAAAT GNCTATCTAA CCTTTNGAAA 60  
 CTTAAAGTGT TCCCAGTCCC CATTATACTT TTTAAACCA CAATAGTCAC ATAAGGAAAT 120  
 AATCTAGCAG CTCATCCCTT TGCATCCAAT GTTTGAACTA TTTTAGAAA GTGCTCTNGT 180  
 TCTGTCAAAG AACCTTCAAC ACAGAAAAAT ACANAAATGA GGGAAATGTA TAATTCCTGC 240  
 AGGAGAGAAG TGTGTTAAC ATGTCAATAN ATGTTCTTAG ANAGTTAAA 289

SEQ ID NO:1998

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02278

SEQUENCE DESCRIPTION:

GATCAGAGAA GCTAGGAGAG CTCCAGCAGG GGCACAGAGG ATTGGNNGCA GGAGGAGTCT 60  
 GGAACACAGC CTTCATGCCC CTTGACCCCA GGCCGACCCT CCCCACACCC TAGGGTACCC 120  
 CAGTCGTATC CTCTGTCCGC ATGTGTGGCC AGGTCTGACA AACACCTGTA GATGACTGNT 180  
 GGCCNAACCT GGGNCCTGNN CAGGAGGTTG GAGCAGNAAG GGCTCTCCCT AGGGGTGGTG 240  
 TNTCTCTCT AGGGTATTGG GNTGCATGTN NTGCACTNN 279

SEQ ID NO:1999

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02279

SEQUENCE DESCRIPTION:

GATCATGAAG GAACACATAG CACCAAGAGA GGCCATGCTA AATCTCGCCC TGTCAGAGGT 60  
 ATCCACACTT CTCCTTTGGG GAAGNCTTCC CTGTCCCCCT TGCATTTCTT TCTAACTCT 120  
 CTGTTACACG TCATTGAAAC TACACTTTTT TGGTCTNNTT TTNTGCTAGA CTGTAAGTTC 180  
 CTTGGGGNCA GGGCCTTTGN CTGNCTCATC TCTGTATTCC CAAATGCCTA ACAGTACAGA 240  
 GCCATGACTC AATAAATACA TGNTAAATGG NAAA 274

SEQ ID NO:2000

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02280

SEQUENCE DESCRIPTION:

GATCTTAACA AAATTCGTAG CAGTGGAACC TTGAAATGCA TGTGGCTAGA TTTATGCTAA 60  
 AATGATTCTC AGTTAGCATT TTAGTAACAC TTCAAAGGTT TTTTTTGTGTT TGTTTTCTAG 120  
 ACTTAATAAA AGCTTAGGAT TAATTAGAAG AAGCAATCTA GTTAAATTTC CCATTTGTAT 180  
 TTNATTTNCT TGAATACTTT TTNCATAGTT ATTTGTTTAA AANGATTTAA AAATCATTGC 240

ACTTTGGTCA GAAAAATAAT AAATATATCT NATAAACAAA

280

SEQ ID NO:2001

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02281

SEQUENCE DESCRIPTION:

5  
10  
15  
GATCTGCATG TTCTCTCTTT GGGTTCAAGC ATTCCTTAC AGAAGAGCCA CCGTGGAAGT 60  
CATGGGTAAA TATGTGTTGA ATTGGTAACT CCCTCTTGGA GAATTTCTTG TGAATTACAC 120  
AGCAATAGGG GAACTCATT AACTGGAGAC ATAATCTCAA TTTGTAAAGT GTGGCCCAT 180  
TTCTAACATT TTNANNTTGC ATACCTCCC CTCTCTTCTC GATTGATGAA ACTAACAAAG 240  
AGGTTAATAA AAGCCCATCT CGTCATGTAA A 271

SEQ ID NO:2002

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02282

SEQUENCE DESCRIPTION:

20  
25  
30  
GATCTTACCC GTGACAAAAT GTGTTCCATG GTCAAAAAAT GGCAGACAAT GATTGAAGCT 60  
CACGTTGATG TCAAGACTAC CGATGGTTAC TTGCTTCGTC TGCCTGTGT TGGTTTACT 120  
AAAAAACGCA NCAATCAGAT ACGGAAGACC TCTTATGCTC AGCACCCNCA AGGTNCGN 180  
AATNCGGGAG AAGATGATGG GNAATCATTG GCCCCGTGAG GGTCAAGGC AAANTTTGCT 240  
TTTGAANGNA AGGGGGGNN AATAATTNGN 270

SEQ ID NO:2003

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02283

SEQUENCE DESCRIPTION:

35  
40  
GATCCCAACA GAAGAACATC GGAGACCAGA GAGAGGAACT CAAAGGGGCG CTGCCTCCGG 60  
GTCTGGGGTC CTGGCCTGCG TGGCCTNTTG GCACGTGTTT CTCTCCCCG CCCGGCCTCC 120  
AGTTGTGTGC TCTCACACAG GCTTCCTTCT CGACCGGCAG GGGCTGGCTG GCTTGACAGC 180  
CACGAGNGTN GGCTCTACCC NACACTGGCT TTGCTGTGTA TACGCTTNTT GCCCTTAAAT 240  
AAATATGCAC ATTTTATCCA TTA 265

SEQ ID NO:2004

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02285

SEQUENCE DESCRIPTION:

50  
GATCCACATT GTTAGGTGCT GACCTAGACA GAGATGAACT GAGGTCCTTG TTTTGTGTTG 60

TTCATAATAC AAAGGTGCTA ATTAATAGTA TTTCAGATAC TTGAAGAATG TTGATGGTGC 120  
 TAGAAGAATT TGAGAAGAAA TACTCCTGTA TTGAGTTGTA TCGTGTGGTG TATTTTTTAA 180  
 AAAATTTGAT TTAGCATTCA TATTTTCCAT CTTATTCCCA ATTAAAAGTA TGCAGATTAT 240  
 TTGCCCAAA 249

SEQ ID NO:2005

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02287

SEQUENCE DESCRIPTION:

GATCAGGAGC AAACAGACCC TGCAAGGTCC TCCAGGCCTG GGGACAGGAA AGCCACTGAC 60  
 CCAGCCCGGG AGGCAGAACCC AGGCAGCCTC CNTGGCCCCA GGCAGCCCTT TTCCCTCCAG 120  
 TGGCACCTCC TGGAAACAGT CCACTTGGGC GCAAAACCCA GTGCCTTCCA AATGAGCTGC 180  
 AGTCCCCAGG CCATGAGCCT CCCGGGAATG TTTAATAAAG GGCCTGGCCA CCTCTCCTCA 240  
 AA 242

SEQ ID NO:2006

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02288

SEQUENCE DESCRIPTION:

GATCTAAGTT TGATAAGAGC CTGTGTGGTG AGTATGGTGT GTATGTGAAG GTGACTTCCA 60  
 TCCAGGACTG GGTTCAGAAG CCATAGCTGA GACTAATGCA AGGCTGGCGA AGCCTTGCTG 120  
 AAAGAAGATT TCAGCTGGAG AGGCAAAGTG GCGGGAGTGG CAGAGTGGTG CGTAAAGTGTG 180  
 GTTAAGTNTG GGTCCANCCT GCATTCTGAG CAATCAATAA AGTNTTCTT TTNCCCAA 239

SEQ ID NO:2007

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02289

SEQUENCE DESCRIPTION:

GATCCTGAAG GTAATACAAT CAGCAACATT AAAACATTTT TTTCAATTTT TGTTACTGAA 60  
 GTAAAATAAG CATTCCACAT TTATAAACAA CAGGTTATTT CAGGAAGATA TTTTCATATC 120  
 TTACAGCGAA AAGTCTTTTC AAACAGAAGC ACCTAATATT TAATATATTA TTTTGTAAAT 180  
 TATTGACTAA CAAAATGATG ACTCGACTGG CGAAATAAAA TACAGTTTTT AAATCAAA 238

SEQ ID NO:2008

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02290

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

5 GATCCTGAGA NCTTCAAGCT CCTGGNNAAT GTNCTGGTGA CCGTTTTGGC AATCCATTTC 60  
 GGCAAAGAAT TCACCCCTGA GGTGCAGGCT TCCTGGCAGA AGATGGTGAC TGGAGTGGCC 120  
 AGTNCCCTGT CCTCCAGATA CCACTGAGCT CACTGCCCAT NATGCAGAGC TTTCAAGGAT 180  
 AGGCTTTATT CTGCAAGCAA TCAAATAATA AATNTATTCT GCTANGNNA AACAAA 236

10 SEQ ID NO:2009  
 SEQUENCE LENGTH:235  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02291  
 SEQUENCE DESCRIPTION:  
 15 GATCATTACC ATTACAGGAA CACAGGACCA GATACAGAAT GCACAGTATT TGCTGCAGAA 60  
 CAGTGTGAAG CAGTATGCAG ATGTTGAAGG ATTCTAATGC AAGATATTTT TCCTTTTTTA 120  
 TAGTGTGAAG CAGTATTCTG GAAAGTTTTT CTAAGACTAG TGAAGAACTG AAGGAGTCCT 180  
 GCATCTTTTN NNGTTTAANC TGCTTCTGTT NAAAANGCCA NCATTCTCT GTTTN 235

20 SEQ ID NO:2010  
 SEQUENCE LENGTH:233  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02292  
 25 SEQUENCE DESCRIPTION:  
 GATCCTGAAG AACTTCAAGC TCCTGGGAAA TATGCTGGTG ACCGTTTTGG CAANNNGTTT 60  
 CGGCAAAGAN TTCACCCCTG AGGTGCAGGC TTCCTGGCAG AAGATGGTGA CTGGAGTGGC 120  
 CAGTGCCCTG TCCTCCANAT ACCACTGAGC TCACTGCCCA TAATGCAGAG CTTTCAAGGA 180  
 TAGGCTTTAT NCTGCAAGCA ATACAAATAA TAANTCTNTC CTCCTAAGAG AAA 233

30 SEQ ID NO:2011  
 SEQUENCE LENGTH:229  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02293  
 SEQUENCE DESCRIPTION:  
 35 GATCCTTGAC GAGGAGAGAG AGCTTGAAAA GCTGTTTCAG CTGGGCCCCG CTTACCTGT 60  
 GAAGATGCCC TCTCCACCAT GGAATCCAA TCTGTTGCAG TCTCCTTCAA GCATTCTGTC 120  
 40 GACCCTGGAT GTTGAATTGC CACCTGTTTG CTGTGACATA GATATTTAAA TTTCTTAGTG 180  
 CTTCAGAGTT TGTGTGTATT TGTATTAATA AAGCATTCTT TAACAGAAA 229

45 SEQ ID NO:2012  
 SEQUENCE LENGTH:223  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02294  
 SEQUENCE DESCRIPTION:  
 50 GATCTGGCAT AAATAAATTN AATAAATATT TTAATGCTCC ATTTTAAAT GTTGCTTTTC 60

55



ATACTAAAGA ATGGTGTAGA CTTGTTTTGC AACTNTAAGG TACCCAGTTA TCAATTTAAT 120  
CAATGTTTTA GAGNAGGAAA TNATTTTTTN GGTAGAAATT GTTCANGAAC CTTAATTGAA 180  
TGCATTAAAT GATGGTGGCA AAATAAACCT ATTAGAAATT AAA 223

5

SEQ ID NO:2013  
SEQUENCE LENGTH:221  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS02295  
SEQUENCE DESCRIPTION:  
GATCAATGCC CTCATCTGCA ATGTAGGGGC CGGTGGACCT GCTCCAGCAG CTGGTGCTGC 60  
ACCANAGGAG GTCCTGCCCC CTCCACTNCT GCTGCTCCAG CTGAGGAGAA GAAAGTGGAA 120  
GCAAAGAAAG AAGAATCCGA GGAGTCTGAT GATGACATGG GCTTTGGTCT TTTTGACTAA 180  
ACCTCTTTTA TAACATGTTT AATAAAAAGC TGAAC TTAA A 221

15

SEQ ID NO:2014  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02296

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SEQUENCE DESCRIPTION:  
GATCTGTAGT GTCATGGGTG CTGCCGAGA CGNAAAGTTGA NCTGGGGGTG CCTGCAGCCT 60  
TCCACTCCTG CCCC GCCTCA CCCACATGC TCCCTGTTT TAATGCTTTC TCTAACTTCC 120  
TCACCCCTTA ACCAAAAAGG TGTGTTTNC TTTGTNCATA TAGCCATTCT NAAATATNAG 180  
TAATGTAAAC CTNACTTTAT TAAAAAATTA TCCAGCAAA 219

25

SEQ ID NO:2015  
SEQUENCE LENGTH:216  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS02297  
SEQUENCE DESCRIPTION:  
GATCAGGTTT GTTGAGTTT TTAGCCTAAT TCCAAAGCAT GGAAGAGTGC TCTAGGTAGG 60  
AAAGAAAGCT TTTTCTTACG ATTTGTAGCT ACCTACTGTG CCTGACTTGG TGCCTGTGTG 120  
AGGATTAAGC CCTTAGTCTG CTCTTGCAAT TATTCAAATG ACAAATTAAA TTTGCTTTTG 180  
TAATAACAAT AAAAGTTGTC ATCTTCCCTT TTGAAA 216

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40

SEQ ID NO:2016  
SEQUENCE LENGTH:210  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

45

CLONE:HUMGS02298  
SEQUENCE DESCRIPTION:  
GATCCTGCCA TCACTGCTGC AAAGAGAACA CGAGACTCAA GGAAACTCCT CCTCCACCGC 60  
AGCCCAACTG TGCCTGCTAG TNTCCCGTG CACACAGGCA GCTCCAGGGG GCTCTGGTTG 120

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CCAACAAACA GCATTTGTAA ATGGTCTATT AGCCTTCATT TATACTGCCT AACAATTATT 180  
TGAAGGAATA AATTGATGTC AATGGCTAAA 210

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SEQ ID NO:2017  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS02299

SEQUENCE DESCRIPTION:

15

GATCTAGCCT GATTCCTGCG TGTCCGAAAG AACTTAACGT TTTAAAGGTN ATTGTNAAGT 60  
AACTGTGTGG GGTTCCTAATG CCAGTTTCCT AATTCATCT CACTGGAGAT GTTTAAAGTT 120  
GGCCTCTATC CTAATGACTC AAAACTTGGT TCTTAACTAC CATGATTGCT TTTNAGGGCC 180  
CGGAATTATA AATATATATN ATATTTAANT TGTTTGAAA 219

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SEQ ID NO:2018  
SEQUENCE LENGTH:208  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02300

SEQUENCE DESCRIPTION:

25

GATCCGGGGC ACAAAGAGGG TGGGGAACAT GGGGGCTATA CTGGGGAAAAG CAGCCATGCT 60  
CCCCCNACC TCCAGCCGAG CATCCTTCAT NAGCCTGCAG AACTGCTTTC CTATGTTTAC 120  
CCAGGGGACC TCCTTTCANA TGAAGTGGGA AGAGATGAAA TGTTTTTCCA TATTTAAATA 180  
AATAAGAACA TTA AAAAGCA ACCCCAAA 208

30

SEQ ID NO:2019  
SEQUENCE LENGTH:202  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02301

SEQUENCE DESCRIPTION:

35

GATCTCAAGG CTGCCGTACT GGAGGCCATG ACTGCCTTCC GCAGAGCAGG TGCTGACATC 60  
ATCATCACCN ACTACACACC GCAGCTGCTG CAGTGGCTGA AGGAGGAATG ATGGAGACAG 120  
TGCCAGGCCC AAGAACTAGA ACTTTAAAC GTTCCCGGGG CCTCAGACAA GTGAAAACCA 180  
AAGTAAATGC TGCTTTTGA AA 202

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SEQ ID NO:2020  
SEQUENCE LENGTH:224  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

45

CLONE:HUMGS02302

SEQUENCE DESCRIPTION:

50

GATCTTCTTT GAGACAAGGC AGGCTGTGGC CATGTAGCCC CATCACACTG TGTTTGTNAT 60  
TGTCTGTGTG TCTGTCTCCC CCACCAGACT GTGAGCTCCA TGAGGGCAGG GACCGTGTCT 120  
TGCCGTTCT CTGTATCCCC AGTGCTTGA ACAGAGCGAG TGCTCACTGT GTATTTAATA 180

55

AATGGACAAA GAGAGAGGAT GACCCTCACG GGGAGACAGA GAAA

224

SEQ ID NO:2021

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02303

SEQUENCE DESCRIPTION:

GATCGGCAAA TGCATTGGCC TCCTGGTTAA GCACGTTTGG GGGATAATTT TCTCTTCTTT 60  
 AGGCAATGAT TAAGTTAGGC AATTTCCAGT ATGTTAAGTA ACACACTTAT TTTTGCCTGT 120  
 GTATGGAGAG ATTCAAGAAA TAATTTTAAA ACCGCATACA TAATAAAAGA CATTGTTGCA 180  
 TGGCTTATAG TCAAA 195

SEQ ID NO:2022

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02304

SEQUENCE DESCRIPTION:

GATCTGTGCC GTGGTCCTGA GGCAGTTGTC TCCACACAAG TACCTCTAGA ACAATCCCCT 60  
 TTTTCCATC AAGCTGTAGC CTGCAGAGAA TGGAAACGTG GGAAAGGAAT GGTATGTGGG 120  
 GGAAATGCAT CCCCTCAGAG GACTGAGGCA TAGTCTCTCA TCTGCTATTG AATAAGACC 180  
 TTCTATCTTG AAA 193

SEQ ID NO:2023

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02305

SEQUENCE DESCRIPTION:

GATCTNCCCT GCATCCTGAC CAAGACCCCA ACCGTGCCCC CAACAGACTC CCCCTGGGAG 60  
 ATTCAGCCTA TTTACTGATG AGGAAAGTGA AGCCGGGTCT CCTGTCTCCC CAAATTCATT 120  
 GCACCTACGA TATAGTCCAG GATTGGGTAG CAAGATTAAA CACAAGCGCT TCAAATTGAT 180  
 GAAAACCACA AA 192

SEQ ID NO:2024

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02306

SEQUENCE DESCRIPTION:

GATCCCTAAC TACCAACCCC CTGAAGGCAG GTACAATGAC ATCACCAAGG TGTACACACA 60  
 AGTGGAGTTT AAGAGATAGA CTTGCAGGCT GCTATCCTTA ACATGCTGCC CCTGAGAGTA 120  
 GGAATGACCA GGGTTCAAGT CTGCTTCCA CAGAATCAGG CATNCTGTTA ATAAATACTG 180  
 GTTTAATCAA A 191

# EP 0 679 716 A1

SEQ ID NO:2025

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS02307

SEQUENCE DESCRIPTION:

10 GATCGTATTT CAGTTTTTTG GGTCAATATA TGAACAATGT GTGAACCAGA ACGTATGGTA 60  
TTTGACATCA AAGCTATGTC TTGGCATATG TTTATGTTGA TATACTTGAA TTCATTTAAA 120  
ATGGAATGTT AATTACATCG ACTTCTTACT ATAAAAATA AAAAGTTATT GTCCAGTGCA 180  
CAGAAA 186

SEQ ID NO:2026

15 SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02308

20 SEQUENCE DESCRIPTION:

GATCCATTGA GAAAGAGATG ATGTAATAAA TAATTAAGAT TAGTAATAAT ATTATCAGGG 60  
GTGATTATGA CCAGTTGAAT AATCTCTTTC CCTGAATTA TTTAGCTAAC AAATTAAGTC 120  
TCCCAAATAT NTAAANTAAT GTAAANTCAT ATTNACTGC CCATTATTAA CTAAAAATATT 180  
TNTGTNTGAC TTTGAGCACC AACTGGTAAT ACTAGTAAAT ACCCATGTCA TGCAGATGGC 240  
25 TGGGCGAATA AGAGATGTCT AAAAATATGC ACTGGTCTTG GGAAACATGG CACAAGTAAG 300  
GNTATCATAT ATGANGTCTG GTTTATTTTA TGTCTGATT CTTTTTGANT GAGTAGTTNG 360  
GGACTCCANT TCTAAGGNTN 380

SEQ ID NO:2027

30 SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02309

35 SEQUENCE DESCRIPTION:

GATCTCTCCA CAGGGCTTGT TTTCCAAAGA AAAGTATTGT TTGGAGGAGC AAAGTTAAAA 60  
GCCTACCTAA GCATATCGTA AAGCTGTTCA AAAATAAGTC AGACCCAGTC TTGTGGATGG 120  
AAATGTAGTG CTCGAGTCAC ATTCTGCTTA AAGTTGTAAC AAATACAGAT GAGTTAAAAAG 180  
AAA 183

SEQ ID NO:2028

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS02310

SEQUENCE DESCRIPTION:

GATCTGCAGC TGCCTGGGA CTTGAATCCA TGCAATGTTT AGAGTGTGAA GTCAGTTACT 60  
50 TGTGATGTT TTCTTACTGT ATCAATGAAA TACATATTGT NATGTCAGTN CTTGCCAGGA 120

ACTTCTCAAC AAAATGGAAT TTNNTTTTNC AGTATTTCAA TAAATATTGA TATGCCCAGC 180  
CTGNTAAA 188

5

SEQ ID NO:2029  
SEQUENCE LENGTH:178  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS02311

SEQUENCE DESCRIPTION:

GATCCATGCT GATTTTATT GCACAAGAAT TAGGTTTGAA CTCTTGAGCT GGAACCTCAG 60  
CAAACTAGAG TATATATTGT TCAGTATNNC TTTGGAAACA TTTCATTAAT GTACTTGTCT 120  
TACANAAATT TCTGAACTTT AGTAAAAAAA AAATAAAGTT AAACTTTTAA AACTCAAA 178

15

SEQ ID NO:2030  
SEQUENCE LENGTH:176  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS02312

SEQUENCE DESCRIPTION:

GATCGGTATG TTTTGAAAAG AGTAATTTAA CTTTGGGTG CCAGGAAATG GGTCTTCTCA 60  
AAGTCCATTG CCGGCAATGG GCAGGCCTGC AAATACTGGC ACAGAGCATT AATCATACAC 120  
CTTATTAACG GTGAGGTGAA TAACTTTGAA ATAAAGTTTT AGAGAAATGT TTCAAA 176

25

SEQ ID NO:2031  
SEQUENCE LENGTH:174  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS02313

SEQUENCE DESCRIPTION:

GATCCGCCTG GCAGCCATTG CAGAGTCAGG GGTAGAGCGG CAAGTACTTT TGGGAGACCA 60  
GATACCCAAA TTCGCCGTTG CCACTTTACC ACCCGCCTGA ATCCTGGGAT TCTAGTATGC 120  
AATAAGAGAT GCCCTGTACT GATGCAAAAT TTAATAAAGT TTGTCACAGA GAAA 174

35

SEQ ID NO:2032  
SEQUENCE LENGTH:172  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40

CLONE:HUMGS02314

SEQUENCE DESCRIPTION:

GATCCAGAAG TTATGGTGGC TTTCCAGGAT GTGGCTCAGA ACCCAGCAAA TATGTCAAAA 60  
TACCAGAGCA ACCCAAAGGT TATGAATCTC ATCAGTAAAT TNTCAGCCAA ATTTGGAGGT 120  
CAAGCGTAAT GTCCTTCTGA TAAATAAAGC CCTTNCTGAA GGAAAAGCAA CN 172

45

SEQ ID NO:2033  
SEQUENCE LENGTH:170

50

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02315

SEQUENCE DESCRIPTION:

GATCTCAGGA CCTCTTTACA CTTTCAAAG TTAATAAGA CTCTGAAGAG CTTTCTTTA 60  
TGAGGTATA TCAATATTTA CTACATTAAG AATTAAACA GAAAATTAA AGTAGGTATT 120  
TATTGATTTA TTAAACAAT AAAAATAATA AAGTATTACA TGCTAACAAA 170

SEQ ID NO:2034

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02316

SEQUENCE DESCRIPTION:

GATCCGTTTG CTGTGAACCC TATGTTATTT CCATGTGTCA AGTGGGTCTT GTGTTGCCAG 60  
CTTCTATTTG AAGATTGCGT TTGCACTCAG TGTAAGTTTC TGTCAGCAGT AGTTTCACCC 120  
ATTTGCATGG AAAAATTAA AGCTAATAAA GCAATTAA AAGCACAAA 169

SEQ ID NO:2035

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02317

SEQUENCE DESCRIPTION:

GATCCCACAG TCTCAGCCCT GCTTACTAGT GAGAAAGACT GGCAAGGTTT CCTAGAGCTC 60  
TACTTACAGA ACAGCCCTGA GNCCTGTAAC TATGGGCTCT GAAGGGGGCA GGAGTCAGCA 120  
ATAAAGCTAT GTCTGATATT TTCCTTCACT AATATGAAA 159

SEQ ID NO:2036

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02318

SEQUENCE DESCRIPTION:

GATCCGGGGN AGCTAGGATG GGGAACCTGC CACAGCCAGA ACTGAGGGGC TGGCCCCAGG 60  
CAGCTCCCAG GGGGTAGAAC GGCCCTGTGC TTAAGACACT CCTGCTGCCC CGTCTTGAGG 120  
GTGGCGATTA AAGTTGCTTC ACATCNTCAA A 151

SEQ ID NO:2037

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02319

SEQUENCE DESCRIPTION:

GATCTAACAT CAACTAACA GCTTTCAGAA AGGAGACTNT TGNCATCTTT TCACCAAGGA 60

GTATATTTGT AGAGTAATAT ATGTGTGGAA NTTNAAATT ATATCATTTG ACATGATTTA 120  
 TGAGGCTTAT TTAAGCTGGA GTNNCCN 148

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SEQ ID NO:2038  
 SEQUENCE LENGTH:143  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02321

10

SEQUENCE DESCRIPTION:  
 GATCTGGTCT AGTTAACCTA GAAGTATTTT TGTCTCTTAG AAATACTTGT GATTTTATA 60  
 ATACAAAAGG GTCTTGACTC TAAATGCAGT TTAAAGAATT GTTTTGAAT TTAAATAAAG 120  
 TTACTTGAAT TTCAAACATC AAA 143

15

SEQ ID NO:2039  
 SEQUENCE LENGTH:142  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02322

20

SEQUENCE DESCRIPTION:  
 GATCTGGAGG AGGTGAAGGC CAAGGGACCT GCTTCTATTA GCCCTTCTCC ATGGCCCTGC 60  
 CATGCTCTCC AAACCACTTT TTGCAGCTTT CTCTAGTTCA AGTTCACCAG ACTCTATAAA 120  
 TAAACCTGA CAGACCATGA AA 142

25

SEQ ID NO:2040  
 SEQUENCE LENGTH:156  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02323

30

SEQUENCE DESCRIPTION:  
 GATCGAAAGA AGAACATCAT GAAAAANAAA TNAACTTTGC TTAGTGGATT AGACTCCTTT 60  
 GCTGAAGTCA GTTATTCATC AAGAATGCAA TTAGACTAAT TGTGAATAAA TGATTGAATG 120  
 AAGATATAAT AAATAAAAGC TATAATTATA GATAAA 156

35

SEQ ID NO:2041  
 SEQUENCE LENGTH:138  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02324

40

SEQUENCE DESCRIPTION:  
 GATCTCTCCT TCAGTCTGCT CTGTTTAATT CTGCTGTCTG CTCTTCTCTA ATGCTGCGTC 60  
 CCTAATTGTA CACAGTTTAG TGATATCTAG GAGTATAAAG TTGTCGCCCA TCAATAAAAA 120  
 TCACAAAGTT GGTTTAAA 138

45

SEQ ID NO:2042  
 SEQUENCE LENGTH:137

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02325

5 SEQUENCE DESCRIPTION:

GATCCACAGG CAGAGCCAAG GGAAGGTGTG ATTCTNTGAG GAAAGAGTGA TTCTGATATA 60  
TGTACTTGTC ACATTGGTGT TGGACACATT TGCGCCAAAA GTATGGTAAT NCTATTATNA 120  
AATAATTCTC TGAGAAA 137

10

SEQ ID NO:2043

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS02326

SEQUENCE DESCRIPTION:

GATCCAAACT GGAANCAGCT CAAATNTCCA TCAATAGCAG AAAGATAAAC AAATGTNGGG 60  
ATGTNCAGAG CTTGAAATAT GACACANTAT AAAAGGACAA ACTATTAAAA CTCACAACAG 120  
CATGGATAAN TCTN 134

20

SEQ ID NO:2044

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS02327

SEQUENCE DESCRIPTION:

GATCCAAGCA GGCCTTGAAT GCAATNGCAA GTGGTTTATA GTCCCTTGCT CTTACAACTT 60  
GCAGGGACAT GTGGTTATTT AGAAATTGTG ACTGAGCGGA CCCAAGAATN TAAATAATAT 120  
TCATAAACCT AAA 133

30

SEQ ID NO:2045

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS02328

SEQUENCE DESCRIPTION:

GATCACCTGT AGGGAAATGA AGTGTNCCCT GGAACAAGGA GGTGGGGGCA NTGTGGCCCC 60  
TTCCCCAACT GGGGGTGGAC AGCTGTNTCC TGGGGTGGGT TGGTATTAAA GAGGAAAGCN 120  
ATTTTTTGGA AA 132

40

SEQ ID NO:2046

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

45

TOPOLOGY:linear

CLONE:HUMGS02329

SEQUENCE DESCRIPTION:

GATCCAGGA ACTGTGGGCA CCCATTTTCT GTGTCTCCA GCCCATTTCC ACTCCTAGTT 60

50

55



EP 0 679 716 A1

TGTCATGGAT AATNTTTGTT GTTCCTGTG TGATTTTTCG CATCAAAATA AAAATTTGAG 120  
ACTCGTTAAA 130

5 SEQ ID NO:2047  
SEQUENCE LENGTH:130  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS02330  
SEQUENCE DESCRIPTION:  
GATCCAAGGT CAAAAAACA AATNCATCAA TTCAGCACAC CACCAACTNA NAGGCTAAGC 60  
ATCTTACTGC TAATTCATTG ANGCTGCCAT TTGTCAAGTG CCAAATTGAN TTATTGATTT 120  
GTCAATANTN 130

15 SEQ ID NO:2048  
SEQUENCE LENGTH:130  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20 CLONE:HUMGS02331  
SEQUENCE DESCRIPTION:  
GATCAGATAT AAAAAATAA AGTTTTTNAT TTCATTAAAT ATTTAATTAA AACTGCTAAG 60  
TTTGAAAATT TTTACCAAGA AATANTTTTN ANAAATTTTN CTAAGTTGAT AAAGGCTTTT 120  
25 AAGCAATAAA 130

SEQ ID NO:2049  
SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear

CLONE:HUMGS02332  
SEQUENCE DESCRIPTION:  
GATCTATATT CCCTTATTGC ATTTTCCTTA TGTATAATTT TCCAGATGGT GATGTTACTT 60  
35 TTCAGTGTAC TCATATGTCT CATTTTCATC TAAAATTAAA TGGCAGGAAA CAAGGACTGC 120  
ATAGAGAAA 129

SEQ ID NO:2050  
SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
40 TOPOLOGY:linear

CLONE:HUMGS02333  
SEQUENCE DESCRIPTION:  
45 GATCAAAAGC TTATTCNTTT TTTTTTTTTT TTCTTTGGTG TAAAGCCAAC ACCCTGTTTA 60  
AAANANATAA TTTTTTTTAA TCATTTTGCN TCTTTTTTTT TTGCTTCATT NAATAAAAAAN 120  
TGGAAGAN 129

50 SEQ ID NO:2051  
SEQUENCE LENGTH:148

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02334

SEQUENCE DESCRIPTION:

GATCTGAACA CCACAGCCCC TGTACTTGGG TTGCCTCTTG TCCCTGAACT TCGTTGTACC 60  
AGTGCATGGA GAGAAAATTT TGTCCTCTTG TCTTAGAGTT GTGTGTAAAT CAAGGAAGCC 120  
ATCATTAAAT TGTTTTATTT CTCTCAAA 148

SEQ ID NO:2052

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02336

SEQUENCE DESCRIPTION:

GATCCANCTN TNTCAACCTC CCAAGTAGGA TTACAAGCAT ACGCCGACGA TGCCCAGAAT 60  
CCAGAACTTT GTCTATNACT CTCCCCAACA ACCTAGATGT GAAAACAGAA TAAACTTCAC 120  
CCAGAAAACA AA 132

SEQ ID NO:2053

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02337

SEQUENCE DESCRIPTION:

GATCCATCCT TCCTGCCTCC AAGGAGGATA CACAGAGAAT GGCTTCCTGT TGTTTTGTTT 60  
ATTTTCTTAA CGTGTACAGA TGGAACTTC ATTTAAAAAT AAAACAAAA CAACTCAAAA 120  
AGGAAA 126

SEQ ID NO:2054

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02338

SEQUENCE DESCRIPTION:

GATCAAAAAA GCTCACGTCG TATTTCTTCT TTCTCTTCT CTTTCTAGA AATTGGGTGT 60  
TTGTACCAGA ATGGAATTTT GCTTCTCGGT TATCCTGTGC TTCAGATGAT TATAATCTAA 120  
CCCAAA 126

SEQ ID NO:2055

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02339

SEQUENCE DESCRIPTION:

GATCAAATCT TACAGTTCAT CACAGAATCC ATGTTGGTGA TAAATNCTAT AAAAGTAATA 60

GGGGTGGTAA GAACATCAGA GANTCCACAC AGGAAAAAAA ATCTATAAAA NGATTCTTTG 120  
TGAAA 125

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SEQ ID NO:2056  
SEQUENCE LENGTH:124  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS02340  
SEQUENCE DESCRIPTION:  
GATCCACAG AAATGTTTGG GAGAGCGGGA GGTTCCTCC AAGTTCTTCT 60  
CCCTCCAACC AGAGTTGTGT CTAACCTTAG GCATCTTTA ATAAATNTNA TTGCGACTCT 120  
GAAA 124

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SEQ ID NO:2057  
SEQUENCE LENGTH:207  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS02341  
SEQUENCE DESCRIPTION:  
GATCACTTCT GAATAAGCAG TTTGCCTTTA TAAAACTTG CTGCCTGNCT AAAGATTAAC 60  
AGGTTATAGT TTAAATNTGT AATTAATGCT ACCATCTTGC AATAAAGTGA CAATTGAATG 120  
NAACAGGGTT TTTCAAGTTG TATAATTCTC TGAAATACTC AGCTTTTGTC ATATGGGTAA 180  
AANTTAAAGA TGTCATTGGN CTACAAA 207

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SEQ ID NO:2058  
SEQUENCE LENGTH:120  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02342

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SEQUENCE DESCRIPTION:  
GATCTTTACT CTTGAGAAAT GAATAAGCTT TCTCTCAGAA ATGCTGTCCC TATACACTAG 60  
ACAAAAGTGA GCCTGTATAA GGAATAAATG GGAGCGCCGA AAAGCTCCNT AAAAAGCAAA 120

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SEQ ID NO:2059  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02343

40

SEQUENCE DESCRIPTION:  
GATCCAAGGT ATCCNTAACA NTGGAGCAGC CAAGTTTNTT TTCAGGCACA ATGACCCTGA 60  
CCACCTAAAG AAACCTNTAG AGAAGTNTAA CCCTAAGATA CCCAAAATTT TGGCCTTTN 119

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SEQ ID NO:2060  
SEQUENCE LENGTH:127  
SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS02345

SEQUENCE DESCRIPTION:

GATCCCTCT TCTCAGACAG CGCCAGGCCG GGGTGGGGCC GGGGTGTTGGG CCGAGCCCCA 60  
CAGCTGCCCC CCTCCNTCC CNTTTGTAT AATTTAATAA AGAAATGGTC GCGCTTCTGT 120  
TTTAAA 127

SEQ ID NO:2061

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02346

SEQUENCE DESCRIPTION:

GATCGAGGTG GAGAAGATGC GGCGGGCGGA GNCTTATNAC CGNNTAGAGA ACAGCCCACA 60  
GNTGGATGGG AGCCCCCAG GGCTCGAGGG TCTGCTGGG GGCATTGGGG AGAAAGN 117

SEQ ID NO:2062

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02347

SEQUENCE DESCRIPTION:

GATCTGCTGA GGACACATGC GCTTTGTAG AATTTAACAT CTGGTGTTTT TCTGAAAAAA 60  
TATATATACA TATATTGCTT TATTTGAAAC AAATNAAAAT ATGCTGCATT TGAAA 115

SEQ ID NO:2063

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02348

SEQUENCE DESCRIPTION:

GATCTGGAGG AGGTGAAGGC CAAGGTGCTG CCCGCTGGGC CTCCAACGG GCCCTCCTCC 60  
CCTCCTTGCA CCGGCCCTTC CTGGTCTTTG AATAAAGTCT GAGTGGGCGG CAAA 114

SEQ ID NO:2064

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02349

SEQUENCE DESCRIPTION:

GATCCAAAGT ATCAGGTCTG TTAGTGGCCA TCAGCACTTT AATATTGCCT CGAGGAGGAT 60  
TTCTTGGNCN CNNNAAATAA GGTCATTAAG TCTTATGCCA AATTCAGTGC TCCN 114

SEQ ID NO:2065

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02350

SEQUENCE DESCRIPTION:

GATCCTAGAT AAGCAGGTGA AATTTAGGCT TCAGAATATA TCCGAGAGGT GGGGAGGGTC 60  
CCTTGAAGC TGGTGAAGTC CTGTTCTTAT TATGAATCCA TTCATTCAAG AAA 113

SEQ ID NO:2066

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02351

SEQUENCE DESCRIPTION:

GATCTACGCT GTGCCTTGGC AGGGCACAAT GACCTTNTAG ANATCCACCT GTTAGAACGC 60  
CTAGGGGTCT GAACCGGGCT GGNCTGANNC TATCACCTCT TATGCACAN 109

SEQ ID NO:2067

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02352

SEQUENCE DESCRIPTION:

GATCCCAAGG CCTAGCCTGT GAAGGTCTCC TATCGGAAGA NTACCCCAT NNAATGGGAA 60  
GTGGAATTCC TGGTCAANTT GGTCTTNATG CTCTGGAAGA CGTAAGAN 108

SEQ ID NO:2068

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02353

SEQUENCE DESCRIPTION:

GATCTTAAGC AAAAATACTC ACTGAAATAG TATGTGGATG AATTCACCTA CTTACAATTT 60  
TATGGTTTCT TTGTAAATAA TAAATGTGAA TCTCAATTCT GCTTTAAA 108

SEQ ID NO:2069

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02354

SEQUENCE DESCRIPTION:

GATCCTNGGC TCCACCTGGG TGGCCCTGAC CACGGGAGCC TTGGGCCTAG AGCTGCCCTT 60  
GTCCTNCCAG GACCCCNCC TGGCCACTGC CCGCCTACTN NCTN 104

SEQ ID NO:2070

SEQUENCE LENGTH:408

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02355

SEQUENCE DESCRIPTION:

GATCAGAGCT GCTGAGTTCA GGATGCCTGC GTGTGGTTTA GGTGTTAGCC TTCTTACATG 60  
GATGTNAGGA GAGCTGCTGC CCTCTTGGCG TGAGTTGCGT ATTCAGGCTG CTTTGTCTGC 120  
CTTTGGCCAG AGAGCTGGTT GAAGATGTTT GTAATCGTTT TCAGTCTCCT GCAGGTTTCT 180  
GTGCCCCCTGT GGTGGAAGAG GGCACGACAG TNCANGCGCA NGTTCCTGGG CTCCTCAGTC 240  
GCAGGGGTGG GATGTGAGTC ATGCGGATTA TCCACTCGCC ACAGTTATCA GCTGCCATTG 300  
CTCCCTGTCC TGTTCCCCA CTCTCTTATT TGTGCATTG GTTTGGTTTC CTGTAGTTTT 360  
AATTTTAA TAAAGTTGAN TAAAANTATA AAAANAAGAG NNGGCGNN 408

SEQ ID NO:2071

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02356

SEQUENCE DESCRIPTION:

GATCAAAAGC TTATTCATCT TTTTCTTTT TCCTTTGGTG TAAAGCCAAC ACCCTGTTTA 60  
AAAANCATAA TTCNTTAAN CNATTTTCCC TCTTTCTCNT N 101

SEQ ID NO:2072

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02357

SEQUENCE DESCRIPTION:

GATCAAAAAA AGAGTTTGAA GCTAATTTTG GCAAAATTCA GGCCAAAAA GTAAGGCCAT 60  
TATTTAACCC TGTGGCACCA TTAAATGTTG AAGAATGACA AA 102

SEQ ID NO:2073

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02358

SEQUENCE DESCRIPTION:

GATCTTTTTT GTCAGTTTGT TTGTATGAAA CTAAAGCCNT TATTTGTAA TAGTTCCTGC 60  
TAAACAATG AATAAAACT CAAGGAGCAA CTAA 95

SEQ ID NO:2074

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02359

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCGTCTCT AGGATGATAT GCATGTTTCA AGTGGTATTG AAAGCCGCAC TGATGGATAT 60  
GTAATAATAA ACATATCTGT TATTAATATA AA 92

5 SEQ ID NO:2075  
SEQUENCE LENGTH:101  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02360  
10 SEQUENCE DESCRIPTION:  
GATCTAAGTT AGGAAAAGACG ATGGAGGTGG AATCCTTTAA GATTATNTCC AGTTATTTGC 60  
TTTAATAAAG AAGAAGTTAC CCTTGTCAAA ATCAGAACAA A 101

15 SEQ ID NO:2076  
SEQUENCE LENGTH:87  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02361  
20 SEQUENCE DESCRIPTION:  
GATCTTCATT TATTTTAATG GTAATGGTTT TAAAATATGT TCCTGATTGT ACATATTNTA 60  
AAATAAACAT GTTTTAAAC ATGCAAA 87

25 SEQ ID NO:2077  
SEQUENCE LENGTH:88  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02362  
30 SEQUENCE DESCRIPTION:  
GATCACAAAC ATTCAACAAA AAAGTAACT TATGTGACTT GGCAGTTATT CTATACCATT 60  
TCCTGTCCAT TAAAATTTT AAAGGAAA 88

35 SEQ ID NO:2078  
SEQUENCE LENGTH:85  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02363  
40 SEQUENCE DESCRIPTION:  
GATCCCATTT AATATTTAAA AAAATCAGTA GCACAAATAT ATNTNAATTG TCAACTTACA 60  
AAATAAAATA CATTTACAGT CTAAA 85

45 SEQ ID NO:2079  
SEQUENCE LENGTH:82  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02364  
50 SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

GATCATCAAA AAAGAGGTAA TCTACGTTAT TTCCTATTCT AATGTCTTTT CCTAATAAAA 60  
AACTTCAACT TTCTAAGTTA AA 82

5 SEQ ID NO:2080  
SEQUENCE LENGTH:80  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS02365  
SEQUENCE DESCRIPTION:  
GATCCTTTCG GAATTGCACT TTTACATGTT GGGCGAATTT GTGTCCGTGC TGAAGTTTAT 60  
TAAAGGAAAA TAGATGGAAA 80

15 SEQ ID NO:2081  
SEQUENCE LENGTH:80  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS02366  
SEQUENCE DESCRIPTION:  
GATCAAGCCT TGCTTGAGAT TGGCCTTACC TCTGGNCNTT TTTTGTATA TGAGCTAATA 60  
AATNCTGTTT ATTGTTTAAA 80

25 SEQ ID NO:2082  
SEQUENCE LENGTH:80  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
30 CLONE:HUMGS02367  
SEQUENCE DESCRIPTION:  
GATCCATGAA GTNATTGAGT GGAAANATGC ACGTTNATAC TATTTNAGAG CACAAATAAA 60  
CTCACTATAC AATGGTCAAA 80

35 SEQ ID NO:2083  
SEQUENCE LENGTH:76  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
40 CLONE:HUMGS02368  
SEQUENCE DESCRIPTION:  
GATCAAACCT CAAAGCAGCT TTNACTTGGA ATTAAAAAT AAACAGTTCA AAGATACTCT 60  
ACATTATCAC CNTAAA 76

45 SEQ ID NO:2084  
SEQUENCE LENGTH:70  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
50 CLONE:HUMGS02369  
SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

GATCCATTTT ATGCAGGATT GTGTTGTTTT AACTGTTGTT GAGGAACTA ATAAATAATT 60  
AAATTGTAAA 70

5 SEQ ID NO:2085  
SEQUENCE LENGTH:64  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02370  
10 SEQUENCE DESCRIPTION:  
GATCTAAGAT GTCCCAGGTC CTGGGAAGTT TACTCAATAA AGCTGGCTTT CCCCTGCCCT 60  
CAAA 64

15 SEQ ID NO:2086  
SEQUENCE LENGTH:64  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02371  
20 SEQUENCE DESCRIPTION:  
GATCCGTTGT AATGATGTGA ACATTTTATG AGTTTAAATA AAGTCATCTT ATGGTGTTCAT 60  
TAAA 64

25 SEQ ID NO:2087  
SEQUENCE LENGTH:61  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02372  
30 SEQUENCE DESCRIPTION:  
GATCTTAAAA TCAGTGATTA TCTTTTCTA AATAAAATAT CACCAGAATT CATCAGTTAA 60  
A 61

35 SEQ ID NO:2088  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02373  
40 SEQUENCE DESCRIPTION:  
GATCTAAGAT GTCCCAGGTC CAGGAAGTTT ACTCAATAAA GTGGCTTTCC CTGCCANAAA 60

45 SEQ ID NO:2089  
SEQUENCE LENGTH:66  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02374  
50 SEQUENCE DESCRIPTION:  
GATCTCCGGG CAGCCACCAC CTCCTCGGTC TGCCCCCTCA TTAATAATTCA CGTTCACCACC 60

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CTGAAA

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SEQ ID NO:2090

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02375

SEQUENCE DESCRIPTION:

GATCATGCAA AGAAACTTC CAAAAAGATT TATTAAGTTA AACCAGCCTC TNTNGCAA 59

SEQ ID NO:2091

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02376

SEQUENCE DESCRIPTION:

GATCTCAAAT TGCCTCTGAA CCTTTTATAA GACAGTTTAT CTTCAAATAA ATTTATTTTG 60  
CAATACCACG CAAA 74

SEQ ID NO:2092

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02377

SEQUENCE DESCRIPTION:

GATCAAAGTC TATTTTGCAT AAAATGTCCA ATAATTAAAT ATTGTTATAA AATAAA 56

SEQ ID NO:2093

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02378

SEQUENCE DESCRIPTION:

GATCGGCAGT TGGGAGGGGC GCTCTGAGAT TAAAGAGTTT TACCTCTGAG ATAAA 55

SEQ ID NO:2094

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02379

SEQUENCE DESCRIPTION:

GATCCANTCT TTGACAAACT GAAAAGAACT GAAAATAAAC ATTGCTCTTT CAAA 54

SEQ ID NO:2095

SEQUENCE LENGTH:52

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02380

SEQUENCE DESCRIPTION:

GATCCCTGCC CCTCCCCACT GGGACGGAAT AAATGCTCTG CAGACCTGGA AA

52

SEQ ID NO:2096

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02382

SEQUENCE DESCRIPTION:

GATCTGCTTA TAGAGCAGGA AGAATAAAGC CACCAACTTT TACCTAGCCC GGCTAATCAT 60  
 GGAAGTGTGN CCAGGCTTCA AGTAACTTGA GTTTTAATTT TTTTTTTTC TTGGNAGAGT 120  
 AATGTAAAT TTAAATGGGG AAAGATATTT AANATTTAAT ACTAAGCTTT AAAAAGAAAC 180  
 CTGCTATCAT TGCTATGTAT CTTGATGCAA AGACTATGAT GTTAATAAAA GAAAGTACAG 240  
 ANGACACTTG GCATTCAAAG NTTAAA 266

SEQ ID NO:2097

SEQUENCE LENGTH:451

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02399

SEQUENCE DESCRIPTION:

GATCTAGAGA GTGCTCAGAA TTAGGGCCTG GCATTTGGAA TCACAGGANA TATCATCACA 60  
 GAAACAACTG TTTTAAGATT AGTTCCATCA CTCTCATCCT GTATTTTNAT AAGAAACACA 120  
 AGAGTGCATA CCAGAATTGA ATATACCATA TGGGATTGGN GAAAGACAAA TGTGGAAGAA 180  
 ATCANNGNGC TGGAGACTAC TTTTGTGCTT TACAAAACCTG TGAAGGATTG TGGTCACCTG 240  
 GAACAGTCTC CAATCTATGT TAGCACTATG TGGCTCAGCC TCTGTTACCC CTTGGNTTAT 300  
 ATATCAACCT GTAAACATGT GCCTGTAACCT TACTTCCAAA ATCAAANTCA TACTTATTNG 360  
 AGGAANATTC TGATTTTNTA GANAAAANNT NGAGCNAGGN GATTATANCN TGTTTGCAAG 420  
 TCATGTGGTT TCTTTCTCAA TNGGGGGNNA N 451

SEQ ID NO:2098

SEQUENCE LENGTH:441

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02400

SEQUENCE DESCRIPTION:

GATCCCAAAC TGTTCCCTTT TTCATTCTT GAAATGTTAC CACTACAGAC ATTTTTTNAA 60  
 GGTGAATAAA CAGTTGTNAT GTGCTGTACC TAAATCATG TTAAATCGTA TAAGGAAACA 120  
 TTTCAATACA CTTATACAGG AAGAAAACCTA TAGATGAAGT ACATGTGTGT GATTCACTCT 180  
 GATTCACAGA ATTCTGAGAG TAATATGGAA TAAACAACCT CCACTTAGAT GATAACTGAA 240  
 GCATTTCTTG CCTTGTGAAA ATTTGGNTTT TAAATTGCTG TTAGAATGGG NAATTTGGAC 300  
 ACTTTATATC ATTGTATANT TNCAGACTTT AGNTTCTGTA TCTNTTGGGA ACCATGGTTA 360

TAGCAAAACC NTTGGNAATA ATCCTGTTTC CNANACCNCC CTNNATGTAA ACCTGGTATG 420  
CTTGGCTGGT AACNCCTAAG N 441

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SEQ ID NO:2099  
SEQUENCE LENGTH:440  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS02401

SEQUENCE DESCRIPTION:

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GATCTATGTC TNCTGCCTGG CTCCTAGATG GCTCTCCGGG CAGGTNCTGG CCAAGGACAT 60  
CATCTAGGCA GGGGAGAGC CTGGNCTGAA CAGCTGTNAC CAAAACCTCC TTCTNCCCCA 120  
CCCTGCCCCC TCCACTTCCT GCCCTCTGTT CCATCTTCCC CCTTCCCAA GGCCACAGCC 180  
TTTATTCCAG GCCCAGGGAT GTAGGAGGGG GAAGGAGGAA ACAGGAAGCC CAGAGAGGGC 240  
AAAGGGCCTA CCTCGGGGCG CGAACCATGC CCCANACTAT TATCTCAGGG CTTTCTGGGC 300  
ACTNGCACTT CAGCGTGGCC CACCTGCCCA TGCCCTGAGG CCAGTTNGCG AGGGGTGGCT 360  
CCTGAGGGTT TTTATAACCT TTGTTTGNTA ATGTTTAATT TTTGCATCAT AATTCTACA 420  
TTGTCCCTGG AGTGAAGAN 440

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SEQ ID NO:2100  
SEQUENCE LENGTH:411  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02402

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SEQUENCE DESCRIPTION:

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GATCAAAAGG CTGAAAGGTT TGCTACCCCA GCACGGCATC CCCTACACGA GGCCACAGA 60  
AACTTCCAAC TTGGAGCACT TGGGCCACGA GACGCCCAGA GCCAAGTCTC CAGAGCAGCT 120  
GCGGGGTGAC CCAGGACTGC GTGGGAGTTT GTGACCTTGT GGTGGGAGAG CAGAGGTGGA 180  
CGNGGCCGAG AGCCCTACAG AGAAGCTGGC TGGTAGGACC CGCAGGACCA GCTGACCAGG 240  
CTTGTGCTCA GAGAAGCAGA CAAACAAAG ATTCAAGGTT TTAATTAATT CCCATACTGA 300  
TAAAAATAAC TCCATGAATT CTGTAAACCA TTGCATAAAT GCTATAGTGT AAANAAATTT 360  
AACCAAGTGT TACTTTAAAC AGTTCGTACA AGTAATGNTT ATAATTCTAA A 411

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SEQ ID NO:2101  
SEQUENCE LENGTH:408  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02403

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SEQUENCE DESCRIPTION:

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GATCTGGAAA GCTTGAGCCT CCTTGGGTTT GTCTACAAAT TGGAAGGAAA TATGAATGAA 60  
GCCCTGGAGT ACTATGAGCG GGCCCTGAGA CTGGCTGCTG ACTTTGAGAA CTCTGTGAGA 120  
CAAGGTCCTT AGGCACCCAG ATATCAGCCA CTTTCACATT TCATTTTCATT TTATGCTAAC 180  
ATTTACTAAT CATCTTTTCT GCTTACTGTT TTCAGAAACA TTATAATTCA CTGTAATGAT 240  
GTAATTCTTG AATAATAAAT CTGACAAAAT ATTAGTTGTG TTCAACAATT AGTGAAACAG 300  
AATGTGTGTA TGCATGTAAG AANGAGAAAT CATTTGTATG AGTGCTATGT AGTAGAGAAA 360  
AAATGTTAGT TAACCTTTGTA GGAAATAAAA CATTTGGACTT AACTAAA 408

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# EP 0 679 716 A1

SEQ ID NO:2102  
SEQUENCE LENGTH:397  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02404

## SEQUENCE DESCRIPTION:

GATCCGAGAG GTGGCCAACA AAGTCAAGGT CCCCCTGCTG GATTTAGGCA GCCCCCAACT 60  
GGCCATGCAC TCTATCCGGN AGATGGCCTG CACCACAGGA GTCCTCCANA CCCTNACCCT 120  
CTTCAAGGGC TTCTTTAAGC TGTTCCTTC TCTAAGCCAT AATCTCTNAG TGGATTGAGC 180  
CCTCTTGGA AGACTTCTCT GCCATCCCTT TGCACCTGAN AGGGGAAGTT CTCAGCTGAG 240  
CTGAAGCTGG ATTATTAAAG TGGATTGTAA CTCAGACTCT CCGTGCTACG CTTATTTGGA 300  
GACTAGAGGA GTGGGAGTTG AGCCTGGCTT GAACCTTTGG AACCAGAAAA GTTGGGGAGC 360  
AGGTGGAGGA GGCCACACTC CTGGGAGCTT GATGGTN 397

SEQ ID NO:2103  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02406

## SEQUENCE DESCRIPTION:

GATCAGCCCT TTTCCCATC CTGCCCTATG GTTCTCTAGC CACCTGTGCA TGCATGTGTA 60  
TTTCTGCCTN GTTCTATGGT GTGTGGATGT GTGTGCATGA ATCTGTCATA TAGAGGGGGT 120  
CCGAGCTGGA ATCCTAGAGC ATTGCTGCCC TGGGGCCTGA TGTCTTGGC TTCCTCAGAG 180  
CATGTAACAG GAAATTAAAT GGGATGAGTG TTTGGTAAA 219

SEQ ID NO:2104  
SEQUENCE LENGTH:380  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02408

## SEQUENCE DESCRIPTION:

GATCCTACCT CCAACTCCTG ACTCTATAGG TCTCACTCTT TTTTATTGT CCTANNNTA 60  
CATAACATAA AATTTATAAA TTAAATATTC TAGGGTATAG TTCAGTGGTA TTAAGTACAT 120  
TCACACTGAT GTGCAACCAT CATTATCATC CATTCCCAA ACTTTTCATC ACCGCAAATA 180  
GAAAAGCTGT ACCCATGAAA CAATAACTTC CATTGCCTCC CCCTCAGCCT TTGGTAACCT 240  
CTATTCTACT TTCTGTTTCT ATGAATTTGA CTGTTCTAGG TACCTCATAT AAGTGGAAATC 300  
ACACAATATT TGTCCTTTG TGTCTAACTT ATTTCACTTA GCATGTTTTT AAGATTTATC 360  
TGTACTGTAC CATGTATCAN 380

SEQ ID NO:2105  
SEQUENCE LENGTH:378  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02409

## SEQUENCE DESCRIPTION:

GATCTGTGCT CTCCTAGCCC AAGAGACCCC TGGAGGGGCT GGAGTTTAT CCAGCGNCTC 60  
 GTCGTATGTT TGGCTGAGCA CCTGTGGCCT GGGTGCAGGT TAACTTCTTG TTATCAGGAG 120  
 CCCACTATGC AGAGGCCAAA GGTCGGCAGC CAGCGAGGCT ATGAATTGGA CTTTTTGGT 180  
 ATCTGTGTNA CTGNTCTGTG NCCATNCTTA GNCAACTTGC TGGCGTGACA AGTGGCCACA 240  
 AGTAACACAC CAGGTACCCA GAGNAGGGTG GACAGGAGAG ACCTGAATNA CAGCAGTANG 300  
 GAATTCTCTCA ANGNTGTGNC CTCGCCCATG AANTTGTTC AANTTGAAGG TNANNAGGGN 360  
 CACCAATCAG GGTGAGN 378

SEQ ID NO:2106

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02411

## SEQUENCE DESCRIPTION:

GATCCAGAAG TACAAGGTGG TCCTGGCCCC GGAGACGGNG GAGTTGAAGA GTGTGGCCCG 60  
 CATTGTCCTG GTTCCCAATA AGAAAGTGGG CCTGCAGTTC CTGCAGAGAC AGTGCTGAGC 120  
 TGAGTCTCCG CTTGTCTGGG GCTTGTCTTA GAGGCTCCAG CTCTGGCACA GTGGTTCCTG 180  
 GCTGTGCCA TGTCTCANAT GAGGAGGGAG AGAAGGAGGC CGCCAGACTC GAGAGGTGGG 240  
 AGGAACTCCT TGCACACACC CTGAGCTTTT GCCACTTCTA TCATTTTGA GAACTCCCTC 300  
 TCAGCTAAAA GGCCACCCTT TTATCGAATG CTGTCCTTGG GAAGATATAA AATAAAGGGC 360  
 TTTTATTCT TAAA 374

SEQ ID NO:2107

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02412

## SEQUENCE DESCRIPTION:

GATCCAGCCC GACCTGCGAG ANTGATGGAG ACCATGCACC GCATGAGCCA CCTCCCACCC 60  
 GACTTTGAGG GCCGCCAGAC GGTGAGCCAG TGGCTGCAGA CCCTGAGCGG ATGTCGGCGT 120  
 CAGATGAGCT GGACGACTCA CAGGTGCGTC AGATGCTGTT CGCCTGGAGT CAGCCTACAN 180  
 CGCCTTCANC CGCTTCTNA TGCCTGAGCC CGGGGANTAG CCTGNACAG CCGGGAGAGT 240  
 CTGAGGCNTG GTCCTGGTCC CTGTCCGCAN AGAGGCCGTG NNATCACANA GCTANTGTCT 300  
 GAGTGGCTGT CTGGNTCTGC TTTGGGTAAG ACTTTGGGGC CGGCCTCCCA NAATAAGGTG 360  
 TCTCGGAAA 369

SEQ ID NO:2108

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02413

## SEQUENCE DESCRIPTION:

GATCAGAGCC AAGAAGCGTC TGCGGCAGAG TGGGGAAGAG TTGCCGCCAA CCTCCTAGGC 60  
 GCCCGGCCCA GTCCTCTTTG ACCCCTGGGG CAGGGCAGGG GGCAGGGAGA GACAAGGCTG 120

# EP 0 679 716 A1

CTGCTATTAG AGCCCATCCT GGAGCCCCAC CTCTGAACCA CCTCCTACCA GCTGTCCCTC 180  
 AGGCTGGGGG AAAACAGGTG TTTNATTTGT NACCGTTGGA GCTTGGATAT GTNCGTGGCA 240  
 TGTGTGTGTN TGTGTNANAG TGTGAATGCA CAGGTGGGTA TTAACTCTGT ATTATTCCCC 300  
 GTTNTTGGAA TTGNNTTCCC CNATGGGNCT GGGGTACTTT ACATTCAATA AATACTGTTT 360  
 AACCCAAA 368

SEQ ID NO:2109

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02414

SEQUENCE DESCRIPTION:

GATCACAGGA AGTGGAGGAG CCAGAGGTGC CTTTGTGGAG GACAGCAGTG GCTGCTGGGA 60  
 GAGGGCTGTG GAGGAAGGAG CTTCTCGGAG CCCCCTCTCA GGCTTACCTG GGCCCCCTCCT 120  
 CTAGAGAAGA GCTCAACTCT CTCCCAACCT CACCATGGAA AGAAAATAAT TATGAATGCC 180  
 ACTGAGGCAC TNAGGCCCTA CCTCATGCCA AACAAAGGGT TCAAGGCTGG GTCTAGCGAG 240  
 GATGCTTGAA GGAAGGGAGG TATGAGACCG TAGGNANAAN GGCACCATCC TCGTACTGTT 300  
 GTCATATGA GCTTAAGAAA TTTGATACCA TAAATGGTA AAGACTTGAA AAAAGTANAA 360  
 NATGTTTN 368

SEQ ID NO:2110

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02415

SEQUENCE DESCRIPTION:

GATCTTGGTT TTGATGTGGA CATAGGCCCT CTTTCCAGA CTCCTCGTGA AGTGGCCCAG 60  
 CAGGCTGTGG ATGCGGATGT GCATGCTGTG GCGGTAANAC CCTCGCTGCT GGTCATAAAA 120  
 CCCTAGTTCC TGAATCATC AAAGAACTTA ACTCCCTTGG ACGGCCAGAT ATTCTTGTCA 180  
 TGTGTGGAGG GGTGATACCA CCNTCAGGAT TATNAATTTC TGTTTGAAGT TGGTGTTC 240  
 AATGTATTTG GTCCTGGGAC TCGAATTCCA AAGGCTGCCG TTCAGGTGCT TNATGATATT 300  
 GAGAAGTGTT TNGAAAAGAA GCAGCAATCT GTATAAAATA AAAATATCAC AAGAGAACAC 360  
 CTGTACTN 368

SEQ ID NO:2111

SEQUENCE LENGTH:365

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02416

SEQUENCE DESCRIPTION:

GATCGAAAGA AATCTAAGTG ATACGGCCCA ATGAAGCTAA AATATAGCCT TCTGTTAAGC 60  
 AAATAGTATT TCCTTTCCCC AAGTAGTTCA TTTTCTAGAT GCTTGTCAAA TGAATTAATG 120  
 TCCTCTGATG AAGAGTGTC TCCGTTTCT AAGGTCTTCT CAATCTCAGC AATAGAGCTT 180  
 CCCAGCAGCG TTCAAGACAC ATCATTTATA CACAGGCACA GGGGCCTTCC TGAAATGGGT 240  
 GCATTTTAC CAACTACAAT CATGTAATTT TTTTGGAAAT TTTTAAAT TTTGNTNCT 300

EP 0 679 716 A1

TTACATTACA ATTGGGTGAA ACACATTTTA CAGCTCTCAA TAAATGTTTG CTGGTCGCTC 360  
TGAAA 365

5 SEQ ID NO:2112  
SEQUENCE LENGTH:363  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02417

10 SEQUENCE DESCRIPTION:  
GATCAACGAT TACGTGGAGA AGGGTACTCA AGGGAAAATT GTGGATTGG TCAAGGAGCT 60  
TGACAGAGAC ACAGTTTTTN CTCTGGTGAA TTACATCTNC TTTAAAGGCA AATGGGAGAG 120  
ACCCTTTGAA GTCAAGGACA CCGAGGAAGA GGACTTCCAC GTGGACCAGG TGACCACCGT 180  
15 GAAGGTGCCT ATNATGAAGC GTTTAGGCAT GTTAAACATC CAGCACTGTA AGANGCTGTC 240  
CAGCTGGGTG CTGCTGATGA AATACCTGGG CAATGCCACC GCCATCTTCT TCCTGCCTGA 300  
TGAGGGGAAA CTACAGCACC TGGAAAATGA TTGACCAAAA TACCAAGTCT CCCCTTCTTC 360  
ATN 363

20 SEQ ID NO:2113  
SEQUENCE LENGTH:362  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02418

25 SEQUENCE DESCRIPTION:  
GATCCCAGTC GCATACCAGG TGTCTCCTC CAGGTCGTGA ACGGCAAAGG CACTGCCCGC 60  
ATCGCCATAG CAGGTGTCTT CTTGGTACTT AGACATGCCA GCACAGAAGG TGTGTTTCATT 120  
CAGTATGGGC TGCACCCTTA CAGGGCTCTT CGGTGTCTTC CATCCAGGAC TGGGTTTCAGA 180  
30 AGACCATAGC TGAGAACTAA TGCAAGGCTG GCCGGAAGCC CTTGCCTGAA AGCAAGATTT 240  
CAGCCTGGAA GAGGGCAAAG TGGACGGGAG TGGACAGGAG TNGATGCGAT AAGATGTGGT 300  
TTGAAGCTTG ATGGGTGCCA GCCTGCATTG CTGAGTCAAT CAATAAAGAG CTTTTCTTTT 360  
GN 362

35 SEQ ID NO:2114  
SEQUENCE LENGTH:362  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02419

40 SEQUENCE DESCRIPTION:  
GATCNGACAG GCACCAGCAA TGACACAGCA TAAACTGTTG GGCACAGGAA AGAGGCTTGA 60  
CACCACCAGC CCACCAGGAA ATGCAGTTCA GCCACCACGA GGACACGAGG AACCTGCACC 120  
45 ACAGCCGCAG TCAAGAGAAT GCTGGTGGTG CCAAGNTGCA GGGTGTGGCC TGCTGGAATG 180  
GAAGCGCATG GTGGTNNCTA TAAAGTCAAT GNCACAGCAC ATGCCAGCA ATCCACTGTG 240  
GGATTNGNGA TGANACTANG CNCATAAAAC TGTNCGAATT TTNCTGTGCT TTTCATATCN 300  
TCAATNTGAA TCAANTGCTT CATTGGGTAC TGTAAGTGTG GNTACTTNAG TGAATCTCTN 360  
TN 362

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EP 0 679 716 A1

SEQ ID NO:2115

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02420

SEQUENCE DESCRIPTION:

GATCATATAG TAGGTTTAGG TTTAACTTTT TAAGAAATTG CCAAGCTTTT CCAAAGTGGC 60  
TGTCCCTCTT TACATTTCCA CCAGCAATGT ATAATGAATG GTTCAGGTTT CTCCACATTC 120  
TTGTCGGCAC TTGGACTTTT CTGTTTGTG GTAGCCATTC TAGTGGATGC AAAGTGGCAT 180  
CTCATTATGG TTCATTTGCA TTTCTCTGAC AACTAATGAT TTTGAGCATC TTCATGCGAT 240  
TGTTAAACCAT TTGTATATCT TTAGTGAAAT ATCTATTCAA TTATTGCCCA TTTTAAATT 300  
GGNTCACATG GCTNATTAAT GNATTGTAAG AAAGGTTTAC ATATTCCTGG ATACN 355

SEQ ID NO:2116

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02421

SEQUENCE DESCRIPTION:

GATCATGATT TTGTAGTACA GGAAGACTTC ATGAAAGCAG TCAGAAAAGT GGCTGATTCT 60  
AAGAAGCTGG AGTCTAAATT GGACTACAAA CCTGTGTAAT TTAGTGAAG ATTTTGTATG 120  
GCTGCATGAC AGANGTTGGC TTATTGTAAG AATAAAGTTA AAGAAAATAA TGTATGTATT 180  
GGTAATGATG TCATTAAGAG TATATGANTA AAAATATGAG TAACATCATA AAAATTAGTA 240  
ATTCAACTTT TAAGATACAG AAGAAATTTG TATGTTTGT AAAGTNGCAT TTATTGCAGC 300  
ANGTTACAAA GGGGAAGTGT TGAAGCTTTT CATATTGCT GCGTGACATN 350

SEQ ID NO:2117

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02422

SEQUENCE DESCRIPTION:

GATCCGCAGN CAGAAGCTCT GCCCTTCTGT ATCCTATGTA TGCAGTGTNN TTTNCTTGC 60  
CAGCTTGGGC CATTCTTGCT TAGACAGTCA GCATTGTNT CCTCCTTAA CTGAGTCATC 120  
ATCTTAGTCC AACTAATGCA GTCGATACAA TGCCTAGATA GAAGAAGCCC CACGGGAGCC 180  
AGGATGGGAC TGGTCGTGTT TGTNCTTTTN TCCAAGTCAG CACCCAAAGG TCAATGCACA 240  
GAGACCCCGG GTGGGTGAGC GCTGGCTTCT CAAACGGCCG AAGTTGCCTC TTTTAGGAAT 300  
CTCTTTGAA TTGGGAGCAC GNTGNNCTCT TGAGTTTGA GCTTTTAAAA GTACTTTNTT 360  
TACCACATTT GGAAA 375

SEQ ID NO:2118

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02423

## SEQUENCE DESCRIPTION:

GATCTCTAAC CAGAAATAAA CAGGAAGACT CAGTNGTTTA CAAAAGACAT TTTAGTTTTA 60  
 CACGTACAGA AAATTCTACC CNGGCATTAC AGAATTCTTA GACTTCTTAA ATTCCTGATT 120  
 5 TTCCTTGGTA TTTACATTTT GATAAGGGAG CCAATGGTTC TTCAAACATT TGAAAAGAAC 180  
 ACATACACAC TGGACAATTT CAAACGNTAC AAACAAACGC AACTGTCCTT CTTTCTCATT 240  
 CCTGTCCTTC AGCCACCCAG TTTCTTCTCC CCTGAGGGAA TCAGTTATCA TTNGCTGGGT 300  
 CATACTTCCA GATTATCCTG TGCCTATGTA AGTGTGTGN 339

SEQ ID NO:2119

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02424

## SEQUENCE DESCRIPTION:

GATCTGGGAC GTNCACGAGT NAGGGGCTGG CCACCCAGCC CACAGCCTTG CCTGACCACC 60  
 CTCCAGCAGA TAGACGCCGG CACCCCTTCC TCTTCCTAGG GTGGAAGGGG CCCTGGTNCN 120  
 20 NGCCTGTAGA CCTATCGGNT CTCATCCCTT GGGATAAGCC CCAGTCCAGG TCCAGGAGGC 180  
 TCCNTCCCTG CCCAGCGAGT CTTCCAGAAG GGGTGAAAGG GTTNCAGGTC CCGACCACTG 240  
 ACCNTTCCCG GGTGNCCTCC CTCCCCANCT TACACCTNAA GCCCAGCACG NAGTAGNCTT 300  
 TGAACAGAGG GAGGGAAGGA CCCATGGGTC TCCN 334

SEQ ID NO:2120

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02425

## SEQUENCE DESCRIPTION:

GATCAAAGAG AAAATAAAAA ATCGCTACTT CCCTGCCTTT GAAAAAGTCT TAAAGAGCCA 60  
 TGGACAAGAC TACCTTGTG GCAACAAGCT GAGCCGGGCT GACATTCATC TGGTGGAACT 120  
 NCTCTACTAC GTCGAGGAGC TTGACTCCAG TCTTATCTCC AGCTTCCCTC TGCTGAAGCT 180  
 35 CTCCAGGACA CTGGCCCCC AACTGTATC TCTACTGAG AAAAGGTGGT CCCATGGCCC 240  
 TGAAAACCAG AATNAGCAAC CTGNCCCACA GTGAAGAAGT TTCTACAGCC TNGGCAGCCC 300  
 AAGGAAAGCC TCCCATTGGA TGAGAAATCN 330

SEQ ID NO:2121

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02426

## SEQUENCE DESCRIPTION:

GATCGAAGTA AAATAGAAAT GGGACTNGCT TTCCACAGGA AGTAAACTGC TTCAGAGCCC 60  
 ACAGTCCCCT GCTCAGTGTC CGGAAAGAAG TCAGTCATCC CTGTGGCAG TAAATCTTCC 120  
 CACAGGCCGT CCATTAGAGA TTAACTAGA TATGTTCAAT AGAAAGAGTC TGAGGCAAGT 180  
 GGAATGAGG NNCGGAAACT TAGGTTGGGA GAATATTTT NNTNTATTCA TTCTGTTTGC 240  
 50 TTAATTCAGA GTACAGTTTG TGCTATTTC TATCTGTACT CCAGGCAGAA ATATAACTTG 300

AAAATACTGT GTCTAAAGAA ATTTCAN

327

SEQ ID NO:2122

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02427

SEQUENCE DESCRIPTION:

5  
10  
15  
GATCCTCGTC ATCAAGGATG GCTGCATCGT GGAGAGGGGA CGACACGAGG CTCTGTTGTC 60  
CCGAGGTGGG GTGTATGCTG ACATGTGGCA GCTGCAGCAG GGACAGGAAG AAACCTCTGA 120  
AGACACTAAG CCTCAGACCA TGGAACGGTG AAAAAAGTTT GGCCACTTCC CTCTCAAAGA 180  
CTAACCCAGA AGGGAATAAG ATGTGTCTCC TTCCCTGGC TTATTTTCATC CTGGTCTTGG 240  
GGTATGGTGC TAGCTATGGT AAGGGAAAGG GACCTTTCCG AAAAACATCT TTTNGGGGAA 300  
ATAAAAATGT GGACTGGTGC GAGN 324

SEQ ID NO:2123

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02428

SEQUENCE DESCRIPTION:

20  
25  
30  
GATCTGAACA TTCAAAAGAA AGCTTTGGAA AAAAAGAGCT GGCTGGCCTA AAAACCTAAA 60  
TATATGATGA AGATTGTAGG ACTGTCTTCC CAAGCCCCAT GTTCATGGTG GNNCNNTGGT 120  
TATTTGGTTA TTTTACTCAA TTGGTTACTC TCATTTGAAA TGAGGGAGGG ACATACAGAA 180  
TAGGAACAGG TGTTTGCTCT CCTAAGAGCC TTCATGCACA CCCCTGAACC ACGAGGAAAC 240  
AGTACAGTCG CTAGTCAAGT GGTTTTTTAAA GTAAAGTATA TTCATAAGGT AACAGTTATT 300  
CTGTTGTTAT AAAACTATAC CCACTGCAAA AGTAGTAGTC AAGTGTCTAG GTCTN 355

SEQ ID NO:2124

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02429

SEQUENCE DESCRIPTION:

35  
40  
45  
GATCTCAGAA CTGAAGGCCG CCCTGACATG AAGACTGAGC TCTTTTCCAG CTCATGCCCA 60  
GGTGGAATCA TGCTGAATGA GACAGGCCAG GGTTACCAGC GCTTTCTCCT CTACAATCGC 120  
TCACCACATC CTCCGAAAA GTGTGTGGAG GAATTCAAGT CCCTGACTTC CTGCCTGGAC 180  
TCCAAAGCCT NCTTATTGAC TCCTAGGGAA TCAAGAGGCC TGTGAGCTGT CCAATAACTG 240  
ACCTGTAAC TCACTAAGT CCCCAGATGG GGNACANTGG GGAGNTNGAG TTGTTGGAGG 300  
GAGGAAGCTT GGAGACTTCC CAGN 324

SEQ ID NO:2125

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS02430

SEQUENCE DESCRIPTION:

GATCCATCTT CATCCATTGC ATTGGAACT NCTTTATGCT GCTGCAGTCT GCAAAGTCTA 60  
 GAGCTTTTAT CAGGCCATGT CATACCCAAG AAAGCACCTA TTAAAGAAA AAACAATTCC 120  
 CTGAGCTCTC AACTCCAAGT TGTAAGATTG GTGTCTTCCT TGTCTTACT TAAAAAGTC 180  
 ATGTGTTAAT TTTNNTCCTG CCTGTATTG TATGCAAAAT GTCCTCTATC TGCTATNAAA 240  
 GAAAAGCTAC GTAAACCACT ACATTGTANC CTTCTAAGTN ATTNTTAATT AGNAGGGNAT 300  
 TATNTTGCAG TACCANTTGG GAAA 324

SEQ ID NO:2126

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02431

SEQUENCE DESCRIPTION:

GATCGTGAAG ACCTGCTGAG CCAGCCTGTT CTCCGGGCCT GAATGTCTGG GGTGCTTGTG 60  
 CCTTTTCTGA GAAGCGTTGT GACTGCTCAA CATCCCCATC AAGGTTTGAG TCCACAAAAG 120  
 TGGACCTCCC TATCATGCTT CCCCTTCCCT CTAGCATGTG GGAAGGGACT GCTGTGAAGA 180  
 ATGNCAGATG TGGGGCCTCT GCCAAGTTCT TGCATTGCTA AATAAGGGCT TCCTCTGCCT 240  
 TCTACCTACA GTGCATTGA ACTGCCTTCT GAAAGAGGTC CAGGGAGGGA TTTAGGAAAT 300  
 AAAGNTTCTA CCTATTTGAA A 321

SEQ ID NO:2127

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02432

SEQUENCE DESCRIPTION:

GATCCTAAGC GAAGATGGAT TTCAGTTCAT CAAATCATCA TTAATGACTT TATGTATTAT 60  
 TTGCACAGGG AGAATTGAAA CTGAGTATAA TCAATAAGCT AGATACGAAA TCAGTTTCTC 120  
 AAAGTGAGCT TCAGAAAGGG GCATTTTGTA CTCTTGTTT TGCATAACTG GTTTTGTTT 180  
 TTTGCAGAAT TAACTATAAC ANTCACTGGC TACCGAAGTA AACTGATGTA CTGAATTCCA 240  
 TAATACATAA CATTCAATTT TTACCACTNC TGTTTAGCGA ACTTGTATAC TTATTTCTCT 300  
 TTCAGNTTAA AAAAAGAAA 319

SEQ ID NO:2128

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02433

SEQUENCE DESCRIPTION:

GATCACACCT GAAAGCAGTG GTCCAGCTC TGTGCTGTGG GACATCACAG GTCCTAAACA 60  
 GTGATAGAGA AAGGGCTGGG GAGTGGCAGC TGGAATCTCT GCTCCGTCT GAACATCTGG 120  
 ACACACATGT CAGAGAATCT TTGCATTAAT TGGACTGCCC AATCTATTG GTGATTAAAT 180  
 GGCTGTGCGG TGAGGGGAGA ACCCTGGGCA GTCTGGAGAC TGAGGTGCCA TTCTCGGCTA 240

EP 0 679 716 A1

GAGACACCAC CCAAAGAAGA GATGGGCTGG CTAATAAGA CAAGTNTCAG TTGAATAAAT 300  
GTCTTTAAAC CTAAC 315

5 SEQ ID NO:2129  
SEQUENCE LENGTH:311  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02434  
10 SEQUENCE DESCRIPTION:  
GATCATTGTC CCTACAGACA CCCAGAACAT CTTCTTCATG AGCAAAGTCA CCAATCCCAA 60  
GCAAGCCTAG AGCTTGCCAT CAAGCAGTGG GGCTCTCAGT AAGGAACTTG GAATGCAAGC 120  
TGGATGCCTG GGTCTCTGGG CACAGCCTGG CCCCTGTGCA CCGAGTGGCC ATGGCATGTN 180  
15 TGGCCCTGTC TGCTTATCCT TGGAAAGGTGA CAGCGATTCC CTGTGTAGCT CTCACATGCA 240  
CAGGGGCCCA TGGACTCTTC AGTCTGGAGG GTCCTGGGNC TNCTGACAGN AATAAATAAT 300  
TTCGTTGGAA A 311

20 SEQ ID NO:2130  
SEQUENCE LENGTH:309  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02435  
25 SEQUENCE DESCRIPTION:  
GATCCCAACT GCTCCTGCGC CGCCGGTGAC TCCTGCAAAT GCAAAGAGTG CAAATGCACC 60  
TCCTGCAAGA AAAGCTGCTG CTCCTGCTGC CCTGTGGGTT GTGCCAAGTG TGCCAGGGC 120  
TGCATCTGCA AAGGGGCGTC GGACAAGTGC AGCTGCTGCG CCTGATGCTG GGACAGCCCG 180  
CTCCCAGATG TAAAGAACGC GACTTCCACA AACCTGGATT TTTTATGTAC AACCTGACC 240  
30 GTGACCTTTT GCTATATTCC TTTTCTATG AAATAATGTG AATGATAATA AAACAGCTTT 300  
GACTTGAAA 309

35 SEQ ID NO:2131  
SEQUENCE LENGTH:307  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02436  
40 SEQUENCE DESCRIPTION:  
GATCCTGGCC TGCAGTTCC TATCCNTGA CCCAGAACAG CTCACCAAGG AGCTGCAGCA 60  
GCATGTGAAG TCAGTGCAGC CCATACAAGT CCCAAANAAG ATAGAGTTTG TTTGAACCT 120  
GCCAAAGCTG TCACAGGGAA ATTCAACAGA CCAAACCTCG NGNCAAGGAG TGGAAGATGT 180  
CCGAAAAAGC CCGTNCAGT GAGNCGTCTA GGAGCATTCA TTTGGATTCC CTCTTCTTTC 240  
45 TCTTTCTTTT CCCTTTGGGC CTTGGCTTAC TATNATGATA TGAGTCCTTT ATGAAGACAT 300  
GATGAAA 307

50 SEQ ID NO:2132  
SEQUENCE LENGTH:306  
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS02437

SEQUENCE DESCRIPTION:

5 GATCCTGGTG GCGACCATGG AGAGGAAACT GGAGGGCAGG GATGGAGCTG AAANCTTGGC 60  
 GGCCAGAGA GAGGTCCACC CCAAGCAGCC TGAGCCCTCA GCCACCCCCC AGCTCCCTGG 120  
 CAGCTCCCCT CCACCTGCCA ATGTCAGCGC CACACTGGTG TCTGAAAGGA ATAAGGAGAA 180  
 CAGGACAGAC TAACTTTTTA AATGATATGA AGAAATCAGA GGTGAAAATT GTACATTGGG 240  
 10 AATATATTTA TGCAAATTTT ATTGAAATTT ATTGTAAATA AAGATTTTCT CAGTGGTCTA 300  
 GANAAA 306

SEQ ID NO:2133

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02438

SEQUENCE DESCRIPTION:

20 GATCTGGGCT GGTCCCTTTC CCATAAAATN AGGTCCCTGG TTGTATGTTC CCATAGCACC 60  
 CCATACTTCC TCTCTNAGAA TAATCATTTT CCTTGTAATG CTCAGCATCC GCATCCTGCT 120  
 TGACTGCAA CTTGCTGAAG GTAGGGACTG TTTGTCTTGG ACTTCGCTGC CAGTCCTTAG 180  
 AACAGTGTCT GGGACACAGT GTGTTCTCAA ATATTGTGTT CTGGAATAAA TGAATGACCT 240  
 25 AAATCAGTCT TTTAGGGATT TACTGTAAAC CACCATGGGA AAATTAAATA AATGCGGGGA 300  
 AGGAAA 306

SEQ ID NO:2134

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02439

SEQUENCE DESCRIPTION:

35 GATCTGACCC CACAGCCTTT GGCCTGCTCA CCCGACCAGC CTGGGCCGCA TTCCCTGCAG 60  
 GACCTCCCGG GTCAGGCAGG GCGGCCCTT GCTCCACACA CTGCTGCATC TTGGGTCTCA 120  
 GGGACCCAGA CAGATGGACT TACATGGAGC TGGGCACTGC CCTGCCTCAA CAGGGTCCAT 180  
 TGCTCCTCG CCTCCAGAAC TTGAGCAGG GAAGTGGGCA CCCTGAGGCC TCCAGCACCA 240  
 40 GTTCCGTCAT TCTCGTTCCT GGGGAACCCC CACTCTGACC TGTATTAAA GTTCACATTT 300  
 TGA AAA 305

SEQ ID NO:2135

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02441

SEQUENCE DESCRIPTION:

50 GATCAACCTG AGAAAAATTG CTGAGCTCAT GCCAGGAGCA TCAGGGGCTG AAGTGAAGGG 60  
 CGTGTGCACA GAAGCTGGCA TGTATGCCCT GCGAGAACGG CGNGTCCATG TCACTCAGGA 120  
 GGACTTTGAG ATGGCAGTAG CCANGTCAT GCAGAAGGNC AGTGAGAAAA ACATGTCCAT 180

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CAAGCANTTA TGGANGTGAG TGGACAGCCT TTGTGTGTAT CTCTCCAATA CAGCTCTGTG 240  
GGCCAAGTAA A 251

5 SEQ ID NO:2136  
SEQUENCE LENGTH:301  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS02442

## SEQUENCE DESCRIPTION:

GATCTGCATC CCCAAAAGTA TCACTCCTTC TCGAATCCTT CAGAACATCA AGGTGTTTGA 60  
CTTCACCTTT AGCCAGAAG AGATGAAGCA GCTAAATGCC CTGAACAAA ATTGGAGATA 120  
TATTGTGCCT ATGCTTACGG TGGATGGGAA GAGAGTCCCA AGGGATGCAG GGCATCCTCT 180  
15 GTACCCCTTT AATGACCCGT ACTGAGACCA CAGCTTCTTG GCCTCCCTTC CAGCTCTGCA 240  
GCTAATGAGG TCCTGCCACA ACGGAAAGAG GNAGTTAATA ANNGCCATTG GANGCATNAA 300  
A 301

20 SEQ ID NO:2137  
SEQUENCE LENGTH:302  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02443

## SEQUENCE DESCRIPTION:

GATCCGAGAG GGCATGGCCG CCCTGCAGTC TGACCCCTGG CAGCAAGAGC TCTACCGCAA 60  
CTTCAAAAGC ATCTCCAAGG CCTTGGTGGA GCGGGGTGGT GTGGTCACCA GCAACCCACT 120  
TGGCTTCTGA ATACTCCCGG CCAGGGCCTG TCCCAGTTAT GTGCCTTCCC TCAAGCCAAA 180  
25 GCCGAAGCCC CTTTCCTTAA GGCCTGTT TGTCCCGAAG GGCCCTAGTG TTCCAGCAC 240  
30 TGTGCCTGCT CTCAAGAGCA CTTACTGCCT CGNAAATAAT AAAAATTTCT AGCCAGGTCA 300  
AA 302

35 SEQ ID NO:2138  
SEQUENCE LENGTH:297  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02444

## SEQUENCE DESCRIPTION:

GATCATCCAG AAGGAGCCCG TTGAAGTGGC CCCAAGCCAG CTCTCTGCAT TTCGTACTCT 60  
CCTGTTTTCT GCACTTGGTG AAGAGGAGAA GATGATGGTG AACAACTATC GCCCACTTCA 120  
ACCCTTGATG AACCAGGAAGG TCTGGGCGTC CTTCCAGGCC ACTAATGAGG GCACAAGGTC 180  
CTAGAGACAT TAGGTCCACA TGAATAGCAG AACTGACTTT GAAGGAAGGA AGCGTTGTTT 240  
45 CCCAAGTTTC ACAATGTGAT TGTACATGAC TTCTGAAATT AAAAAGAGAG CATGAAA 297

50 SEQ ID NO:2139  
SEQUENCE LENGTH:295  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

55

CLONE:HUMGS02445

SEQUENCE DESCRIPTION:

5 GATCTATGCC AGCAAAACAT CATTTTGAGA CAAACATTTT TGTGGCAGAT GTTTTTCCTA 60  
 AAAAGTACTA TATCATCCAA GAAATATTTG AGTAAATCC CTGTTCTTT TGGGTGACAT 120  
 TAACTGACAT TTGCTTTTT TCAAGACCTA ATAGAAAATA AGAAAGCCCA TAATGTATTT 180  
 AGAAACAGGA ATCCTCAGAG CAATTCTCTG TATTCTCATA TAATTCAAT GTAAAACAGA 240  
 AACATATTG ATGTGTTGGT GATAGGCTTG AATTATTTAA AACTTCAAAA ACAA 295

SEQ ID NO:2140

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02446

SEQUENCE DESCRIPTION:

15 GATCGAGGCT GCAGGATATG CTCAGACTCT AGAGGCGTGG ACCAAGGGGC ATGGAGCTTC 60  
 ACTCCTTGCT GGCCAGGGAG TTGGGGACTC AGAGGGACCA CTGGGGCCA GCCAGACTGG 120  
 20 CCTCAATGGC GGA CTGACTG ACATTGACTG ACGGGGACCA GGGCTTGTTT GGGTCGAGAG 180  
 CGCCCTCATG GTGCTGGTNC TGTGTGTGT AGGTCCCCTG GGGACACAAG CAGGCGCCAA 240  
 TGGTATCTGG GCGGANTCAC AGAGTTCTTG GAATAAAAGC AACCTCAGAN CAAA 294

SEQ ID NO:2141

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02447

SEQUENCE DESCRIPTION:

30 GATCTGGTTG GTGGATGAAC AAGTGTCACG CTGGACATCT CAATGGNGTT TATTACCAAG 60  
 GTGGCACTTA CTCANANGCA TCTACTCCTA ATGGTTATGA TAATGGCATT ATTTGGGCCA 120  
 CTTGGANAAC CCGGTGGTAT TCCATGAAGA ANCCACTATG AAGATAATCC CATCAACAGA 180  
 CTCACAATTG GAGATGACAG CAACACCACC TGGGGGGAGC ANACAGGTGG AGACGTTAAA 240  
 35 NGCCGTTTAN TGNGTTTTCT NTTTAAAGNC TTTATCTGAC CNGGGGTANN GN 292

SEQ ID NO:2142

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02448

SEQUENCE DESCRIPTION:

45 GATCGGAAAA AAATTCCTTGA ACGCAAAGCC AAGTCTCGAC AAGTTGGAAA AGAGAAAGGC 60  
 AAATATAAAG AAGAACTTAT TGAGAAAAATG CAGGAATAAA TAGAACCTGT TGTGCAACCA 120  
 CGGTTTAACC GGAGATTTTG AGGCTAGGGT GTGTTCTTT CGAACTTTTC GGAATGTCTG 180  
 GAACATTTCA TTTCTGTTT TGTTACCTGT GCCTCTGTAA ATCTACTTTT GCAATTTTAA 240  
 GTAATAATTT TATGAATAAN AATGGGAAAT GCTTCCTAAA 280

---

 SEQ ID NO:2143



SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02449

SEQUENCE DESCRIPTION:

GATCCCATAA CAGGCTACCC CTTGGCCTCA TGCTGGAGTT GTGTGTGTCT GTCTTCATCC 60  
 CAGGCTGAGC TCCTTGAGGT GAGGATGTTG TGCTGTTTGC CTCCCTCACA GTGCCTTGGT 120  
 CTTAGTGGAT GCCCAGTTGT CTTGTGAATG ACTTTTAAGA AGTGTACTTA AGAGAAAAAT 180  
 CCTACCNTAT NNNNGTAAT TACAAGTCAT GTTTTGTNG CTTAAAGGTG ATAAATCAGT 240  
 GTATATNATN NGNTAATGTC CATTAAAGCC AGTTTTTAAA 280

SEQ ID NO:2144

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02450

SEQUENCE DESCRIPTION:

GATCCTAGAG CCTGACGTTT AGTGAACCCA TGTTTCTGGG TGGGTGAAAG GGGCCCAACC 60  
 CTGCCCACTT CAGCCCAGCC CGCCCAAGGG GACTTGTGCC AGCAGAACAT GTNGGAGGAA 120  
 GAAGCCCCGT TTCCAGGGCA TCCGCAGCCC AGGGTAGGGA GAAATATTCT CTCCACTTTG 180  
 GGGGAGAGTT CTTGCTCTCG ACCTAGTGGT TTCTACTCTC ACCGACTTAT TCTGATTTC 240  
 GAAATAAAAT GAAATGTCTT ATTTTGGGA AAGTTAAA 278

SEQ ID NO:2145

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02452

SEQUENCE DESCRIPTION:

GATCCCACTG GGGCCTNTGG GAAGGNGACA GACTTATNAC TAGATGATTC GCTGGTGTCC 60  
 ATCTTTGGGA ATCGACGTCT CAAAAGGTTA TCCATGGTGG TACAGGATGG CATAGTGAAG 120  
 GCCCTGAATG TGAACCAGA TGGCACAGGC CTCACCTGCA GCCTGGCACC CAATATCATC 180  
 TCACAGNTCT GAGGCCCTGG GCCAGATTAC TTCCTCCACC NNTCCNTATC TNACCTGCCC 240  
 AGCCCTGTGC TGGGGCCCTG CAATTGGAAT GTTGGCCAGA TTTCTGCAAT AAACACTTGT 300  
 GGTTTGCGGG TCAAA 315

SEQ ID NO:2146

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02453

SEQUENCE DESCRIPTION:

GATCCCAGGA CCATTTGGCT AGTGTGCCTA GGTGACCACA TGATTGCTGT TTTACCAGGA 60  
 ATGCAGCATC CCATTGACAA AACAAGTGCT CTGAGAAGGT TTAAATACT ACAGNGAATA 120  
 TGGGANCACA GNCCTTGAAA TTTAGCTGAG TTGTAACAGC TGAAACTCCA AGAGGTGTCT 180

EP 0 679 716 A1

TCCTTGTTTN GAGGTGNACT AGTGTGCTT CCAGAGGGCA GCTTGAAACC CGTAAAGCCT 240  
GTTTTGGGGA ATCCTTTTTT GNCTTGCTTT GNTTN 275

SEQ ID NO:2147  
SEQUENCE LENGTH:274  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02454

SEQUENCE DESCRIPTION:  
GATCATCAAT GATTTATTGG CACGTTCTAT TGGGATGGTC GAAGTTAATA CAGTAGACAA 60  
ATACCAAGAT AAGGGACAAA AGTATTGTCC TAGTATCTTT TGTTAGAAAGT AATAAGGATG 120  
GAACTGTTGG TGAACCTCTG AAAGATTGGC GACGTCTTAA TGTGCTATA ACCAGAGCCA 180  
AACATAAACT GATTCTTCTG GGGTGTGTGC CCTCACTAAA TTGCTATCCT CCTTTGGAGA 240  
AGCTGCTTAA TCATTTAAAC TCAGAAAAAT TAAA 274

SEQ ID NO:2148  
SEQUENCE LENGTH:266  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02455

SEQUENCE DESCRIPTION:  
GATCGCAGAG AAGGCAGCTG ACATTATCAA GGGGCAGCCT GCACTCTGGG ACAAAGATGT 60  
CCCTGTCTAC AAGCCCAGGA CGCTGGCCAC CCAGCGCTAA GACAGTTGCT GCTGGAGGAT 120  
GACCAGGGAA GCCCCTGAT AAGCCAAGAG GGCCAGCACA GCCCTTGCTC CCAGGCTCCT 180  
GCCTGAAACT ATCTAGCACA CTAGGACCCA GGTGGTACCC TACTCAGTGG CTGAGAATTG 240  
GATAAAGTCT TGGGAAATGA GACAAA 266

SEQ ID NO:2149  
SEQUENCE LENGTH:265  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02456

SEQUENCE DESCRIPTION:  
GATCTTTAAC AAATGTTTTA AGCAATTTTA AAAAGGCAGG ATGTTATTGA CATTATACAC 60  
TGAAGTCTTA ACATTTTAAC ATTTATAGTG CTTATTTGCA AAATTGTATA ATTAGGAATT 120  
ATTTCAGAGA CAATGTTTTT TTTTTCAGGT GAGTAGTTGC CGCGTAATAT CATTGGAGTA 180  
CATTCTTTAT ACTGTTTGTG AAATTAATAC TAGCATATTA AGTGTACAAA TAGATTTAGA 240  
AAACAATAAA AAATTGCATG CTAAA 265

SEQ ID NO:2150  
SEQUENCE LENGTH:264  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02457

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCCTAGTG TTTTAATTAC CTGTGTGCAG CTATTTTAAA TAGCATTTTA CTTGAATAAT 60  
 ATGTATGTTG TCATTGTTTC ATGCTATACT TTGTGGGATA AAACCTGGGA ATGAGTGTGG 120  
 TAAGAAATTT ATAAAGTTTT GCTTTTAAAA CGTGGACATA ACTCATTTTT CTAGTTTTTG 180  
 ACAATTGTGT GTTTTAGTGT CTAGTCTGCA GAGAGCTGTG TGATTAATAA ACGTGAATT 240  
 AACAGAATTT CCTCTCCCTG TAAA 264

10 SEQ ID NO:2151  
 SEQUENCE LENGTH:259  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02458

15 SEQUENCE DESCRIPTION:  
 GATCCTGGGC TCATAGGCAG TCCCTTTCAC TTCCTTGTCT TGCTCCCTGC TATGCTGGAG 60  
 ATGAATGTGA CTAAAAGGGC CATCTTGCTG GCTTAATGTG TGGCTGGAGA GACCAGCCTG 120  
 GAGACAATGT GGCAAAATGG GCGCCTTCAT CCAGTCTGTC TAAGCCCTGT CGACTTGGGG 180  
 AGGTGATTC TTTCTGGTT CTATATGTNA AGCAAAATAA ATGTTTTAAA ATTAAAAGCA 240  
 NNAAAGCAGA ATGTGAGTN 259

25 SEQ ID NO:2152  
 SEQUENCE LENGTH:255  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02459

30 SEQUENCE DESCRIPTION:  
 GATCAAAGCT GGACTGGAAA TTGTATCGTG TAATTATTTT TGTGTTCTTA ATGTTATTTG 60  
 GTACTCAAGT TGTAATAAAC GTCTACTACT GTTTATNCCA GTGTCTACTA CCTCAGGTGT 120  
 CCTATAGATT TTCCTTCTAC CAAAGTTCAC TTTCACANTG AAATTATATT TGCTGTGTGA 180  
 CTATGATTCC TAAGATTCC AGGGCTTAAG GGCTAACTTC TATTAGCACC TTACTGTGTA 240  
 AGCAAATGTT ACAA 255

35 SEQ ID NO:2153  
 SEQUENCE LENGTH:248  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02461

40 SEQUENCE DESCRIPTION:  
 GATCTGTGCA GCAAAGCACC ATGGTACATG TNNTACCTAT GTAACAAACC TGCACATCCT 60  
 GCACATGTAC CCTGGAACCT AATAAAAGTT GGAAATTTT AAAAAGAATG AATAAGACCT 120  
 GGTATTTGAT AGCACAACAG GGAGACTATA GTCAACAGCA ATTTAATTGT ATATTTTAAT 180  
 45 ATGACTAAAA GAGTATAATG GNTTGTGTTGT AACACAANTA AATGCTTGAG GGGATGGNCA 240  
 CCCCNA 248

50 SEQ ID NO:2154  
 SEQUENCE LENGTH:245  
 SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS02462

SEQUENCE DESCRIPTION:

5 GATCTTAAGC TTTGATAAGA GCTGTCCTGT GGCTGAGTAT GGTGTGTATG TNAAGGTGCT 60  
TCCATCCAGG CTGGGTTTCAG AAGCCATAGC TGNGACTAAT GCAAGCTGGC CGAAGCCTTG 120  
CTGAAAGAAG CTTTAGCTGG AGAGGCAAAG TGGCGGGAGT GGCAGGAGTG GATNNGATAA 180  
GATGTGGTTT AAGTNATGGG TNCAGCCTGA TTCTGAGCAA TAATAAAGAN TTTCTTTTGC 240  
CCAAA 245

SEQ ID NO:2155

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS02463

SEQUENCE DESCRIPTION:

20 GATCCAGGAA GCTCCCAAAC CAGAGTGTGA GAAGGCACTT CTTGCCTTTC AGGAGAGTAA 60  
GAACCTCTGC GAANCATGGA GAACCTTATG CAACAATTAA AGGAAAGTGG CATGACAATG 120  
GAGGAGCTAA AATATTCTCT GGAGCTGAAG AAAGCTGAGT TGAAGGCAAA ATTGTTGTAA 180  
CACTACAGCT GAGCAGATGT AATAGAAATA AACCTATGAA TAAATTTNCT TCTTGGTTCT 240  
GAAA 244

25 SEQ ID NO:2156

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02464

SEQUENCE DESCRIPTION:

30 GATCCTATAT CTTGGTNAAT ATGCTCCCAG ATACTTTAAA CATGGCAACC TTTTGGCCTA 60  
AGAGAATGTT TGTTTCATGGA AAAAAGCTTT TGAGATGAGA GGGTGTCTTA CTTTCTTGTG 120  
GCAATTGATT TTCTGTTTAA ACACCCCTTTG GGTAAAACTT TGCAAAGAGC TTTTATAATT 180  
35 NGTTTTACTG AATTGTATGG AGATTGTATA CCAAGTAAAG CTCTTTTAAA TTACAAA 237

SEQ ID NO:2157

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS02465

SEQUENCE DESCRIPTION:

45 GATCCACGCT GGGCCGAGGA TGGGACGTTT TTCTTCTTGG GCCCGGTCCA CAGGTCCANT 60  
GACACCCTCC CTCCAGGGTC CTCTCTTCCA CAGTGGCGGG CCCACTCAGC CCCGAGACCA 120  
CCCAACCTCA CCCTCCTGAC CCCCATGTAA ATATTGTTCT GCTGTCTGGG ACTCCTGTCT 180  
AGGTGCCCCT GATGATGGGA TGCNCTTTAA ATAATAAAGA TGGTTTTGAT TAAA 234

50 SEQ ID NO:2158

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02466

SEQUENCE DESCRIPTION:

GATCCCTAAG CTGTAGAACA TTTTAACGTT GATGCCACAA CGCAGATTGA TGCCTTGTAG 60  
ATGGAGCTTG CAGATGGAGC CCCGTGACCT CTCACCTACC CACCTGTTTG CCTGCCTTCT 120  
TGTGCGTTTC TCGGAGAAGT TCTTAGCCTG ATGAAATAAC TTGGGGCGTT GAAGAGCTGT 180  
TTAATTTTAA ATGCCTTAGA CTGGGGATAT ATTAGAGGAA GCAGATTGTC AAA 233

SEQ ID NO:2159

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02467

SEQUENCE DESCRIPTION:

GATCTGTGCA CACTTTCTAA ACAGCTTGTN ATGCAAGTNT GAGCCTATTG TGTTACTTGA 60  
CCTTATTTTG GAAGTTTTGA ATTGGCCTAG GAGGAAACCC AGAAATGAAC CAGGGGTATG 120  
TNATCACTTT TTNATATCA AGTCCTCACC CTCCTNCCAC ATAATGCTCT ATCCGGCTAA 180  
GGTTGGAAC CTGAAGTTGG AGAAGGTGGA ATAAAGTTAC ACCTGGAAA 229

SEQ ID NO:2160

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02468

SEQUENCE DESCRIPTION:

GATCCCTGCG AATTACGAAA ACTACTACAT CCATGATTGC CCCAACCCCC TTGGGGTGGG 60  
GCAGAAGGTG AAGCATCCCA ACTGACTAGA GACTCAGGCC CTGCAGGNCC TTATAGAACC 120  
TGTGGCCATC CCTGAGCACC CTGCCACCAG GTGACCTCGG CCATACTCAC TGCCCCCCTT 180  
GGGCACCCAC TCACNTAGA ATAACTTAA CAGTGTCCCG TGGTAAA 227

SEQ ID NO:2161

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02469

SEQUENCE DESCRIPTION:

GATCTTACGA TGCCCTCTGT ACTGACCTGA AGGAGACCTA AGAGTCCTTT CCCTTTTTGA 60  
GTTTGAATCA TAGCCTTGAT GTGGTCTCTT GTTTTATGTC CTTGTTCTTA ATGTAAAAGT 120  
GCTTAACTGC TTCTTGGTTG TATTGGGTAG CATTGGGATA AGATTTTAAC TGGGTATTCT 180  
TGAATTGCTT TTACAATAAA CCAATTTTAT AATCTTTAAA TTAAAA 226

SEQ ID NO:2162

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02471

SEQUENCE DESCRIPTION:

5 GATCTGCCTT GCTCACTATT TGCCTATTGG CATATATGAT TACTTTGCTA AAAGACATTT 60  
TGGCCAAGAC AAGCCCATNT CCAGAGCTCT AAGAATGCCT AACTACAAGA AAAAGGCCAC 120  
CTAGGCAATG GAAGCCCTCA AAGAAGTCGG AATGTCATAG TCTTGAAATG AAAGGGAAAC 180  
TGGGAAACTG GGTTTCTCAT TAAAGTTGTT TCCCACTCTN TAAA 224

10

SEQ ID NO:2163

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS02472

SEQUENCE DESCRIPTION:

20 GATCTAATTT GATAACAAC ATGGCTTGTG TGAAACTGA GCAGGTGTTT GTTTACCCAT 60  
AGTGTCTGT GTAGTTATTG CTTANTCTGC AGAAAATAAT GACTTAGATG AGATGTCTGA 120  
CTTGCTTTCA CTTATTAAAC ATGTTACCA TGGGATGATG TCTGTAACAT CAGATATTGT 180  
TCAACTAGAC TAGGATTAA TAAAAATTGT GAAAGCTTAA A 221

25

SEQ ID NO:2164

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02473

SEQUENCE DESCRIPTION:

30 GATCTTAATT TACAGTTCCA TGGGATTAAA ACAAGTTTGC ATTTATGTAA TTTGCATTAC 60  
TTTAAAAATT ACAACAACAT AATCTCTGAA ACTTACTTCA ATCAATTCAC ATCCCTACAA 120  
CTGTTAAGAT TTATTTTGTG ATTAGNATCT TATAGTGGGT ATTCTTTTNA GTGCTGATAT 180  
TTCTATTCAT TAAAATCCTG TGNACACAAA 210

35

SEQ ID NO:2165

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS02474

SEQUENCE DESCRIPTION:

45 GATCCTGCAT TAAATTTTAA TTTGTGAAAA TTTGAAAATT ATGAGCTATA ACTTATAAAG 60  
TTTGCCCTTCT TATGNCTAAA ATCTTTTAAA GGATTATTTG CATTTATGTA AAAGTGGAAA 120  
TGAAGTTATA TATGAGTGCA AAGAAATTGA CTTCTGCTCA AATATGTGTT GATACCCTAC 180  
AGTAAATTGA ATTAAATTTT TATCCCAA 209

50

SEQ ID NO:2166

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

# EP 0 679 716 A1

CLONE:HUMGS02475

SEQUENCE DESCRIPTION:

GATCAGTCAA TTTTCCGTCG TCCGTAACCA GCGGGCCCCT GGTCAAGTNC TGGCTCTGCT 60  
 5 GTCTTGCCT TCCATTTCCC CTCTGCACCC AGAACAGTGG TGGCAACATT CATTGCCAAG 120  
 GGCCCAAAGA AAGAGCTACC TGGACCTTTT GTTTTCTGTT TGACAACATG TTTAATAAAT 180  
 AAAAATGTCT TGATATCAGT AAA 203

SEQ ID NO:2167

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02476

SEQUENCE DESCRIPTION:

GATCTGGACT TCGAACTTT CCTCATGGAT TCTGAATAAA AGAAACACTC TACACCTCTT 60  
 15 AAATCAAGGT CATGTAGATA ATGACTTTGT TATAAATGCT ACAGCTGTGA GAGCTTGTTT 120  
 CTGATTTTCAT TGTTGCTTC TGTAATTCTG AAAAACTTTA AACTGGTAGA ACTTGGAATA 180  
 AATAATTNGT TTTAATTTAA 200

SEQ ID NO:2168

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02477

SEQUENCE DESCRIPTION:

GATCTTAAGT GTCTCCTTGC TCTGGTAAAA GATAGATTTG TAGCTCACTT GATGATGGTG 60  
 25 CTGGTGAATT GCTCTGCTCT GTCTGAGATT TTTAAAAATC AGCTTAATGA GAGTAATCTG 120  
 30 CAGACAATTG ATAATAACAT TTTGAAAATT GGAAAGATGG TATACTGTTT TTAGAGGAAT 180  
 AAACGTATTT GTGGTTTAAA 200

SEQ ID NO:2169

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02478

SEQUENCE DESCRIPTION:

GATCCAAATC CCAGCTCTAC TGTCTCGTCC GAATTAGCCT TGGGAAAATC ATTTATATGC 60  
 40 TAAATAATTT ACCTTTTAT CTAGGAGATG AAAAGAGGAT AATGTTTCCT TCCATAAAGA 120  
 AAGTTCTTGT AAGAATCAAA AGAAATGGTG AGCTTTAAGT GGTTTGTAAC CCATAAAACA 180  
 CATCATAAAA GTTCAAA 197

SEQ ID NO:2170

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02479

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

5 GATCCATGNC ATCTCTCTCT TGCCTGAGGG GAAAGAGAGA TGGGCCAGGC AGAGAACAGA 60  
 ACTGGAGGCA GTCCATCTAG GGAANNNNAC TGTGAGGCCA TACTTGTGAA ACGTCTGGAC 120  
 TGCTATTCTA GAGCTTTTAT TTGNGTGTGT TCGTTGCACA NCTTGTTTTA AATGTTTAAT 180  
 AAAAGCTTTA TAAACTTTAA A 201

SEQ ID NO:2171

10 SEQUENCE LENGTH:218  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02480

SEQUENCE DESCRIPTION:

15 GATCCCCCAA GTACAGGCGC TAATTNTTGT GATAATTTGT AATNGTGACT TGTACTCCCC 60  
 GGCTGGCAGC GTAGTGGGGC TGCCAGGCCC CAGCTTTGTT CCCTGGTCCC CCTGAAGCCT 120  
 GCAAACGTTG TCATTGGCAG GGAAGGGTGG GGGGCAGCTG CGGTGGGGNG CTATAAAANT 180  
 GACAATTAAA CGNGACANTN GTNTTTTATT TCCTNAAA 218

20 SEQ ID NO:2172

SEQUENCE LENGTH:195  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 25 CLONE:HUMGS02481

SEQUENCE DESCRIPTION:

30 GATCCTTGCA GGGAGCTTGG AACCTTAGTG CACCTACTTC AGTTCAGAAC ACTTAGCACC 60  
 CCACTGACTC CACTGACAAT TGACTAAAAG ATGCAGGTGC TCGTATCTCG ACATTCATTG 120  
 CCACCCCCNT CTTATTTAAA TAGCTACCAA AGTACTTCTT TTTTAATAAA AAAATAAAGA 180  
 TTTTATTAG GTAAA 195

35 SEQ ID NO:2173

SEQUENCE LENGTH:194  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02482

SEQUENCE DESCRIPTION:

40 GATCCGGCAA CATCAACCCG AGTCATTCGT TCTGTGGAGG GACAAGTGA CTCAGGGCAG 60  
 CGCAGGCTGA CCACAGCACA GCCAACACGC ACCTGCCTCA GGAAGTGGAC GAAACCGGTG 120  
 GGGCTGGTTC TGTAATTGTG TGTGATGTGA AGCCAATTCA GACAGGCAAA TAAAAGTGAC 180  
 CTTTACACT GAAA 194

45 SEQ ID NO:2174

SEQUENCE LENGTH:192  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02483

50 SEQUENCE DESCRIPTION:

55



EP 0 679 716 A1

5 GATCAAATGG AAAGGAGAGG AAAGAACTCA GTGCTGCCTA TTAGTAGTTA ATTCTGTCAC 60  
 TCACCACTAC ATCACTTGAG ACAAATCTAT GCCACTCAGA ATCTCCTTCT TTCCTGGACT 120  
 TAACTCTAAT TCTAGAGTCT CTGTTACTGC TTGGGCTATA CCTGGGCATA CTAATAAAGT 180  
 ATGGTATTGA AA 192

10 SEQ ID NO:2175  
 SEQUENCE LENGTH:192  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02484  
 SEQUENCE DESCRIPTION:  
 15 GATCAGAACT GTTACCAAAA AACAACTGTC AGTTTTATTG AGATGGGAAA AATGTAAACT 60  
 CGANNNTTAT TACTTAAGAC TTTATGGGAG AGATTAGACA CTGGAGGTTT TTAACAGAAC 120  
 GTGTATTTAT TAATGTTCAA AACACTGGAA TTACAAATGA GAAGAGTCTA CAATAAATTA 180  
 AGATTTTGA AA 192

20 SEQ ID NO:2176  
 SEQUENCE LENGTH:187  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02486  
 25 SEQUENCE DESCRIPTION:  
 GATCGTCTTG GAAGGGAGTG GTTTTCAGAG ACATTTTCAGA AAGTGAAGGA GAAACTCAAG 60  
 ATTGACTCAT GAGGACCTGA AGGGTGACAT CCCAGGAGGG GCCTCTGAAA TTTCCCACAC 120  
 CCCAGCGCCT GTNCTGAGGA CTCCCTCCAT GTGGCCCCAG GTGCCACCAA TAAAAATCCT 180  
 ACAGAAA 187

30 SEQ ID NO:2177  
 SEQUENCE LENGTH:187  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02487  
 35 SEQUENCE DESCRIPTION:  
 GATCATTGAA ATGCTGAAAA TTTTAACAGT CTTCTTAAAA GTATTGAGGG GGCAAAAATT 60  
 ACCAATTATG GTATACAAAA ATAAGCCTAT AAATGTNTTT CACATTGCTA ACTTGAGTTT 120  
 40 CAGTTGATTC AGTTTGTAAT AACTAGTAAT GAGCTTCTGT TTACAATAAA AATNCTGTAA 180  
 ATTGAAA 187

45 SEQ ID NO:2178  
 SEQUENCE LENGTH:186  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02488  
 50 SEQUENCE DESCRIPTION:  
 GATCAGTTGC TTATAGATAA TGTTC AATGA CCTCAAGACA TATATTTTGG AGAAATTATC 60

55

ATTTTAAAAA ATTTGGTCTA TACTGATTGT TTCTACTGAT TCCAATATTA TTACTTATAA 120  
CACTGACCTC TGAAAAATAT TTTGTNCACA AGAAATAATA AAGTATAATG ATTTGTNGCA 180  
NNNAAA 186

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SEQ ID NO:2179  
SEQUENCE LENGTH:179  
SEQUENCE TYPE:nucleic acid

10

TOPOLOGY:linear  
CLONE:HUMGS02489  
SEQUENCE DESCRIPTION:

15

GATCCACAAG GCCTGAGGAG CAGTGTGGGG GGACAGACAG GAGGTGGATT TGGAGACCGA 60  
AGACTGGGAT GCCTGTCTTG AGTAGACTTG GACCCAAAAA ATCATCTCAC CTTGAGCCCA 120  
CCCCCACCNC NTTGTCTAAT CTGTAGAAGC TAATAAATAA TCATCCNTNC TTGCCTAAA 179

SEQ ID NO:2180  
SEQUENCE LENGTH:179  
SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear  
CLONE:HUMGS02490  
SEQUENCE DESCRIPTION:

25

GATCCAATGG AGCCTGGNGA GGTGTGCCCA GAAAGCTTGT CTGTAGCGGG TTTTNTGAGA 60  
GTNAACACTT TCCACTTTTT GACACCTTAT CCTGATGTAT GGTTCAGGA TTTGGATTTT 120  
AATTTTCCAA ATGTAGCTTG AAATTTCAAT AACTTTGCT CTGTTTTTCT AAAAATAAA 179

SEQ ID NO:2181  
SEQUENCE LENGTH:177  
SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear  
CLONE:HUMGS02491  
SEQUENCE DESCRIPTION:

35

GATCTGTCCA CTCCTGGTCA TTGGTGGATG TTAAACCCAT ATTCCTTTCA ACTGCTGCCT 60  
GCTAGGGAAA ACTGCTCCTC ATTATCATCA CTATTATTGC TCACCACTGT ATCCCCTCTA 120  
CTGGGCAAGT GCTTGTCAG TTCTAGTTGT TCAATAAATT TGTTAATAAT GCTGAAA 177

SEQ ID NO:2182  
SEQUENCE LENGTH:176  
SEQUENCE TYPE:nucleic acid

40

TOPOLOGY:linear  
CLONE:HUMGS02493

45

SEQUENCE DESCRIPTION:  
GATCAAAAAA CCACAGGGCT TTTGGGCACT GCCTCCTTGG GAAGTTAGTG GCCACAGAAG 60  
AGAGATGAAA CCTGTAAGAA GTCTGGAGTC TTTTGGAAC TCAGCCATTT CCCCAGGTTG 120  
TTACTTTCTT AGTATGTACA GTCTTCTCAG GATGAGCAGT AAAACCTTTG AACAAA 176

50

SEQ ID NO:2183

55

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02494

SEQUENCE DESCRIPTION:

GATCCTAAAC TCTCTAGCTT AAGTGTAAT GAAGTACAGT AGTTTCCCTA CTGAACCCTA 60  
CCTCTTGTGT CCCTGGAACC TTCTAGAACA CCTGCCTTCT ACCCTCTGGT TGGGAGATGC 120  
AGCCACCACA TCCCTTCATA TCATACTGTT TTGAATAAAT TTTCAAATCC TTAAT 175

SEQ ID NO:2184

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02495

SEQUENCE DESCRIPTION:

GATCCGGAGG GCCCAGGAGA ACCGGAGCGT GCTTCAGGGT GCCCGCAGAA CAGGAGCTGC 60  
TCAGCCAAGA ACTGTGGCGG CGGCTGCTGC CAGGATGCCG AAGATACCCC ACTAGCACCC 120  
CTNAGGGGGT CATGTGGTCA ATAAAAGTCC TTAGCTGCTG CCTAAA 166

SEQ ID NO:2185

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02496

SEQUENCE DESCRIPTION:

GATCAAAATC AAGAAATCCG GGCATCACAG AGAAGTTGGG TTTAGGACAG CAGGTGCTGT 60  
TCCGAGACTC AGTCCTAAAG GGTITTTTTT CCCACTAAGC AAGGGGCCCT GACCTCGGGA 120  
TGAGATAACA AATTGTAATA AAGTAACTTC TCTTTCTTC TAAA 164

SEQ ID NO:2186

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02497

SEQUENCE DESCRIPTION:

GATCAGCCCC TTAATATNAG TTCTAGAGCA GGTCTTCTGT TCCAGAAGGG GAGAAGCATA 60  
GAGGGCCTGT GAGCTCACGT GTGTTCTTTG TCATAGGGGT GAAAACTAA CTTCAAGTGT 120  
CCCTTGTTTG AAATAAATT AGCAGAGTCA CTTTCTATCT TAAA 164

SEQ ID NO:2187

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02498

SEQUENCE DESCRIPTION:

GATCTAATGG TTTTATAAAT NAAAGTTCCC CTGGACAAGT TCTCTTGCCT GCCACCATGT 60  
AAGATGTACC TTTGCTACTC ATTCACCTTC TGTCATGATG GTGAGGCCTT CCCAGCAATG 120  
TGGAAGTGTG AGTCCATTAA ACCTCTTTCC TTTATAAATT AAA 163

SEQ ID NO:2188

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02499

SEQUENCE DESCRIPTION:

GATCCTAACC AGGTAACCTG GTCCTNTGAA TTGAAGCTTA TCATATACCC AAAGCCTTGA 60  
CTAGAAATAC CTAATAGAA TACCATGGTC ATTGGAAAAA ATAGATAGTN TTNTAAAGTA 120  
TTATTNAAT AAATCCTAAA GTNTGTCTNT CTTCTCCTCA AA 162

SEQ ID NO:2189

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02500

SEQUENCE DESCRIPTION:

GATCCTGGCC ATGAATGAAA AGGATAAGAA GAAAGAGAAG AAATGAAGTG ACCATCCAGC 60  
CTTTCCCAAT NAGACTTCCT CTCCTTCCAC CCCTCATTTT CTTTTTGCAC ACATTACAGG 120  
TGGTGTGTTC TGTGATAATG AAAAGCATCA GAAA 154

SEQ ID NO:2190

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02501

SEQUENCE DESCRIPTION:

GATCAAAGCC AGCNACCCCC ACCCCAACAC ACTCGGTGTC CCANTCATAC TAGGGCCTGT 60  
GTAAATCCCA GCCTGGCCAT ACCCTCAACC TCAGTGGGCT GGAAATNACA GTGGGCCCTA 120  
TAGCAGTGGC AGAATAAACT CAGNTGTGTT CAAA 154

SEQ ID NO:2191

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02502

SEQUENCE DESCRIPTION:

GATCGCCCCA CTGCAATCCA GCCTGGGAGA CATAATTCOA ATCTATTTTG GTCTTATATC 60  
TTCTTATGTT TGTGTTATTT CATGTGTGCC AGTTTCTCTT TTTTTCACAA CAATTTATCA 120  
ATTGTGCGCA ATAAAAATNA TTTACCTTTT AAA 153

SEQ ID NO:2192

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02503

SEQUENCE DESCRIPTION:

GATCATGGTG ATTTTACTGC TGCTTGTGGC TATCGTGGTT GTTGCAGTCT GGCCGACCAC 60  
CAGCAGTNAC ACCTGCCAAT NACAGATGCA AGCCCAACAC CCTTTTGGTA CGCAAAACCT 120  
GCTCTCAATA AATTCCCCCA AAGCTCTGAA A 151

SEQ ID NO:2193

SEQUENCE LENGTH:371

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02504

SEQUENCE DESCRIPTION:

GATCCCAGGA ACCTTCCTNC TCCAGGGCAG CACAGGACTC AGCCATGTNT GGACCGGCC 60  
TGCTGAGGCT ACAGTCACTC TGGAAGCTCT GCGCTTCATC AGGNNGCAGG ACTGTGGCGG 120  
GAGGGGTCCT TGAAGATGGG TGTGGGGAGC AGTGGGTCAG GAAGTGGGAG CCAGAGGTTT 180  
GACTCACTTT GCTTTATTTT TCAGGCTACA ATACAGGTCA GAGACAATGG CTTATAAAGG 240  
TTTAGTGTGG TCTCAGGATG TGACAGGCAG TCCAGCCTGA CCTTTCTGCA CACTCCAGAC 300  
AAACTTCCCA GACAAGCTCC TTTGTGCCTC TACGTGGAGA GGGTGTGGGA AAGTTATCAC 360  
ATTAAAAGGT N 371

SEQ ID NO:2194

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02505

SEQUENCE DESCRIPTION:

GATCAAGAAA GAGATGGAGG AGGAGGACTG AGCCCAGAAT TCACTAGGTT CGAATCCAGA 60  
NAGCAGTGTG GAAAAAAAAA ACCAAAAANC AACTGNCCAG TTGTTGATAA CCACTAAGAG 120  
TCTCTATTAA AATTACTGAT GCAGAAA 147

SEQ ID NO:2195

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02506

SEQUENCE DESCRIPTION:

GATCTGTGTC ATTNCCCATG AGGGGCCGGG GCAGGTGGCT GGGTGGGGGC ACAGGCTGGA 60  
GTATTCTNAG TTCTACTGGT TCTACACTGT GAGGTGGCAA TGGGATTTCG TCAGATGCCA 120  
CCCAATAAAA TGCCTGTAAC TTAAG 145

SEQ ID NO:2196

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02507

SEQUENCE DESCRIPTION:

GATCGCTACT CTTAAGAATA TACATGTATG TATTCATAGG AACATTTTTT CTCAATATTT 60  
GTATGATTCG CTTACTGTTA TTGTGCTGAG TGAGCTCCTG TGTGCTTCAG AAAAAAATAA 120  
ATGAGACTTT GTGTTTACGT TAAA 144

SEQ ID NO:2197

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02508

SEQUENCE DESCRIPTION:

GATCAGCTGG AAGCTCACTA GTCATCTCCT GCCCAATCCC CAGAAACCCT GATTCAGGTC 60  
TGCAGGCTCC TGCGGGCTCA CCACGGCTGC TGGCTCCGGT ACCATGTAAN NCCTAGGAAG 120  
GTAAAGGNGC AGGCAACCTC AAA 143

SEQ ID NO:2198

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02509

SEQUENCE DESCRIPTION:

GATCCAGTGA GATAGAATAC ATGTAAGTNT GGTTTTGTA TTTAAAAAGT GCTATACTAA 60  
GGGAAAGAAT TGAGGAATTA ACTGCATACG TTTTGGTGTT GCTTTTCAAA TGTTTGAAAA 120  
TAAAAAAAAT GTTANGANAA A 141

SEQ ID NO:2199

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02510

SEQUENCE DESCRIPTION:

GATCCCTTGT GGCTATGCAG ATACCTACCT CACAGAGTTG TTGTAGAAGA CTGGTGGTTT 60  
GGTTCAAACC TTGTGATTAA AGAGTTTGTC AAGCATTTTA TTCTTTTGAA TAAAAGCAAC 120  
ATATCNAAAA CATTAAA 137

SEQ ID NO:2200

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02511

SEQUENCE DESCRIPTION:

GATCCCTGTT TAACTCCAAA TTACAGTCGG ACTTGGATAC ATCATTTGTA ACATTGTAGG 60

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AAAGAAAAAA GTCTTGGTTN TGAAAAACGA TTTGCATTGG GGTAATAA AGTGACCATG 120  
CTTTTGTCT GTAAA 135

5 SEQ ID NO:2201  
SEQUENCE LENGTH:135  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02512  
10 SEQUENCE DESCRIPTION:  
GATCCAGCTC AAGTGCCATC CTGCCAGTGG CCCCCAGACT GTGGGGTTGG GACGCCTGGC 60  
CTCTGTGTCC TAGAAGGGAC CCTCCTGTGG TCTTTGTCTT GATTTTNCCT AATAAACGGT 120  
GCTATCCCCG CCAA 135

15 SEQ ID NO:2202  
SEQUENCE LENGTH:133  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS02513  
SEQUENCE DESCRIPTION:  
GATCACTACT GCTCTGGAG TTCCTTCTCC TAAAGCTAAG GCCAGCCTCC ATCACAAATG 60  
CCCATAAAT CTGGCTCGTC TTTGATGAAC AATAAATATT TTTGAACAA ATAAATAACT 120  
25 GCCCTGCATT AAA 133

SEQ ID NO:2203  
SEQUENCE LENGTH:138  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS02514  
SEQUENCE DESCRIPTION:  
GATCCTCCCG CTGGCTTCCA GACAGACCTG GGATTTTGGC AGTCATGCCG GGTGATGGTG 60  
35 TTCCTGCGGA GACCCTCAGT TGTCTATTG CTCCTAGCT TCCCTGCAAT AAAATCAAGC 120  
TGCTTTTGTT GGAATAAA 138

SEQ ID NO:2204  
SEQUENCE LENGTH:130  
40 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02515  
SEQUENCE DESCRIPTION:  
45 GATCATTTCA CCTGATGTTT TTAAAGCATC CTAAGTACAG TAGAGTAGAA AACTNATTTT 60  
TTTGTTAATT GTACACTGAA TAATGCCTTT AAAAAATCAA AATAAAATTA ACAAATAATG 120  
GTGAATGAAA 130

50 SEQ ID NO:2205  
SEQUENCE LENGTH:176

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02516

SEQUENCE DESCRIPTION:

GATCTCCTAT GTTACCAATG TGTATCGTCT CCTTCTCCCT AAAGTGACT TAATCTTTGC 60  
TTTCTTTGCA CAATGTCTTT GGTGCAAGT CATAAGCCTG AGGCAAATAA AATTCCAGTA 120  
ATTCGAAGA ATGTGGTGTT GGTGCTTCC TAATAAGAA ATAATTTAGC TTGAAA 176

SEQ ID NO:2206

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02517

SEQUENCE DESCRIPTION:

GATCATGTTA TGAATTTGTA ACATTCACAC AACACCTCAC TTTTNAATCT ATAAAAGAAT 60  
TGCACGTATG ANAAACCTAT ATTTNAATAC TGCTGAAACA GACATGAAAT AAAGAATTTA 120  
AGAATGAAA 130

SEQ ID NO:2207

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02518

SEQUENCE DESCRIPTION:

GATCTAGCTT CTGGCTCTGT GTGTTTATTG ACCAGTGGTG TGCCTTGAGA AACCAGAACT 60  
CTCTGAATTT CAGTTTGTG TCTNTNTAAA TGAAGAAGGT TGTAATAAAA AAAATCTCAA 120  
GTTTCAAA 128

SEQ ID NO:2208

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02519

SEQUENCE DESCRIPTION:

GATCCGTCAT GGNCAACGAG AAGCACAGCA AGAACATCAC CCAGCGCGGC ATACGTCGCC 60  
AAGACCTCGA GAAATGCCCC CGAAGAGAAG GCGTCTGTAG GCCCTGGTTA TTGGCTCTCT 120  
TCACTTTTGT NGTCTGTGGT TCTGCAATTT TCCAGATTAT TCAAAGTATC AGGATGGGCA 180  
NNTGAAGTGA CTGACCTTAA NTGTTTCCAT TCTNCTNTGA ATTAACTTA ACTCATTCCT 240  
GATGTTTGAN CCCTGGTTNA ACAATTCAGT AAANATCTGC TAGAATNCTT NCTATCATNT 300  
TCATGTGCAT TCAAGNTTCT CATNGCATCC ANGTTCTAGN CAACACAGN 349

SEQ ID NO:2209

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



CLONE:HUMGS02520

SEQUENCE DESCRIPTION:

GATCACCAGG CAGCGACCTC CGCNCACCCC AGCAGTCGCG AGCCTCGGCC CAGCCANAGG 60  
 AAGCGNTGCC GNCGGACCTG ACTGACTTCC CAGTGGAAGT GCCTTCTTNG GCTGGGACAG 120  
 CCNTTTN 127

SEQ ID NO:2210

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02521

SEQUENCE DESCRIPTION:

GATCTGGGCC ACTTCCTCC TTCCAGTCAT GAGTAATCAT CAAGGAGCAA GTTGGAGTGT 60  
 TTCAGGTGTA TATTTGTAG AACCCAAAAG ATTGGAGCCT TAACAATAAA CATCAGCACT 120  
 AAGAAA 126

SEQ ID NO:2211

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02522

SEQUENCE DESCRIPTION:

GATCTTTTCAT AAAGCAGAAT GGTACGTATC GGATTGTTTT AATGTTATAT ATTGGATTGT 60  
 ATTCGTTGTT ACAAACCAA TATTCTATGG AGAATGAAAA AAATAAAGGA CTAAATTAAC 120  
 TGGAAA 126

SEQ ID NO:2212

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02523

SEQUENCE DESCRIPTION:

GATCTCGCAA AGTTATTCTT CCACCATGGC CAACAACGAA GGACTTTTCT CCCTGGTGGC 60  
 GAGGAAGCTG AGCAGACCCC TGTGATGCCT GTNACCTCAA TNAAAGCAAT TCCTTTGACC 120  
 TGTCAA 127

SEQ ID NO:2213

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02524

SEQUENCE DESCRIPTION:

GATCAATGTA CTTTTATAA ACTTGCCATA GATATCTCAG ATTTGAAACC TCAAGACAGA 60  
 TTTATTATTC TTAAATGCTG TATGATAATG AAGAAAAATA AAAATTTATT TCTTGCAAAG 120  
 TTA 125

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SEQ ID NO:2214

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02525

SEQUENCE DESCRIPTION:

GATCAGTTTG GAGAGTAGGG GGCCACTCAT ATTCTGGGCT CCTGGAACCA ATCCCGTGAA 60

AGAATTATTT TTGTGTTTCT AAAACTATGG TTCCAATAA AAGTGACTCT CAGCGAGCAA 120

A 121

SEQ ID NO:2215

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02526

SEQUENCE DESCRIPTION:

GATCCCCGCA TGGTGTGGG GGTGCTGGTG TGTCTGGTG CCTGGACTTG AGTCTCACCC 60

TACAGATGAG AGGTGGCTGA GGCACCAGGG CTAAGCAATT AAACCAGTTA AGTCTCCAG 120

GAAA 124

SEQ ID NO:2216

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02527

SEQUENCE DESCRIPTION:

GATCAAAAAG GGGTCTGAGG TTGCATCAGG GAGACAACTG TAATGATATA AGCAATAGTT 60

GAGAACCTGA CAGCAAGTAA TAAGACAGGA AGAATAAAC TAGAAGAAGT CAGAATGAAA 120

SEQ ID NO:2217

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02528

SEQUENCE DESCRIPTION:

GATCTGAGTT CTGAGCAAGT CAGACTCCTT CCTTTGGCC TCCAAAGCCA CAGATGTTGG 60

CCGGCCCACC TGTTTAACTC TGTATTTATT TCCAATAAA GAAGGGCTTC CAAAGGCAAA 120

SEQ ID NO:2218

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02529

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCGGAACT GTAAAGCTAT AATCCCCAGA ATTAAAGTTT TTATTATTTT TTATACATTG 60  
TAAAACATAG ACGTTTATTT ATGTGATTAA NTTCTATTAA AATTTACATG CTAAANTAAA 120

5 SEQ ID NO:2219  
SEQUENCE LENGTH:115  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS02531  
SEQUENCE DESCRIPTION:  
GATCCAGTTT TTCTTGGGAG GTTGTATCTG GTCATAAGGT AAACATTCTA TATATTCTAT 60  
GCCTGCTCTA GAATTGAAAG ACTTCAGCAG TATTAAAGCA TTTTTTAATC TTAAA 115

15 SEQ ID NO:2220  
SEQUENCE LENGTH:122  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20 CLONE:HUMGS02532  
SEQUENCE DESCRIPTION:  
GATCTGTATT TGTATATGCT GATGCAATGA TAAAAATCAC TGTAATAGNT TCATTGTGTT 60  
GTACTGGATG CAAAGCTAGA AAATATTGCA ATANNTGAGA CCGATGAAAG ACTTCTCTGA 120  
AA 122

25 SEQ ID NO:2221  
SEQUENCE LENGTH:110  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30 CLONE:HUMGS02534  
SEQUENCE DESCRIPTION:  
GATCTTGGGC AAGTTAATCT CTGGGAACTT TGGGTTTCTT ATCCTCAAAA AAGGCGATGG 60  
AAGGNCTGGG NCNCGTGATT AAATAAAAGC AACGCAAGAA AAATGCCAAA 110

35 SEQ ID NO:2222  
SEQUENCE LENGTH:109  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40 CLONE:HUMGS02535  
SEQUENCE DESCRIPTION:  
GATCGATGGT ACTTTTGTAA AATGCTTTAT TGCAAAAAAG TGGCTAGGGT TTTACAAGGN 60  
CTATGAAGAA ACATATTAAG GTTAATAAAG CTTTTTATTG AGTGTTAAA 109

45 SEQ ID NO:2223  
SEQUENCE LENGTH:105  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

50 CLONE:HUMGS02537

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## SEQUENCE DESCRIPTION:

GATCCTCCCT TAGAGCATTT GGAAGAGTGT GGCCCTGCCA ACACCTTGAC TTCAAAC TTC 60  
TGGCCTCCAT AACTATGAAA TAAATNCTTG TTGTTTAAAG CCAAA 105

SEQ ID NO:2224

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02538

## SEQUENCE DESCRIPTION:

GATCTGTCCA CTCTGGTGT CAAAGATTTT ACTCATCTTC TTAGTACATT CTATGTATTT 60  
NATATGTATA ATTTTATACA ATTAAAAATA GATTTTNGTC TAGTGAAA 108

SEQ ID NO:2225

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02540

## SEQUENCE DESCRIPTION:

GATCTTATAT CATTACAGTA GCCTTTTTGT AGAATCCATC CTATTTTCCA CATGGATAAT 60  
CATGTCATGA AGAATAAAGA CAGTTTACT TCTTTCCTTA AA 102

SEQ ID NO:2226

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02542

## SEQUENCE DESCRIPTION:

GATCCCAGGG GAGGGGTCTC TCCTCCCACC CCAAGNCATC AAGCCCTTCT CCTGCACTC 60  
AATAAACCTT CAATAAATAT TCTCATTGGT CAATCAGAAA 100

SEQ ID NO:2227

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02543

## SEQUENCE DESCRIPTION:

GATCTGCTGC TTCCAAGTTG TGTGACCTTG GCTAAGTCAC TTAACCTTTC TGATTGTCAT 60  
TTCGCTTTT AATAAAGTGG GTCTGGTGAA CAAGAAA 97

SEQ ID NO:2228

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02544

## SEQUENCE DESCRIPTION:

GATCCCACTG TATGGCTATA CGGTATTTTA TCAGTGCATC CACTGTCGGG TTTTCCCTT 60  
TGTGGACTAT TATGAATAGT GGACGCTTGT GTGCAAA 97

SEQ ID NO:2229

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02545

## SEQUENCE DESCRIPTION:

GATCAGGTGA GCTGTGTCCA GAAAACCAAC GAGAAGGAGT GGAAGGAGGA ATGAACGTTT 60  
CATTCTCGTT AATAAAGGCA TTATCCTAAT TAAA 94

SEQ ID NO:2230

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02546

## SEQUENCE DESCRIPTION:

GATCTAATCT ATTCCTGGGG CCATAACTCA TGGGAAAACA GAATTATCCC CTAGGACTCC 60  
TTTCTAAGCC CCTAATAAAA TGTCTGAGGG TGTCTCATGA AA 102

SEQ ID NO:2231

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02547

## SEQUENCE DESCRIPTION:

GATCATATAT TTGTGGCATA CAGTGTGATG TTTTGACATG NATATAATTT TGTATACAAT 60  
GTGGAATGAT TAAAACAAGC TAATTAACAT AAA 93

SEQ ID NO:2232

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02548

## SEQUENCE DESCRIPTION:

GATCTGCACT TCCTCCCCTT TCACCTACCT GTACACCTAA CCTGGCCTTA GACTGAGCTT 60  
TATTTAAGAA TAAAATCGTG GTGGTGGTCA AA 92

SEQ ID NO:2233

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02549

## SEQUENCE DESCRIPTION:

GATCAGTGGC TGCTGGGTGG CGGGTACCCT TNCTCAGATG CCTGGCAGGN CTGGNTGGCG 60  
ATTCATAAAG ACCTCGTGT GATTCCCCAA A 91

SEQ ID NO:2234

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02551

## SEQUENCE DESCRIPTION:

GATCTAACCC CTTACCCATC TNTCTACTGC TGGACTGTGG AGGGTCACCA GGTTGGGAAC 60  
ATGCTGGAAA TAAAACAGCT GCAACCAAA 89

SEQ ID NO:2235

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02552

## SEQUENCE DESCRIPTION:

GATCTTTTTG AGAGAAACAA ATGAGGATTG TAAAGTTTGG GGAATTACCT CTGTAGCATT 60  
GTGAAAATAA ACTTTGATTA AGCTGAAA 88

SEQ ID NO:2236

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02553

## SEQUENCE DESCRIPTION:

GATCACCTCG GCGTCTGTTT TGTATGCTCT TTACCTATGG ACTAGTTTGT GGACGGCTAA 60  
GAAATACAGC CTCAGCATTG ATTTGAAA 88

SEQ ID NO:2237

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02554

## SEQUENCE DESCRIPTION:

GATCTTAAGG AGTGTAATTT GCAATCTAAT TTTATCCTCT TACTCTGTGT TGTAAACCA 60  
TATACAATAA ACGGTGTTTA TGGAGAAA 88

SEQ ID NO:2238

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02555

## SEQUENCE DESCRIPTION:

GATCTGGCTG TGAGGCCCTC AGGGCAGGGA TACAAAGCGG GGAGAGGGTA CACAATGGGT 60  
ATCTAATAAA TACTTAAGAG GTGGAATTG TGGAAA 96

SEQ ID NO:2239

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02556

## SEQUENCE DESCRIPTION:

GATCCGGGGA CCAGGGGCTG ACCTCCATTC GTACCCCACT GCTTTGGAGN TGATGGGACT 60  
ATCAATAAGA ACTCTGTTCA CGCAAA 86

SEQ ID NO:2240

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02557

## SEQUENCE DESCRIPTION:

GATCAAACCA TTNACCTGG AGTTTGGTAC TGGTTTAACT TTCTCTNAAT CTGTATAAGA 60  
AAAATGAAGA CAATTGAACT TTCAAACAAA 90

SEQ ID NO:2241

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02559

## SEQUENCE DESCRIPTION:

GATCCAAGTT TTGCGGGGTC TAAAGCTGTG TGTGTTGAGG GGGATACTAA GTTTATGAAA 60  
AAGAATAAAA AACACAACCA CGAAA 85

SEQ ID NO:2242

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02560

## SEQUENCE DESCRIPTION:

GATCTCGCCA CTNTTCTCCA ACCTGGGCAA TAAAGCAAGA NCCTGTCTTC AAACAAGCAA 60  
ATAAAAACTT CTTATCCTG CAAA 84

SEQ ID NO:2243

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02562

## SEQUENCE DESCRIPTION:

GATCCTGTTA GCTTTCTGAA TGTCTGTGG TTGAATGTGT TTTGCTTAA ATAAAGCTTT 60  
TGGTATTTGT TTAAATTAAA 80

SEQ ID NO:2244

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02563

## SEQUENCE DESCRIPTION:

GATCCCAACC GTTTGGCACA GCTTTGGCCA CAGCCAGGCC CCTCTGGAAT TGTCTTATT 60  
AAACCAGTTT CCCGAGAAA 79

SEQ ID NO:2245

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02564

## SEQUENCE DESCRIPTION:

GATCCGGGTC AATGCTTCGT TTTCTAAAGG ATGCTGCTGT TGAAGCTTTG AATTTTACAA 60  
TAAACTTTTT GAAACAAA 78

SEQ ID NO:2246

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02565

## SEQUENCE DESCRIPTION:

GATCTTGGTT TTCCATGAAT ACAGCATGTA TAATAAAAAT TTAAAGAAAT AAATGTTATT 60  
CTACTTTATT AACAAA 76

SEQ ID NO:2247

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02567

## SEQUENCE DESCRIPTION:

GATCTTCTGC CGGGCGTGCC CCAGAGGACA GTGGGTGGAG TGGTCCTACT TATTAAATGT 60  
CTCAGCCCCT CAAA 74

SEQ ID NO:2248

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02568



## SEQUENCE DESCRIPTION:

GATCTCACCT TTGCAAAGTT GGATAGTCAA TTTGTTTTTA GAGGAAATAA AACACTTATT 60  
CTGTGATTTT AAA 73

SEQ ID NO:2249

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02569

## SEQUENCE DESCRIPTION:

GATCTGGAGA GAAAAACATT CAAACCATTG CATCATACAA AAAAAAGGCT ATTAAAAATT 60  
GGATTATAGC AAA 73

SEQ ID NO:2250

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02570

## SEQUENCE DESCRIPTION:

GATCAGAGTA AGAATGTCTT AAGAAGAGGT TTGTAAGGTC TTCATAACAA AGTGGTGTTT 60  
GTTATTTACA AA 72

SEQ ID NO:2251

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02571

## SEQUENCE DESCRIPTION:

GATCAAATCT GTACAGTTTC TATTGTTCCA GATTTTTTTA AGTTTGTATT AAAAGCATGA 60  
TACATAATAG TAAA 74

SEQ ID NO:2252

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02572

## SEQUENCE DESCRIPTION:

GATCTTTTCA GTGTTTTTTC ACTTTAGCTA TGTGGATTAG CTAGAATGCA CACCAAAAAA 60  
ATACTTGAGC N 71

SEQ ID NO:2253

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02573

## SEQUENCE DESCRIPTION:

GATCCAGGAG GGAGCCACCC CCAAGGACCC TGCCAGCCAC AGACCTCCAA TAAAGACAGC 60  
ATGGAAACAA A 71

SEQ ID NO:2254

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02574

## SEQUENCE DESCRIPTION:

GATCTGATGT GAATTCAGAT TTCCAATCTT CTCCTAGCCA ACCATTTTCC TGGAATNAAA 60  
AATTCAGTAA A 71

SEQ ID NO:2255

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02575

## SEQUENCE DESCRIPTION:

GATCCAGAAG TTCTAAATCC AGGATTTTAA TTAGTAACTC AAATAAAATG CCACACATTT 60  
TCATACAAA 69

SEQ ID NO:2256

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02576

## SEQUENCE DESCRIPTION:

GATCATAGTA GTGCCGCTGT TGAGTGATAA AGCAACTTGT CATTAAAGAT GTGTGTNCAG 60  
ACATGGAAA 69

SEQ ID NO:2257

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02577

## SEQUENCE DESCRIPTION:

GATCCCAGCC CAAATNNGCC CATTACACA ATCAGGAGCN AAATAAATTA CTGTTGTCTT 60  
AACACTAAA 69

SEQ ID NO:2258

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02578

## SEQUENCE DESCRIPTION:

GATCTTCAGC TGTTTGCCCG TNCTTATTAC ATAAACTGAA AACAGGATAA AAACGGAGTG 60  
CAATGAAA 68

5

SEQ ID NO:2259

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS02580

SEQUENCE DESCRIPTION:

GATCTGTCAA AGATATGAAC ATGAAAGAAC AGCTTATTTT AATAAACCCA CTTTACATAC 60  
AAA 63

15

SEQ ID NO:2260

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS02581

SEQUENCE DESCRIPTION:

GATCAAAAGT AAATGTTCTC TTTGCCATTT TAGATGGAAA AATAAAAAAA ATTAAAAAGT 60  
AAA 63

25

SEQ ID NO:2261

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS02582

SEQUENCE DESCRIPTION:

GATCTACATG AAGGAAGTGT AGATGATGTA TTTTTTTCAT CTTTTTTGTT AACTGATTG 60  
CAATAAAAAT GATACTGATG GTGAAA 86

35

SEQ ID NO:2262

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS02583

SEQUENCE DESCRIPTION:

GATCCCTTTT TTATTTTGTG GTTTTTTAAT ATAGTATAAA AATCCTTTTA AAAAAACAAA 60

45

SEQ ID NO:2263

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50

CLONE:HUMGS02585

SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

GATCAAAACA GGATTCCATT GACCTAATTA TATTAAGCTA ATAACTAAT TTTTGAATT 60  
TTTGAAA 67

5 SEQ ID NO:2264  
SEQUENCE LENGTH:58  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS02586  
SEQUENCE DESCRIPTION:  
GATCAATATT TATTGACTTG TAGTAACTGC CACCAATAAA GCAGTCTTTA CCATGAAA 58

15 SEQ ID NO:2265  
SEQUENCE LENGTH:55  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02588  
20 SEQUENCE DESCRIPTION:  
GATCAATAGA CTGTACTTAT TTTCCAATAA AATTTTCAAA CTTTGTACTG TTAAA 55

25 SEQ ID NO:2266  
SEQUENCE LENGTH:53  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02589  
30 SEQUENCE DESCRIPTION:  
GATCATTCTC AGTATCCACT GTCTATGTAC AATAAAGGAT GTTTATAAGC AAA 53

35 SEQ ID NO:2267  
SEQUENCE LENGTH:53  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02590  
SEQUENCE DESCRIPTION:  
40 GATCCATTNN TTTTGTGAAT GTGCTAAATA AAAAGTGTTA TNAATTGCTG AAA 53

45 SEQ ID NO:2268  
SEQUENCE LENGTH:52  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02591  
SEQUENCE DESCRIPTION:  
GATCCTGCAT CCCACTCCCT GGGAGCCAAT AAAGTGCATT TTCACAGGCA AA 52

50 SEQ ID NO:2269  
SEQUENCE LENGTH:50

55

# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02592

SEQUENCE DESCRIPTION:

GATCACAAAG TCAAAAACCC ATAAGAAAAA TTGAAAAAGC TACAAGCAAA

50

SEQ ID NO:2270

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02593

SEQUENCE DESCRIPTION:

GATCATATTT TCTATTAAAG TGGCTAACAC CTGGCTACTC TTACTGTAAA

50

SEQ ID NO:2271

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02612

SEQUENCE DESCRIPTION:

GATCTGTAAA TAAATCAGT GCACTGTGAA TCACACCCAG CCCCTTTCCC TGCTGTGTGG 60  
ATTAGGTGTC AAGACACCTA GTTCTTTCTG GGGCCACCCG GCTGGCCTCA CTGCTTATAT 120  
TAAGGCTCCT CCCAACTCTC ATTTTCCTTT GGAAAAACAAG ACTTTTTTCC CCATGGTTAC 180  
CGCTGAGATA CTGGGGCTGT AGTAGTATAA AAGCTCACAG TTCCTTCTGA GTGCTGAAAA 240  
GAGTGCATGA GTTGCTTCGA AATAAAAGGG TCAAGCATTC CTACCTGAAA 290

SEQ ID NO:2272

SEQUENCE LENGTH:556

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02627

SEQUENCE DESCRIPTION:

GATCTGTGCT TCCNACTCAC ATGTNAGGCC ACGCCATCCT CTTGCTGAAN CCCTATTGAT 60  
GCTTTCTAAC AGGTTCTCGT GTCTCTCCCT GACCAGGCC TCTTACAGAC TGCAGAATTA 120  
CCATCCACAG TGTACATTGG ATGAGAATGT GTCACCACCA TGCTTAGAAC CACTCTATC 180  
ACTGACAGGT CAATATCTGA GCTCCTTGGC ACAACACACA TGTCCAGGGA GTGGCCAGTA 240  
ATTAGTTGTG CCTGGAGTAT TGAGAGCATC AGTGGCCGGG AACATCAGGC AAGATGTGAT 300  
GTTTTAAAGA GCCTTGAATG CCATGCTAAG GACTTNGAAC TGCATTGCAC AGCCCATGGG 360  
GAGCTCTGGA AGGTTTAAAA GCAGNGAAGA NCCTTGCTT TGTCTAAATT CTGTAAGTCT 420  
CAAGCACTTC TGCTTTCCTT CATAGNACTT TGTAAATTAT TTCAATTGGC TTGGTTNATT 480  
TTTTNCNNA TTTTCCCTT AAATTTCAAN GTTTTGGGC GGGATTAAAT NNTGGCTTTT 540  
TTGNTCNCNT TTAAA 556

SEQ ID NO:2273

SEQUENCE LENGTH:527

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02628

SEQUENCE DESCRIPTION:

5 GATCTGAACA TCTGGCCCAA GTGAAGCATG GCATATAGTG CCCTTGGAAG AAAATTAGGC 60  
 CTCAAATGAC AGTAGCATTG AAGTGTTTGC TGCAGAGTTG AGGGAAACCC CCAGCCACCC 120  
 TCCCGGAATC CGAGATAGGG TGGCACATCT GTCCTGACAG ACGAGGAGTG TAACTNAACC 180  
 10 AGGAATATTT CCTCCATTCC TGCTCTCCCA CTGCACACAG GGTGGTGGCA CATTATCCCT 240  
 CTGGGGGGTG GGGACGCTG TTGTTTTGGC TCAATTTGGG TTTGTTGGTC ACATGGAGCT 300  
 CTTCCATTTC GTTtagctga ATAATGAGTT GTTCCTAGAG GAGACAGCCT GTCTCTCCTT 360  
 GTTNCCNCA AAGCCCATGN CCTGNCGTGG TGGANCTGGG GCTTTTGGNT GGGGAGGGGN 420  
 CCAACAATG GATNTNTTN CCTTNTCTCG AATTCCAACG GANTNNAATG TNCAAAGGCC 480  
 15 CTTTNGAAAC TTGNGGGGAA ANTtAATTNC TNTNCCCTNG NNGTGGN 527

SEQ ID NO:2274

SEQUENCE LENGTH:458

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02629

SEQUENCE DESCRIPTION:

25 GATCAGCAGC CAATATGGGT TTGTTTGGTT TTTTAATTC TTAAAAACAN CCTNTAGAGG 60  
 AATAGAAACA AATTTTTATG AGCATAACCC TATATAAGA CAAATGAAT TTCTGACCTT 120  
 ACCATATATA CCATTAGGCC TTGCCATTGC TTTAATGTAG ACTCATAGTT GAANTTAGTG 180  
 CAGAAAGANC TCAGATGTAC TAGATTTTCA TTGTTTATTG ATATGCTCAG TATGCTGCCA 240  
 CATAAGATGA ATTTAATNNN NNNCAGCCAA AGCAATATAC TCTTACATGA TTTCTAGGCC 300  
 30 CCATGACCCA GTGTCTAGAG ACATTAATTC TAACCAGTTG TTTTGCTTNT AAATGAGTGA 360  
 TTTCCATTTT GGGGAACAGG TTTCAAATGG ANTATATNTA CATGGGTAAA ATTCCCCTGT 420  
 GCTAGTGTAG GNCTTTCCTN GGGGAATGTT TTATGGGN 458

SEQ ID NO:2275

SEQUENCE LENGTH:452

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02630

SEQUENCE DESCRIPTION:

40 GATCGACTAC AAGCCAGCCC CTANGCACCT GCTGCTACAT CATGAAGNTA NCTCCAGAGA 60  
 GCATCCCCAG TCTTGAGGNT CTCAATAGAA AAGTCCACAA CTTCCAGGCC AAGCCCGCAG 120  
 TGCCTACGTC TAAGCTGGGC CAGGCAGAGG GNCGAGATGC AGGCTCAGCA CCCTCCGGAG 180  
 GGGACCCGGC CTTCTGGGN NTNGCCGTNA NCACCCTGTG TGGCGAGGTG CCGCTCTACT 240  
 45 ACATCTAGGA CGNCTCCGTG GAGCAGGGTC AGTGAAGCC CCAACGGGAA AGGAAACGCC 300  
 CCGGGCAAAG GGTCTTTTGC AGCTTTTGCA GACGNGCAAG AAGCTGCTTT CTTCCACAA 360  
 CCGNAGGACC AAAACCTTG GAGAAANTGN GNAGNTTGGN GGAGATGGAT TTGGGAGTTT 420  
 GGCAANAGGG TTGGACCCNA NGNGGGCCCG GN 452

50 SEQ ID NO:2276

# EP 0 679 716 A1

SEQUENCE LENGTH:451

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02631

SEQUENCE DESCRIPTION:

GATCTTGTTT ACTTTTGGAC ATCAAGCCCA TCACTGCCAG CCAGTNAAGA AGGATTCCAG 60  
CCTATGCCCT CAATCACAAT AAGACCACCA GATGACCAAC ATCTTCCTAC TGCAAATACT 120  
TGCATTCTC GACTTTACGT CCCACTCTAT TCCTCTAAAC AGATTCTCAA ACAGAAATTG 180  
TTACTCGCCA TTAAGACCAA GAATNTTGGC NNNGTGTAGA GTATAAAAAG TGTGTATTGC 240  
TGTGTAATAT TACTAGCAAA TTTTGTAGAT TTTTNTCCAT TTGTCTATAA AAGTTTATGG 300  
AAGTTAATGC TGTACATACC CCCTGGTGGT ACCTTAAAGA GATAAANTGC AGACATTCTT 360  
TGCTGAGTTT ATAGCTTAAA AGGCCTAAGG GAGCACTAGC AANCATTTTG GGCTATATTT 420  
GGGTTTGCTA GGTACCAAC TTTCTGGGG N 451

SEQ ID NO:2277

SEQUENCE LENGTH:446

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02632

SEQUENCE DESCRIPTION:

GATCCAGCCA GGCATCTCGG CGCTTTGGCA CCATGAGTTC TATGTCTGGG GCCGACGACA 60  
CTGTGTACAT GGAGTACCAC TCATCGCGGA NAAGGCGCCC AGCAAACATG TACACCGCT 120  
CTTCAAGCGC TTTAGGAAAT NATNCTTAGG CAGGGTACTT CGTTCAAGAC CGGCGCTTGG 180  
CACCCTTGTT GGAAAGGNT TTTCAGCATA ACATTTTCCT TCCACCTCTT TGACCTTCCC 240  
TCCAGCGTTG GCCAAATTGT GCTGAGGAAG ATGCATCAAG NGNTTGGCTG TGCCCTCATA 300  
GGTCATCTAG GGTTTTATAA AGGAGGAGGA GACAATATTT NTTCAAATT TTTGGGAGT 360  
GGGGTCATTT TCTGTATATA AANAATGTTA ATATTTAAGG TGTAGTTTAT GTTACCGTTC 420  
TGAATAAACA GATTNGGCCA TTNAAA 446

SEQ ID NO:2278

SEQUENCE LENGTH:425

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02633

SEQUENCE DESCRIPTION:

GATCCACACC TGACCCTGTT GGGTCGAGTT AGGNTGGGCC TTGGTCTGCA CTGTAGCACC 60  
TNTGTTCTTT GAGTTCACAT CATGAATGTG GTGACTTNCC AGNTACCATA TCAGGCTTAA 120  
CCTAGCACAT CCTATTTCTT TNCTTCTATG ATATCCAAAT TGGACTGACC TCACTTCAAA 180  
GTTGCTGTCC CATTTTGTCA CCCTATCTTA TCTCGGGGAA ATTGCAGACT GATGGCCAGA 240  
CCAACTCTGT TGAAATTCTT GCATAGAGCA AACCTGTGCT CATTTTAAAG TGGCATGGGA 300  
GAGGCCCCCA GCCTAGTAAA GCCTAGTCTG TGTCTTCACA GTGCTGGTAG NATGNNGTTT 360  
GTGTGTATAA ATATATGATA TAGGATTGAT AATATGTTNN CTAACGGCCA TATTATTGAA 420  
GGGCN 425

SEQ ID NO:2279

SEQUENCE LENGTH:414

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02634

SEQUENCE DESCRIPTION:

GATCTGCCTT AACTCCAAC TACATGTTTT GGTCACTATT ACAAACTGTC ATCCCAGAAT 60  
GATGCTGCAG AGGCTAGGGC TAGGACACAG ACCAGTGTTT CCATGTGGGA ATTCCCTCCC 120  
AGTATTTCCT AGGAANNNTA TGTTTTTTGA ATCCATAATC CCTAGAAAAA TCAGTTGAGG 180  
AAATGAGAAG TATTGTAATT ATNCTGTGAA TAGTAACACT TACCATTATG GAGACATCAC 240  
TAGTTTGAAA GANTCCAAC TCAATCAAATN TTAACGTACC GAGTTGAAGG NTACAAGANC 300  
TGAGACAGGA GCATAGCAGA GGAGAAACGG TCACCATCTC ATTAGCCCTA TTTTTTGGNT 360  
TGNTGTGATG CCATTACATC TGAATAATC TGGGCCATNT CAGCTGCTAA TGGN 414

SEQ ID NO:2280

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02635

SEQUENCE DESCRIPTION:

GATCTCACCT TCCTTCGAAT TCGCTCCAAG AAAAATGAAA TTATGGTTGC ACCAGATAAA 60  
GACTATTTCC TGATTGTAAT TCAGAATCCA ACCGAATAAG CCACTCTCTT GGCTCCCTGT 120  
GTCATTCTT AATTTAATGC CCCCCAAGAA TGTTAATGTC ANNNNGTCA GTGGACTAGC 180  
ACATGGCAGT CGCTTGGAAC CCACTCACAC CAATCCAGTG ACCGTGTGTG GGCTGGNGGC 240  
TCTNTNTCCC NCNCCAACGG AACCCNGTG TGCACCAACC TTTNNCNCAG AGN 293

SEQ ID NO:2281

SEQUENCE LENGTH:400

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02637

SEQUENCE DESCRIPTION:

GATCTGGCAG GGCACCACAG CGCCCCCTAC TGAACCATCA GCATGTCAGT GGCATTTAAA 60  
GCCATGCAGC TGGAGGGGCC ACTGAGATTG TCTCTGAGTA TTACTGAGAA GCAACAGAAA 120  
AGAGCCATGG ATGGAGCCCT TGGGCTCTCT GGGAAATGGG AAATCAGCCA AAGGACTGAG 180  
AAGGAGTTAC CTTAAGGTCA GAGAAAACCA AGAGAGTGTG GTGTTCTGGA AGCTGAGCTT 240  
TCTTTATTCA ACCTCATTCC CTTCTCCAAA TAAGCCACTT GTGTAGTTGG GCCCCTCCAG 300  
GGTTGAAGGC AAGAGGAGAA AGGCACAGCG TTTGGGAAAC AAGACTTTTC CTGCAATAGC 360  
CTGGGGAAGG AATAAAANGG ATAGAGGTGT TTGGGGGAAA 400

SEQ ID NO:2282

SEQUENCE LENGTH:400

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02638

SEQUENCE DESCRIPTION:



GATCTGTCCA ACGCCTGCAG CGTGGATGTG GAGGCGGACT AATCAACNAG TGCTCTGTTA 60  
 TTATTTCTAC CCATCCCTTT TCTCCATGCT AATTTGCTTA GAACTTTAAC ATTGAATGGA 120  
 CAGCAAATGT CATGTTCTGT TTAATTATCA CTCCTTGACC ATTATGTAA TTTCTTTCCC 180  
 TAACAAGGTG ACGCATTGTT TTAAGTAACA ATGACCAACT CATCTACTCT TCTTCCAAAT 240  
 TGTGTAAATT GAANGGGTAA AATGTGGGAA AACGCTAAAT TTGAATGCTA AATTTGAACA 300  
 TTTCACACAA CCAATAATTT TGAAATGCTT CTTNGCAATA TTATNGCGGT TTCGGNACCA 360  
 GGTTAAAAAT NNCTTTCATT TTCAGGNCAT TTTGGTCAAA 400

SEQ ID NO:2283

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02639

SEQUENCE DESCRIPTION:

GATCGATAAT ATAATTTATA ATGAAATTGC TTTATCAGCT ATTAATGTGA ACTACATCAT 60  
 CTTCATATAG CNTTATAACT CATTTGTGCT ATTCCATTTT CCTCTGTTCC TTTTATTTTC 120  
 ACTTCCCTTG TAATGTTAGT CTCTTTGTAC TGATTTCTGA AGAGTTCATT TATGATTAAA 180  
 CATGTTAACA TTTTGTCTAG AATTGCAAAT ATGTTTTTCC TCATTCATTT TACTATGGTG 240  
 TTTTATTTT GGGTTATACA GAAGTNGTAT ATTGAAATAT AATCTNGTNC TGTTTTATGA 300  
 CTTTGGAGTT TTGTGGTTTT TTNAACCAN GTTTACAGTG GNATCCNTNN ATTNGGTATT 360  
 GCCGTCNTAN TNCCNGCAGT TAGGTN 386

SEQ ID NO:2284

SEQUENCE LENGTH:384

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02640

SEQUENCE DESCRIPTION:

GATCTNNTCA AACAGCAAAC GCCCACAGAN GGCCAGAGG NGGTGGTAAT CAGGGTGTGT 60  
 GGGTGNTTT AGGGTTCTTT AGTGTGTTT CTTTCACCCA GGCGGTGGTG GTCCAGCCA 120  
 GTTTGGTGCT GACGGTGAGA GGAAATNAGA ATCTGTTTGC AAATTGTCCA ACCCAGCCCC 180  
 TCAACATGAG GGGCTTCCAT TTTNTGTGTT TTGTAAGGGA ACTGTTTCCT TCATGCCGCC 240  
 ATGTTCTCTGA TATTAGTTCT GATTTCCTTT TAACAAATGT TATCATGATT ANGAAAATTT 300  
 CCAGCACTTT AATGGCCAAT TAACTGAGAA TGTAAGAAAA TTGATGCTGT ACAAGGCAAA 360  
 TAAAGCTGTT TATTAACCTT GAAA 384

SEQ ID NO:2285

SEQUENCE LENGTH:383

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02641

SEQUENCE DESCRIPTION:

GATCTTTTCT ATAATATCCT ACTACTTTGG TTTTCCTAGC TCCATACCAC ACACCTAAAC 60  
 CTGTATTATG AATTACATAT TACAAAGTCA TAAATNTGCC ATATGGATAT ACAGTACATT 120  
 CTAGTTGGAA TCGTTTACTC TGCTAGAATT TAGGTGTGAG ATTTTTTGTT TCCCAGGTAT 180

EP 0 679 716 A1

AGCAGGCTTA TGTTTGGTGG CATTAAATTG GTTCTTTAA AATGCTTTGG TGGCACTTTT 240  
GTAAACAGAT TGCTTCTAGA TTGTTACAAA CCAAGCCTAA GACACATCTG TGAATACTTA 300  
GGATTTGTAG CTTAATCACA TTCTAGACTT GTGAGTTGAA TGACAAAGCA GTTGGACCAA 360  
AAANTTTATG GGCATTTAAA GGN 383

SEQ ID NO:2286  
SEQUENCE LENGTH:424  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02642

SEQUENCE DESCRIPTION:  
GATCTAAAAT ACCTGGTGGC TTTNACAAA AAGCAGATTT TNTTCATGTA CTGTNATGTC 60  
TGATGCAATG CATCCTAGAA CAAACTGGCC ATTTGCNAGT TTA CTCTAAA GACTAAACAT 120  
AGTCTTGGTG TGTGTGGTCT TACTCATCTN CTAGTACCTT TAAGGACAAA TCCTAAGGAC 180  
TTGGACACTT GCAATAAAGA AATTTTATTT TANACCCAAG TCTCCCTGGA TTGATAATAT 240  
ATACACATTT GTCAGCATTT CCGGTCGTGG TGAGAGGCAG CTGTTTGAGC TCCAATGTGT 300  
GCAGCTTTGA ACTAGGGCTG GGGTTGTGGG TGCTCTTCT GAAAGGTCTA ACCATTATTG 360  
GATAACTGGC TTTTCTTCT CTCTTTGGAA TGTACCATTAA NAAATAATTT TTTGAACCAT 420  
CAAA 424

SEQ ID NO:2287  
SEQUENCE LENGTH:378  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02643

SEQUENCE DESCRIPTION:  
GATCCGAAGA GGAAGGGCGG TCCGGGCTCC AACTTAGCT TCGTGGGCAA ACGCAGAGGC 60  
GGGAACAAAC TAGCCCTNAA GACGGGAATA GTAGCCAAGA AGCAGAAGNC GGAGGATGAG 120  
GTATTAACAA GTAAAGGTGA CGCGTGGGCC AAGTNCNNGG CAGAAGTGAA AAAGTACAAA 180  
GCTCACCAGT GCGGTGACGA TGATAAACT CGGCCCTGG TGAAATNACG CCCCTCCCCC 240  
ACCTGCCCAT GGCCTGGGAC TCTCTGCGAT GTACATAACT ATTTAATGCA GCGGCANGTC 300  
GACAGCTTTC CCTGAGAGGA CTTAAAGCA GAAGGAAACC GAGATGCTTC CCGNAAGCCG 360  
TGGACGATTC TCCAAGGN 378

SEQ ID NO:2288  
SEQUENCE LENGTH:370  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02644

SEQUENCE DESCRIPTION:  
GATCTTCTTG ACTATGCCAG TTGTAGTACC AGCTTCTGTA TCTGCACTGA ATTCTGNCTC 60  
AGTAATATGC CTTTGTTTAA AATTTAAATA TTTTTCATT TTTTAACT AGAAAAATAAT 120  
TATAATGAAN NNNNTAAGTA TCTCATTTTA GGATTCTGAT TTACATAGGT ATCACTGTAA 180  
CTTGTGCTGT TTGCATAGGT ATACTCTATC TTGTGCTATC TGCATAAAAT-ATCCAAGTAA-240  
ACACATTGTG ATTTTACATC CGTGCATAGA AAAAAAATC ATCTGAACTC AAATCAATCT 300

EP 0 679 716 A1

GTTGATACTG ACTAGATTGG TGACGTGTTT ATGTGTACCA CTAGTGATAA TGCACGGTCC 360  
TGTACAAGCN 370

5 SEQ ID NO:2289  
SEQUENCE LENGTH:370  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS02645

SEQUENCE DESCRIPTION:

GATCACAGGA ACAGCAGGTG ACAGGCCTAG CTATAGTTAG GAATACACAA GCCGTAAAAT 60  
CGAGTCCTTA CAGCCATACC ACAAGGTACG TCCANNTGGA CTACAAGAAG AGCTTCCTTT 120  
AAAGTTCCTA TTTCAGCATA AAGAGGCTGT CCTTTTTTTT NAGGAATAGT TTGGACCTTG 180  
15 TGCCTCCTGT GGGAGGCTGA GGAAGGCTGA AGGAGAGCTA GCAGATATGC CTGTTACCCC 240  
CTCTCTGGTA CTTGTGGCTT GCTAGTATGT TTTNATGATA ATCTCGGGCA TTGTTTGCAT 300  
TTGTGTTTAT TAATAGGGTT TTTGTTTTTT GTTGTTCCT NTTTTNACAG TAANGGCTGA 360  
ATTACATAAA 370

20 SEQ ID NO:2290  
SEQUENCE LENGTH:367  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS02646

SEQUENCE DESCRIPTION:

GATCTGAAAG GAATGCTAGA AGTGTTTAGA GAGCTGACAG ATGTCCGACG CTAAGGGGG 60  
CATGCNACAG GGGGAATGGC TCGCTTCAGT GCCCTGCTGC TCAAAGCTCT AGGGNAGAAT 120  
30 GCAGTCGGGT AGNCTGTGGG GCTCTAACCC CACAGCAACC TCTAGGGATG ACGTCACTAA 180  
AAACCGATGA AGCCTCCATA ACATTGGTTC CTTACTGACG CTGAGGAGCA NGGCAATCTT 240  
CACACCTTAA CCAATGCTAT TCATGTAGGA TGACCAAGAA ATGAATGTTT CTTACTGAAA 300  
TAATACATAT TTTTGGCATC TTTTGGTTAC CCATAGACTA ATTAAANCTA ATCCNNGGNT 360  
TTATAAA 367

35 SEQ ID NO:2291  
SEQUENCE LENGTH:359  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
40 CLONE:HUMGS02648

SEQUENCE DESCRIPTION:

GATCCTGACA GAGCCCTGAA CAGATTATAT CACTCGGCTA GAGGCACTGC AAAGACGACT 60  
TGGAACATA CAGTCAGGTT CAACTACTCA ATTTTCATGCT GGCATGAGAA GATAATCCTT 120  
45 TGAAACATCA TTAATTGAAG TGATTTTAAA TAGATTTTCT TTTGTAAATC AATGGTTCTT 180  
TTGTGCTTTN GNNNNNCGA ATATTCAATG GGACCAATAT GAACACAGCT TATGATTGTA 240  
TACAAATCCC TTGCCAGCAC ATGAAANCAA ACTGGANTTT GTATATATAA GCATTGTGTA 300  
TGTATTCATG CACAATAATT ATNGANTTAC CTGTATATTT GTGGGAATGC TAATTTAAN 359

50 SEQ ID NO:2292

55

SEQUENCE LENGTH:357

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02650

SEQUENCE DESCRIPTION:

GATCTGTGGG TCCGGCTGNA GGAGAGTGAC ATAGTCCCGC AACTCCANNT TGCCTGTCCT 60  
 GGACAGGCAC ATCTCCACTG AACTGCGGCT CCNTCGCCGT GGGCATTCCC ACCACAGCCA 120  
 GATGGTGGCC AGCAGTGCCT GCCTGTNTCT CTGGACTCCT GTGTTCTGGG TGCTGGTGCT 180  
 GGCTTTCCAA ACAGAGACAC CGCTCCTGTA ACGACTGGAA GCACCAGGCT AAGNACCTNA 240  
 CCCCTCGNAC TTNGAAGGAA TGGGCATTNC NGTACTTCAA CATTCTGGGT CTAGGCCTTG 300  
 TTGGGGCCAA TTCAAGAAGN GGCCTTGTTN TTNGAAAAA GTGGGCCNNG TTTTNAN 357

SEQ ID NO:2293

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02651

SEQUENCE DESCRIPTION:

GATCCTTCTT TTTGGTTTTG GAAATATAAT CATTGTTAAT GTTTTCCTC CAAATAGAAT 60  
 ACTGTTTTAT CCATACAAAT CATAACAGCA TCTATCCCAT GCTAGGGTTG GAAACTGATA 120  
 TTGGTATTAC TTGTGTTTTT CCTTAGTGTG TTTTATTTC CAGTTTCATC TNCTTTTAAA 180  
 AATGAAAATA TGGTGCCTTC CCTCCCTCCA GGAAGACTGG CAAATATTNC CTTTTATTTA 240  
 CTGCTGCTGT GGAGTGATGA GATATGCACT TTA CTCTTA AGATTCAGCA AAAAGCTTTT 300  
 CACTTCTCAG TATATCCAGA ATACATCATA TCTGGGACTT AGGAAAATTT GCCAN 355

SEQ ID NO:2294

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02652

SEQUENCE DESCRIPTION:

GATCTTTTAC ACCACATCAC AGTGANCACA CTGGGGAGAC GTGCTTTTTT GGNAAACTCA 60  
 AAGGTGCTAG CTCCTGATT CAAAGAAATA TTTCTCATGT TTGTTCAATC TAGTTTATAT 120  
 TTNCATTAA AATCCTTTAG GTTAAGTTTA AGCTTTTAA AAGTTAGTTT TGAGAATTGA 180  
 GACACAATAC TAATACTGTA GGAATTGGTG AGGCTTGACT TAAAACTTTC TTTGTACTGT 240  
 GATTTCTTT TGGGTGTATT TTGCTAAGTG AACCTTGTTA AATNTTTNGT TAACTAAATN 300  
 TTTTCCTTAA AATAAAGACT TTTTCACAAA 330

SEQ ID NO:2295

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02653

SEQUENCE DESCRIPTION:

GATCCTATGG ATTTTCCCGG CTGGTTGCCA CTACTNTACA ACATTCANAG CCCACATCCA 60

EP 0 679 716 A1

TCTGTGCCAT TAAGCTTTTT TGAGACATGA GAGATGCCTC TTCCCTGCTG TATGACATGC 120  
 ATTTGGGAAG TTGGAAAGAA ATGACAAAAT CAGGGAGAAA ACATCCAAGC TTCTTACCTG 180  
 TAGATAGAAT CAGCCCTCAC TTGGTGCTTA TTACCAGTTA TTCANGGACA ATAACAACAA 240  
 CAAAATTAGT AGACATNCAT GANGCACATN TTTAGGNCCA AAGGNTAGCA TCAACTTGTA 300  
 TTTNGAAGGG ACTGTAGTTT TCGGCATTTT ATGGCNATTT TTTATNAAAG TN 352

SEQ ID NO:2296

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02654

SEQUENCE DESCRIPTION:

GATCGCAGCC GCTTCGCACG CCGCATCACC CAGGCCCAGG AGGAGCTGAG CCCCTGCCTC 60  
 ACCCCTGCTG CCCGGGCCAG AGCCTGGGCA CGCCTCAGGA ACCCACCTTT AGCCCCCATC 120  
 CCTGCCCTCA CCCAGACCTT GNCCTTCCTCC TCTGTCCCTT CGTCCCCAGT NCAGACCACG 180  
 CCCTTGAGCC AAGCTGTGGC CACACCTTCC CGCTCGTNTG CTGTGCAGC GGCTGCCCTG 240  
 GACCTCAGTG GGAGGCGTGG CTGAGACCAA CTGGTTTGCC TATAATTTAT TAACTATTTA 300  
 TTTTTTCTAA GTGTGGGTTT ATATAAGGAA TAAAGGCTTT TGATTGTAA A 351

SEQ ID NO:2297

SEQUENCE LENGTH:357

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02656

SEQUENCE DESCRIPTION:

GATCCCCGTT CCTGACATCA CAGCAGCCTC CAACACAAGG CTCCAAGACC TAGGCTCATG 60  
 GACGAGATGG GAAGGCACAG GGAGAAGGGA TAACCCTACA CCCAGACCCC AGGCTGGACA 120  
 TGCTGACTGT CCTNTCGNGT NCAGCCNGTG GCCTTGGCTT TTCTAGCCTA TTTACCTGCA 180  
 GGCTGAGCCA CTNTCTTCCC TTTCCCAGC ATCACTCCCC AAGGAAGAGC CAATGTTTTN 240  
 CACCNATAAT NCTNTCTGCC GANCCCTAGT TCCCTCTGCT CAGCCAAGGT TTGTTATCAG 300  
 GTTTTCAGGG GCCATGGGTT CACATTAAGG ATTTAAAAGG GTAGTAATTT GGGGAAA 357

SEQ ID NO:2298

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02657

SEQUENCE DESCRIPTION:

GATCAAATTT NAGTGGCTTT GGACAGAAAA GAAGGCTCTG GATTAAAGCG GGTGGTCACC 60  
 TGTGAGACCA GGTCTACCTT GGGACTGTTA TTAACTGAA TCAGTTATTT CCTTGAAATT 120  
 TCACAGTAGT GGGTGGGCCT GTTTAAGGC TCTGACAGAT ACCACGAAAC ATGANGCNCG 180  
 NNGAACTACA AGACCCCGG GGTCTTCTG AGTGCAAGGC TGAAATGGAC AAGGGCTCCT 240  
 CACGGGGGTG GAGGGAGCCG GAGCCTGCCT TGTGTTCCCT TTTTGACTTG TGACATTTTT 300  
 CAAACACATA ATTTAAAGGA CTTATGCTCT GCTGTCTCAG GAAA 344

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SEQ ID NO:2299

SEQUENCE LENGTH:462

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS02658

SEQUENCE DESCRIPTION:

10 GATCTGGTCC CTGAGAAACA TATTGTGATG AAGTGGAGGT TTAAATCTTG GCCAGAGGGA 60  
CACTTTGCCA CCATCACCTT GACCTTCATC GACAAGAACG GAGAGACTNA GCTGTGCATG 120  
GANGGTCGAG GCATCCCTGC TCCTGAGGAA GAGCGGACAC GACAGGGCTG GCAGCGGTAC 180  
TACTTTGAGG GCATTAAACA GACCTTTGGC TATGGCGCAC GCTTATTTTA GGGCCAGCGG 240  
CAGGGGACTC CAGCCTGCTG GACACTTCAN GTCCAGCTCT CTCCTGACTG GGGCTTNCGA 300  
CTCACAGGAT TGCATCGNCC CAGCTGCTAA CTTNGGGCCG GGGGCCCNTC CCTTNCACAA 360  
15 TATACCTTGG GTTTNTGCA TTTTCCTNN CTGGGTTGGG GTTCAGAGGG GCAATTTCNN 420  
CTTTTAATGG TGTACATATN NCTANATANN CATAATTTTA AA 462

SEQ ID NO:2300

SEQUENCE LENGTH:341

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02659

SEQUENCE DESCRIPTION:

25 GATCAACTTC CCACAAACTG AGGAATGAAT TCCACGAGCC TGTTCTGAAA ATNTGGACGT 60  
AAGACAAACA CGTGCTCGTC CTTTAATGGA GTTCACCAGC ACACTTGTTA ACCAGTCCTG 120  
TTTGCTTCG TCTTTTTTTG TCGTAATAA AGTCAACTGA CCAAGTGACC ATGAAAAGGG 180  
GCTGTCTGGG GCTCCTGTTT TTNAGCTGCT GTTCTTCAGC TCCGACCATG TTGCTGTGTG 240  
ATTATCTCAA TTGGNTTTAA TTGAGGCAGA AACTGAAGCT CTACCAATGA ACTGTTAGAA 300  
30 ACAAGACACA CTNTNGTATT AAAATTGCTT GCAGTAACAA A 341

SEQ ID NO:2301

SEQUENCE LENGTH:339

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02660

SEQUENCE DESCRIPTION:

40 GATCNGTGGC AAAACCAAGT GTGGTCTTTC AGCTTCAGTG TGTTAGCATC CCAGCACCTG 60  
GGATGGGGTT TGTGGGCAAG TTGATTTTGC CACACTGTAG GGCCCAGGTN NNCCCATTCG 120  
CACCGTGAAG CCAAATNCTA GCCCAAGTCT GGTAGAGCAG TCGGGCAGCT AGTTTTCCGG 180  
GGAGGATGAT GTGGTGGGAC AGAGGACCTC AGTGGCCTAT TACGGAGCCC TCTTCCAGA 240  
CTAAATTCAT AGCCGAGAGC TCGGGGGGAT GGTAGAGTTA AAATTTAAAA TAATTTTCTA 300  
45 AATTCTGTAT TTGGATATTA GTGTTTAAGT GGTAATTTN 339

SEQ ID NO:2302

SEQUENCE LENGTH:441

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

CLONE:HUMGS02661

SEQUENCE DESCRIPTION:

5 GATCCAGGGG CTGCCTCTGG CCTCTTAGGG AGCAGAGAGC AGAACTCCGC AGCCCAGCCC 60  
 AGAGGAGTGT CACCTCCCAC CTTTGGAGAG GAATCCTTCC CTCCCCTGGA CAAAGTTGCT 120  
 GACAAGCCCC TGAAGTGGCC TCTCCATATT CCAGCTGAGC CTGAATCTGA CTCTTGAGGG 180  
 TTGGGGCTGC ACTTATTTAT TGCGGGGAGA CAGCTCTCTC TCCCACCTNC TCCCAGATG 240  
 GGAGGAGAGC CTGAGGCCCA AGCAGGACCC GGGGGTTCCA GCCCCTAGCT GCTCTGGAGT 300  
 10 GGGGGAGGTT GGTGGACCAT GGGAGTNCCT GGTGCTGCCC CTNAAGGTGG GACCCAGGCG 360  
 TTNTCAAGCT GTACCCTTT NCCGATGGAA TTTGTGTTT TGAANATNNG TGTCTNNTAC 420  
 TANTTNTTT AAATAAAAAA N 441

SEQ ID NO:2303

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SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02662

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SEQUENCE DESCRIPTION:

GATCATGGCA TCCAAGACCA GAGTCTCAGA ACTCATTAAG AAACAGTTTA CTGGAATGG 60  
 AGAATACCCA TCTGTAATAC AGGTCCTGTC ATTCATTCA TCTCAAATTA TTTTGAATTC 120  
 TTCCCAAATG GCTGCTGGAT TTAGGTGGTA ATAGGGGCTG TGGGCCATAA ATCTGAAGCC 180  
 TTGAGGAACC TTGGGTCTGG AGAGCCATGA AGAGGGAAGG AAAAGAGGGC AAGTCCTGAA 240  
 25 CCTAACCAAT GACCTGATGG ATTGCTCGAC CAAGNCACAG AAGTGAAGTC TGTGTCTGTG 300  
 CACTTTCAC AGACTGGNGT TTTTGGTNCT GAATAN 336

SEQ ID NO:2304

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SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02663

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SEQUENCE DESCRIPTION:

GATCAAGTNA CTTCTGCCCA CCTGGACACA ACACCAAAAA GGCTTCTAAA NACGGGTGTN 60  
 AGTCTTTTNA GCAACCCGGT CCAGTACTGG GAGATACAGC CATCCACCTT CANATGTGTC 120  
 TACGTGCGCT CTGCCATTCA ACTCGGAAAC TATAAGTAAT TCTNAAGAAA GCCCTCATT 180  
 TTATAACCTG GCAAAATCTT GTTAATGTCA TTGCTAAAAA ATAAATAAAA GCTAGATACT 240  
 40 GGNAACCTAA CTGCAATGTG GATGTTTTAC CCACATGGCT TTATTATGCA TAANGCCAAT 300  
 ATTTCTGTGTT TTAAGTAATN GCCTTCAATT NNNAAGNTAA TTTTGGCCTG NCCCANAAAT 360  
 AAA 363

SEQ ID NO:2305

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SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02664

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SEQUENCE DESCRIPTION:

GATCAGAGTT CCTCCTACTT ACAACCCAGG GTGTGAACAT GTNCTCCATT TTCAAGCTGG 60

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AAGAAGTGAG CAGTGTGGA GTGAGGGCTG TAAGGCAGGC CCATTCAGAG CTATGGTGCT 120  
 TGCTGGTGNC TGCCACCTTC AAGTTCTGGA CCTGGGCATG ACATCCTTTN TTTAATGAT 180  
 GCCATGGCAA CTTAGAGATT GCATTTTAT TAAAGCATT CCTACCAGCA AA 232

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SEQ ID NO:2306  
 SEQUENCE LENGTH:330  
 SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear  
 CLONE:HUMGS02665  
 SEQUENCE DESCRIPTION:

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GATCTTAAGT ATAATTACAA GGAAGAAAGT AAGAAGAATA TTCTCTTAGA AGAGAAGGTA 60  
 AAAAACTTT CAGAACAATT GGGAGTTGAA TTAAGTAGCC CTGTTGCTGC TTCTGAAGAG 120  
 TTTGAAGATG AAGAAGAAAG NNCTGTAAAT TTCCCATTT ACTAAAGGTC ACCTATAAAC 180  
 TTTGTTTCAT TTAAGTATT ATTAAGTTAA TAAGTTAAAT ATACTTGGA ATAAGCAGTT 240  
 CTCCGAAGT TAGTATTTCC TTCTCACTAC CTTGGTACCT TTATACTTAG ATTGGAATTC 300  
 TTAATAAATA GAATTATATG AAATTTTCAN 330

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SEQ ID NO:2307  
 SEQUENCE LENGTH:328  
 SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear  
 CLONE:HUMGS02666  
 SEQUENCE DESCRIPTION:

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GATCGACTTA CTCAACATGA GACAATTCAT ACTGGTGTGA ACCACANAAA TGCAAAGAAT 60  
 GTGGTAAGGC CTTAGTCAT TGCTATCAAC TTAGTCAACA TCAAAGATTT CACCATGGTG 120  
 AGAGACTCTT AATGTAATGA GAGGAAAAGC CTTTAGCCAT GGAACATTTT TACTGTTGTC 180  
 ACTATTATNA TGCTATAGTG AAGATTAAAC TAGTTAATAT AGAATATAAA TACTTGGA 240  
 GGCATCTGGC ACATCGTATT TGCTTACTAA ATACATTATT TTTATGATAA TTGTTAGAAT 300  
 TACTAAAAAT AAATCTTATA GAAGGAAA 328

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SEQ ID NO:2308  
 SEQUENCE LENGTH:327  
 SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear  
 CLONE:HUMGS02667  
 SEQUENCE DESCRIPTION:

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GATCTCAGGT ATCAGACCAC TGAGCAACCC ACCGCCAGNC TGCAGGCTTT CAGAGGCCCA 60  
 CCTGGGCCCC GCGTGGCCTG CCCCAGGGTG GGCTCCCAGC GCAACTGCAG GCATCCTCTA 120  
 GTGGGGCCTC TGTAACCCCT AGCAGATGGT GGTGACCCCT CTGAGATGAG GAAGCTGGTG 180  
 ACCTNNGACT GAGCAGCAGC CTATGGGCTC CGGGTCAAGT GCTATTCCCA GCGGATGCCC 240  
 TTCCCTTGC GNCAGTCCCT CTTTCTCTGA GTGTCCAGGC GCNANTGNAA AACAGNAACC 300  
 CTAGGTCTG GAAACTACTT TTTTTN 327

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SEQ ID NO:2309  
 SEQUENCE LENGTH:326

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02668

SEQUENCE DESCRIPTION:

GATCCAGTTG TTATAGTGAA CTCATGGTAA TGGTTTGTGA GAACAATAGA GATTTTNATT 60  
TCTATGTAGA TGAGTTGGTA TGAGAATATA TGGAATTTT AAGGGACTGT TAAATCTTT 120  
GATTTGTAGA CTATTAAATA TACCGTATGC ATAAAGTAAG CCTTTAGCTC TAAGGTAAAG 180  
ACGACACGTT TTCGGTTTGT GACTACAAAT AGGTTAAAA TAGATTTTAA TTTTATTAAA 240  
AATATAATTT AATGCAGGTT GTTTGAAGCA TCTGTCTTCA TATGATGGCA TTAGAACACC 300  
TTGGTATAAT AAAAAGTTAC CGTAAA 326

SEQ ID NO:2310

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02669

SEQUENCE DESCRIPTION:

GATCAAGAAG GAGCTAGAGA CCATTTCAAA GAAAAAAAT GCTTTATAGA GTTTTAAGTA 60  
TGACTTAGAT GGGTCCAGGC AAATAAACTA AAAAGAAGTG AAGGCAACAT GTATCGTCTG 120  
GCAGAACTAA ATCTTGGAGT GGGGTGAGGG ATGAAAGACT ACATATTGGG TACAGTGTA 180  
ACTGCTCGGG TGATGGGTGC GCTAAAGTCG CAGAAATCAC TAAAGAACTC ATCCATGTAA 240  
CCAAACACCA CCTGTACCCC AAAAACGAAA TAAAAAACA AAACCTTGGG GCCCATTCCC 300  
CCTAGGAATG GACTACTGTA AA 322

SEQ ID NO:2311

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02670

SEQUENCE DESCRIPTION:

GATCTAAATT ACCTTGGGTT TCGCATATGT CTATGAAATN CTGTGATAAN GTTTTTCAAT 60  
ACATTGNTTC ACTGGCGTCT GTTTTCANTT TATACTTTTA ATAACTCATC ACTGGTGGTA 120  
CTTTATCTTG AAAAGTAATA TTTTNATAT TTTANCATTG GACAGTGTTA GCCAGTTGTA 180  
ATGATGTATC AGANGTAAAG AAAAACCCAT TAAAGTTATA GCTAATAGAT GCTGTTGGGG 240  
GTAAATTAA TAGTAAANTA ATCCAATATA GCACTNTNNA TGATTNTTA TATAAANGTC 300  
AACTGGTACA TTTCATTGAG N 321

SEQ ID NO:2312

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02672

SEQUENCE DESCRIPTION:

GATCGAAGGG TTTTATAGA ATGTNTTCA AAACCATGCC TGGTATTTTC AACCATAAAA 60  
GAAGTTTCAG TTGTCCTTAA ATTTGTATAA CGGTTTAATT CTGTCTTGTT CATTTTGAGT 120

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ATTTTAAAA AATATGTCGT AGAATTCCTT CGAAAGGCCT TCAGACACAT GCTATGTTCT 180  
 GTCTTCCCAA ACCCAGTCTC CTCTCCATTT TAGCCCAGTG TTTCTTTGA GGACCCCTTA 240  
 ATCTTGCTTT CTTAGAATT TTTACCCAAT TGGATTGGAA TGCAGAGGTC TCCAAACTGA 300  
 TTAAATATTT GAAGGGAAA 319

SEQ ID NO:2313  
 SEQUENCE LENGTH:327  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02673

SEQUENCE DESCRIPTION:  
 GATCGACAAA ACTTTGAACG AGGCTGACTG TGCCACCGTC CCGCCAGCCA TTCGCTCCTA 60  
 CTGATGAGAC AAGATGTGGT GATGACAGAN TCAGCTTTTG TAATTATGTA TAATAGCTCA 120  
 TGCATGTTTC CATGTCATAA CTGTNTTCAT ACGCTTCTGC ACTCTGGGGA AGAAGGAGTA 180  
 CATTGAAGGG AGATTGGCAC CTAGTGGCTG GGAGCTTGCC AGGAACCCAG TGGCCAGGGA 240  
 GCGTGGCACT TACCNNGGGT CCCTTGCTTC ATTCTTGTGA GATGATAAAA CTGGGCACAG 300  
 CTCTTAAATA AAATATAAAT GANCAAA 327

SEQ ID NO:2314  
 SEQUENCE LENGTH:313  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02675

SEQUENCE DESCRIPTION:  
 GATCAACCAC ATGCACATCC TTACTIONACAGA ATCCGTCCTT TCATTTC AAC ATTATAGCAA 60  
 GCTATGATTT TNATATATAA ATATTATATA AATNANGTAT AANACATTAA AAGTTAACTA 120  
 TGTAAGATAT TATNTCTGAA ACAATTTAGC TATATCCACT ATGATTATAA ACTGTGTCTC 180  
 GACCTGTGTT ATNTACANAA GCTGCTTAAA AAAGCATTGA GTTAATTTTN TTAAATATCA 240  
 ACTAAAATAT CATAGTTCTG TGGNNGACAT TGTGTTATAA TGANATAACT GCAACTAGAG 300  
 AAANCTGTAT AAN 313

SEQ ID NO:2315  
 SEQUENCE LENGTH:365  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02676

SEQUENCE DESCRIPTION:  
 GATCGAGGAC ATAAGGAACT AGTCACAGTG TTGCTGCAAC ATAGAGCTGA CATTAACTGT 60  
 NAGGACAATG AAGGCCAAAC AGCTCTACAT TATGCCTCTG CCTGTAAGTT TCTGGATATT 120  
 GTAGAGCTGC TGCTCCAGTC TGGTGCTGAC CCCACTCTCC GAGACCAGGA TGGCTGCCTG 180  
 CCAGAGGAGG TGACAGGCTG CAAAACAGTT TCTTTGGTGC TGCAGCGGCA CACAACCTGGC 240  
 AAGGCTTAAT CAAAAGACTG GAAAAGCTGCA GTCTGTAATA GCATAAGGCT TCCATTATGA 300  
 AAGAAACTA CAGAAATAAT ACTTCTTTTC CACCCGCTT TGGTATGTAT TGGCTTATAA 360  
 AATTN 365

SEQ ID NO:2316  
SEQUENCE LENGTH:308  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02677

SEQUENCE DESCRIPTION:

GATCCTGGAG CTGGCTGGCA ACGCGTGGCT NACAACAAGA AGACCAGGAT AATTCCTCCG 60  
CACCTGCAGC TCGCCATCCG CAACGACGAG GAGTTAAACA AGCTGCTGGG CAAAGTGACC 120  
ATCGCTTAGG GCGGCGTCCT GCCCAACATC CAGGCCGTGC TGCTGCCCAA GAAGACGGAG 180  
AGTCAGAAGA CGAAGAGCAA ATNACCCTGA CGCCGNCCTC AGGGAGCTGN CTNCGNCANA 240  
TAAGGCCCTT TTNATGGTCG TCCCGCAATG CTTTGAATG TGCTGGNTGT CATGGAGGGC 300  
CGGTGACN 308

SEQ ID NO:2317  
SEQUENCE LENGTH:306  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02678

SEQUENCE DESCRIPTION:

GATCTAGATA ACTCATGACA TTTTATTTGA CCAACATAGC ACATGATGAG ATATCAAGGT 60  
AATTAATAATA GCATGCTTGA AAAAAAATA CGTAATCTGT TTCACCTGTA ACTGTTTAAG 120  
CCAATAAACT TTTCAAAATT TATGTAATGT GGGGCTTTTA TGCTAGCACTT TACGTTTTCA 180  
TGCTGCTTAT TGTTTTATTC TACTGAAAAA AATGANNTTC AAGATTCTCA ACTTTNTTAA 240  
TTTCAAAAAT NGTTTATGGT TTTGACTATA GGAATACAAA ANTCCTATT TNGGGNGAAT 300  
AAGAAA 306

SEQ ID NO:2318  
SEQUENCE LENGTH:305  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02679

SEQUENCE DESCRIPTION:

GATCCCCTGG CTCCCCAGCA CACATTCCTT TGAAATAAGG TTTCAATATA CATCTACATA 60  
CTATATATAT ATTTGGCAAC TTGTATTTGT GTGTATGTAT ATATATATAT GTTTATGTAT 120  
ATATGTGATT CTGATAAAAT AGACATTGCT ATTCTGTTTT TTATATGTAA AAACAAAACA 180  
AGAAAAAATA GAGAATTCTA CATACTAAAT CTCTCTCCTT TTTTAATTTT AATATTTGTN 240  
ATCATTTATT TATTGGTGCT ACTGTTTATC CGTAATAATT GTGGGGAAAA GATATTAACA 300  
TCAAA 305

SEQ ID NO:2319  
SEQUENCE LENGTH:303  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS02680

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCGAAATC ACTATAATTT TAACCCTNGT GATTGGAATG AATATGGTTT GTGCTGGAAG 60  
CTCCGAGGTG GAAGAGACTC GTGCAATGGA GATTCTGGAA GCCCTTTGTT GTGCGAGGGT 120  
GTTTTCCGAG GGGTCACTTC CTTTGGCCTT GAAAATAAAT GCGGAGACCC TCGTGGGCCT 180  
GGTGTCTATA TTCTTCTCTC AAAGAAACAC CTCAACTGGA TAATTATGAC TATCAAGGGA 240  
GCAGTTTAAA TAACCGTTTC CTNTCATTTA CTGTGGCTTC TTAATCTTTT CACAAATAAA 300  
ATN 303

SEQ ID NO:2320  
SEQUENCE LENGTH:302  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02681

SEQUENCE DESCRIPTION:  
GATCCCTGCT GAATCCACAG GCCAAAATAG TCAATGTAAC TGCAAATCTA ATTTTCATCCT 60  
CCTTTCCTGA GGCCAACTCA GGAAATNAAA GGACGATTCT AATTTCCTACT GCGGTTACTT 120  
TTGTGGATGT GTCTGCACCT GCAGAGGCAG GCTTCANAGC TCCACCAGCC ATCAATGCCA 180  
GGCTGCCCTT TAACCTCTTC TTCCCGTTTG TTTGACAATG CTCAGATGCA TCAGTTCCTT 240  
AATATACACG TGAAATTTGA AAACGTGTACA TTCGGTGAGA TTAAATTTTA TATACAACCTA 300  
AA 302

SEQ ID NO:2321  
SEQUENCE LENGTH:301  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02682

SEQUENCE DESCRIPTION:  
GATCCAATTA AAAAAAATTA AAACCAATTT AAAAAAAAAA AGANCACAGG AGATTCCAGT 60  
CTACTTGAGT TAGCATAATA CAGAAGTCCC CTCTACTTNA ACTTTTACAA AAAAGTAACC 120  
TGANCTAATC TGATGTNAAC CAATGTATTN ATTTCTGTGG TTCTGTTTCC TTGTNCCAAT 180  
TTGACAAAAC CCACTGTTCT TGTATTGTAT TGCCCAGGGG GAGCTATCAC TGTACTTGTA 240  
GAGTGGTGCT GCTTTAATTC ATAAATCACA ANTAAAAGCC AATTAGCTCT ATAACCTANAA 300  
A 301

SEQ ID NO:2322  
SEQUENCE LENGTH:345  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02684

SEQUENCE DESCRIPTION:  
GATCAAGCGG AAAGAGTTTA AGTGTCTAAC AAACCTAAAG CTACTGTAGT ACCTAAAAAG 60  
TCAGTGTGTG ACATAGCATA AAAACTCTGC AGAGAAGTAT TCCAATAAG GAAATAGCAT 120  
TGAAATGTTA AATACAATTN CTGAAAGTAA TGTTTTTTTN CTATCATCTG GTATACCATT 180  
GCTTTATTTT NATAAATNAT TTCCTCATTTG CCATTGGAAT AGATATCTCA GATTGTGTAG 240  
ATATGCTATT TAAATAATTT ANCAGGAAAT ACTGCCTGTA GAGTTAGTAT TTCTATTTNN 300  
ATATAANGTT TGCACACTGA ATTGAAGAAT TGTGGGTTTT TTCCN 345

SEQ ID NO:2323

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02685

SEQUENCE DESCRIPTION:

GATCTTTTCT AATATGGTAT TACAATGAAA AGAATAAAGA GAAGATTGTA ATTTNCAGTT 60  
 TCATTTTCAA AAACATATTTA CCAAAACAAA TGGAGAAGAA ACATCCAAAA GCACATTCA 120  
 TTTCTCCAAA CTGTGTGTTT TAAATTATAG TTATAAATNG TAAGGTAATT TTAAATTGTC 180  
 CCTCGTATTA TTNCTCCACG CCTGTTTTAG TNTNNGGTCT CCTAAGCTTT TCTCTCATAG 240  
 CGTAGACCTA GGGGAAGGGAT GGGGAAGATTG CCCAGTCCCC GATGGCTGCG CACACAGGN 299

SEQ ID NO:2324

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02686

SEQUENCE DESCRIPTION:

GATCCCTCTG TACAGGCTGG ATGGAAGGGG CCCTCCACAC TTCCTGGGAG GTCAGAGACA 60  
 AACTGTTTCA GAGAGTCAGA TGGACTTCCC AAGACTTGTT GAGAGATGTG ACATGGTTCT 120  
 TGGATTTTCT CTGTAGCAGC CTCCTGGACT TCCTGAGGAC TCGACATTGT CCACAGATGT 180  
 ACTGGCCATT ACATGAAACA AGAAACCAAG CATCTTTGCT GTTGTTAATT ATTATATGTG 240  
 CCATTGTTAC AGGAGATTAT AGGCTAGTCT GTAATAAATT ATCTTATAGC AGCCAAA 297

SEQ ID NO:2325

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02687

SEQUENCE DESCRIPTION:

GATCAGCAGC CGAGAAAAGT ACATCAACAA TCAGCTTGAG AATTTGGTTC AAGAATATCG 60  
 TGCAGCTCAA GCCCAGCTGA GTGAGGCAAA GNAGCGATAC CAGCAGGGAA ATGGAGNGT 120  
 GACGGAAAGA ACCAGACTCC TCTCTGAGGT TNNGGAAGAA TTAGAAAAGG TAAACAAGA 180  
 AATGGAAGAA AAGGGCAGCA GCATGACTGA TGGTGCTCCT TTGGTGAAGA TTAANCNNNG 240  
 CTTNNCANAA CTGAAGCAAG AANCTGTAGN GATGGACATT AGANTTGGCA TTGTGGN 297

SEQ ID NO:2326

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02688

SEQUENCE DESCRIPTION:

GATCCNACTT TAGAAGCCTA CTTTNTAACC AAGGAGCTCA ATTTTTTTTT TAAAGCTTTA 60  
 CTAATCTACC ANAGCATTGT AGATATTTTT TTTTAACATC TATTGTTTAA AATAGATNAT 120

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TATAACGGGG CAGAGAACTT TTTTTCTCT GCAAGAATGT TACATATTGT ATAGATAAAAT 180  
NAGTGNCATT TCATACCATG TATATATAGA GATGTNCTAT AAGTGTGAGA AAGTATATNC 240  
TTAATAGAT ACTGTAATTA TAAGATATTT TAAATTAAAT ATTTTTTGT AAATAAA 297

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SEQ ID NO:2327  
SEQUENCE LENGTH:324  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS02689

SEQUENCE DESCRIPTION:

GATCCTATGT CTGTCTGTCC ACCACGAGAT GGGAGGAGGA GAAAAAGCGG TACGATGCCT 60  
TCCTGACCTC ACCGGCCTCC CCAAGGGTGC CGGCACTCTG GGTGGACTCA CGGCTGCTGG 120  
GCCCCACGTC AAAGGTCAAG TAAGACGTAG GTCAAGTCCT ACGTCGGGGC CCAGACATCC 180  
TGGGGTCCTG GTCTGTNAGA CAGGCTGCCC TAGAGCCCCA CCCAGTCCGG GGGGGNTGGN 240  
GAGCAGTTCC AAGACCACCN CACCNCTTTT TGTAATNTT GTTCATTNTA ANTCAAATAC 300  
AGCGTNTTTT TCANTTCTGG GAAA 324

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SEQ ID NO:2328  
SEQUENCE LENGTH:291  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS02690

SEQUENCE DESCRIPTION:

GATCTGCAGG GGTCTGGGAG TCAGGCCCGG CCTATTGCTT GGGTCTCTCT CTATTTATAT 60  
ATCTAAGTTC ACAGTGTTTC TTATCCCCC TAAGCTTCTA GAGGCTCATG GCCCTGTAGT 120  
TAGGCCTGGC TCATTCTGCA CCTTCCAGG GAGGTGGAAG GACCCTGTGC CCTCCTTCCC 180  
AATCTTCTTT TTCAGGCTCG CCAAGGCCTA GGACCTATGT TGTAATTTA CTTTTATTT 240  
CTAAAGTTGT AGTGAAGCTC TCACCCATAA TAAAGGTTGT GAATGTTCAA A 291

30

SEQ ID NO:2329  
SEQUENCE LENGTH:290  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02691

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SEQUENCE DESCRIPTION:

GATCTAGAAT CTCTTTATGT TCTCCAGAGG AAGGTGGAAG AAACCATGGG CAGGAGTAGG 60  
AATTGAGTGA TAAACAATTG GGCTAATGAA GAAACTTCT CTTATTGTTT AGTTCATCCA 120  
GATTATAACT TCAATGGGAC ACTTTAGACC ATTAGACAAT TGACACTGGA TTAAACAAAT 180  
TCACATAATG CCAAATACAC AATGTATTTA TAGCAACGTA TANTTTGCAA AGATGGNCTT 240  
TANAAGATGC TGTGTAGCTA ANCTGAANTA ATTCATTAC TTATTATTN 290

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SEQ ID NO:2330  
SEQUENCE LENGTH:231  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS02692

SEQUENCE DESCRIPTION:

GATCACTCCG CCTTNTCCTG GGCTCCCGTA GCACACTATA ACATCTGCTG AAGTGTGCT 60  
 GTTGCACCAT ACTTTCTTGT ACATTGTGT CTCCCTTCCC AACTAGACTG TAAGTGCCTT 120  
 GCGGTCAGGG ACTGAATCTT GCCCGTTTAT GTATGCTCCA TGNNGGNCC ATCATCCTGC 180  
 TTGGNGCAAG TAGGCAGGNG CTCAATAAAT GTTTGTGCA TGNNGGNAA A 231

SEQ ID NO:2331

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02693

SEQUENCE DESCRIPTION:

GATCGCCTAC AAGCCAGCCC CTGGCACCTG CTGCTACATC ATGAAGATAG CTGCAGAGAG 60  
 CATCCCCAGT CTTGAGGCTC TCAATAGAAA AGNCCACAAC TTCCAGATNG AATGCTCTCT 120  
 GCAGGCCAAG CCCGCAGTGC CTACGTCTAA GCTGGGCCAG GCAGAGGGGC GAGATGCAGG 180  
 CTCAGACCCC TCCGGAGGGG ACCCGNCTT CCTGGGCATG GCCGTGAACA CCCTGTNTGG 240  
 CGAGGTGCCG CTCTACTACA TCTAGGACGN CTCCGGGTCA TGTGN 285

SEQ ID NO:2332

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02694

SEQUENCE DESCRIPTION:

GATCTAGAGG TTCCANTGCT ATNCTCTCTT CTTGTCTGAG AGCCAGGACC CTGGGGGAAA 60  
 TAACGGGCAA AAAAGCACTT TNAAGACAGA TATAGTGGGA ATTNATAAAC GACTTGATAG 120  
 AAACAGAAAT GAACTGTTTT ATTNATNCT CTGAGGACTC TGCTCATCAC CCANTAGTAC 180  
 CATTTCTTTT CTCAGAATGG ATTCTTTCCC CTATCTATCT AATCATTAGA GATGTAGCTA 240  
 NGAAATTACA TGTATGCATA TGTNTAATAT GTATATGTNT ATGTN 285

SEQ ID NO:2333

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02695

SEQUENCE DESCRIPTION:

GATCTTAAAG CTTTGAGCAC CTGCCATTTT GCCTTGCATC GTTCCCTCG TCATGCATTT 60  
 CCACATATCC ACAAACACAG AACGACTTTA GACAAGCACA TGTTACACCT GTGTGCCAC 120  
 AAGCAGTCAT TCTTGACGGC TCCAGTTTTT ATTTGACACT TGAGTTTAGT TTTCTCTTTT 180  
 ATAAACCCAG TGAATCCTG CACTGGCATT TGGATGTGTG TTAATGCTAT TTGTTTGTG 240  
 TTAAGTAA AACCTTTCTC AGTTTGAAC TGTATTCTCT AAA 283

SEQ ID NO:2334

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02696

SEQUENCE DESCRIPTION:

GATCTATTAA AAAGGTTAAG AGGCCAGGTT ACCCACCANT CCTTGCACTG TNCTGACACT 60  
 TTCCCAGGA GGAACAAG TACAAAGGTT ACGGTGGAGG CATAAGTAGA AGAGATTGTN 120  
 AAGAAGGGTA ATTCATGTNT CTTTGCTCTT NCTGCTTAT GCCTCANTTT GGTTTAAAAA 180  
 CTTCTNTACT GGCAAATGGT GGTATTCAGT GTGGGATAGT GTCATAACTA ATTTGACAAT 240  
 TTATTAATGA TAAATAACA ATAAATGTCT AGCTTTTACA AAA 283

SEQ ID NO:2335

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02697

SEQUENCE DESCRIPTION:

GATCACAAAA AAATCAGTCT TTAAGCATTT GCTTGGAAG GTTTCTTAAN ATNAGGTTTA 60  
 TAATACAACC ATCTGTAATG TATCTNTCGN TTGANCTTGT GGGCCATACA ATTCATTAAAC 120  
 TAGATGNATA CATTGTGGAC AGCATCCTCA CTACCCCTCT CTACTCACTC ACAAAGAACC 180  
 ATGATACACT GGAATGTTTT TNTNTGGAAT CCTCTTTCTA CTCTTGATT AAAATTTTNC 240  
 CCCACTTCAT GATTATATNC AAAATAACA ACTACATCAT AAA 283

SEQ ID NO:2336

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02698

SEQUENCE DESCRIPTION:

GATCAGCTTG CAGAGTCTTG CTTTtaggtt AGATACAAAC AAAGTAAATC ATAGTTGGTG 60  
 TAAATCCAGC AAAAAACAGC TGGCTTTGGA ATGGAGAACA CTACAATTCA AATTTGAAGT 120  
 ATATTGAGAA GAAACTTTG GAATTAGCTT TACATTTGTT TGTAATCTA AACAAATNTG 180  
 CAAAATTGGT CAAAATGTAA GTNTATNGCA TTTTAAAGA TTANTGGTTC CTTTATGTG 240  
 CTGATTTCTT TGTATTCTGT TCTCTGCATT CATCATTCAG GN 282

SEQ ID NO:2337

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02699

SEQUENCE DESCRIPTION:

GATCTGTACC ACACCTTCCG GCCAGCTGTC CTCCTGCTGA TGTCCTCAG TGTCTACAAG 60  
 GCCTTTGTTA TGGAGACCTT CGTCCACCTC TGCTCGCTGG GCAGTTGGGC AGCTCTACTG 120  
 GCCCAGCAG TGGTAACGGG GCTGCTGGCC CTCAGCACTT TGGCCCTGTA TGTCGCCGTT 180  
 GTCAATGTGC ACTCCTAGGC TTGGTGTCTC AGACATTGTA TGTACCTTTT CCCTGNCTCG 240  
 NTCCAGGTTT TTAGTGAAGT AAACAGGTAT TTTGGAAGT TAAA 284



SEQ ID NO:2338

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02700

SEQUENCE DESCRIPTION:

GATCAACGAC AGCCTCCAGT TTCCAATTNG TGAGAGAACA AAGGAACCGG GGCATGCTCA 60  
 NCTATGGCTG CAAGCCNTTC AAGTGAAGCT GGGCACTTAC CCCCTTNATT CCATTCTCCT 120  
 CAGGATAACA GATTAATAAT CCAGAAAGTGT GCACCTGTNG TNTATTCAGG AGATTNTCGT 180  
 TNTGCATAAA GAGACCACTT GAGGCCCTGT AAGCAAAGAC TAATTNGGTC TNAGTCAAAA 240  
 TCTTGGGAAT CTGATNAACT AACACACTCA AATGAAACTN 280

SEQ ID NO:2339

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02701

SEQUENCE DESCRIPTION:

GATCTGGAGC AGGAAGGCCT CGAGGCACAC AGGGGCTGCT GGCCGGCGAG TGGGCCCCAC 60  
 CCCTCTGGGA GCTGGGCAGC CTCTTCCAGG CCTTCGTGAA GAGGGAGAGC CAGGCTTATG 120  
 CGTAANTTCA TAGCTTCTNC TGGCCTGGGG TGGACCCAGG ACCCCTGGGG CCTGGGTGCC 180  
 CTGAGTGGTG GTAAAGTGGA GCAATCCCTT NACGCTCCTT GNCCATGTTC TNAGCGGNCA 240  
 GNTTGGNTTT NNCCTTNAAT AAATNTGCTT TATTNCTCT TCAAA 285

SEQ ID NO:2340

SEQUENCE LENGTH:320

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02702

SEQUENCE DESCRIPTION:

GATCGTAAAC TTGTTGATAA AGAAGATATC GACACTAGCA GCAAAGNAGG CTGTGTCCAA 60  
 CAGGCTACTG GCTGGAGGAA AGGGACAGGC CTGGNATATG GCCATCCTGG ATTGGCTTCA 120  
 TCAGAGGAGG CTGAAGGCCG GATGAGGGGC CCCAGTGTTG GAGCCTCAGG AAGAACCAGC 180  
 AAAAGACAGT CCAACGAGAC TTATCGAGAT GCTGTTTCGAA GAGTCATGTT TNCTCGATAT 240  
 AAAGAACTCG ATTAAGNAAG GNGNCAAGTT CCATGGGATA CAACCTACCT CTTGTTTTGT 300  
 TTGTCTCTCC TTTTCTTTN 320

SEQ ID NO:2341

SEQUENCE LENGTH:519

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02703

SEQUENCE DESCRIPTION:

GATCTGAAAG GAGCAAGGAA CAGCAAGGAA TTATTTTCCA GAATGACACC CGCAGCAGAA 60

# EP 0 679 716 A1

5 TGTGGAGTG GAAATGATGG CTGGCTATGA AGAGGAGGTC AACGTGTGTG GTCTCCTCAG 120  
TCTCTGTCAG AGGGGTGGGG AGGTGGGAAA CAGGAATCCT CTGCAAAGCC CAATCTGCAG 180  
AGTCGAGACC CCTGGTGCTC TCTGCCCCGC TGCCTGGCAC TGGTCCTTTG CAGCCAGCCA 240  
CCAACGGCCC CCTTGCCCTT NCAGAGGCAG AAGCCTNCGT CTNAACCTGC ACCTCTGACC 300  
GTTTNAGCAC CNTTGGGTTN TTACCANGTC CTANAACTCT GANATTTNTT NGTTCTAAAA 360  
GGGGTTTCTA TTTCAACTTG NTGAGTTTGT NTTTTGGGNC CTTCCAATTT GGGNTACCTT 420  
GNTATNTTTN ATGGTTTTAT AAATCCTTNA CTCTTGGNAN GTTTTAATTN TTTACAAAAT 480  
10 CAGGGATAAC TTTNGTTTNA ANACTGGTTT GAAGGAATN 519

SEQ ID NO:2342

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS02704

SEQUENCE DESCRIPTION:

20 GATCCCAACT AATTTTACCG AACCTAAAAC CCACAAAGAG GTTGTTTGTG TTATTGTTCA 60  
ATCTTCAGTT GTAAGAGTAA TTCTCTATTT TNATATTGAA ACATAATTAC TTGATAGCTC 120  
AGGGTCTACA TTTCAATCAA CTTTTTACAC CAAATTCTGC AGAGTGGTCA AAATGGAATA 180  
TTGGGGGCTG TTGTAAACAG AGGCTTAATT TTATTAGAAG TAGCCAGTTA TTTATTAAAG 240  
CATGATGTTA ATAAATAGG CATATTCTGA AA 272

25 SEQ ID NO:2343

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS02705

SEQUENCE DESCRIPTION:

35 GATCTGACAT GATTCCCTCC TGTCTGAAC TGTGGGGTGT GCACATCTCT ACTTGAGTCA 60  
GGTTNAGTA GAGGCTTAGA GACAGTTAGG TGAGAACAAC CAAAATCTTA TCATGGTCTC 120  
AGTCANNATC ATTAGGGGGA ACTCTAGCCA AATNGTTTAA CTTCTGCCTG TGGAACTGGG 180  
GATTGGGTGG GCAGGAAAAG GTGATATCCA TTCTTTCTGA TAACTAGATG GTGCTGAGAA 240  
GCTTTTGAAT AAAAAGTTTG CTAAATGAGA AA 272

40 SEQ ID NO:2344

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02706

SEQUENCE DESCRIPTION:

45 GATCTTTCCC AGGCCGCACC ATTTCTNTCA CTCACATGGA CCCAAGATAN AAGAATGGCC 60  
AAACCCTCAC AACCCTGAT GTTTGAAGAG TTCCAAGTTG AAGGGAAACA AAGAAGTGT 120  
TGATGGTGCC AGAGAGGGGC TGCTCTCCAG AAAGCTAAAA TTTAATTTCT TTTTCTCT 180  
GAGTTCTGTA CTTCAACCAG CCTACAAGCT GGCCTNGCT AACAAATCAG AAATATGACA 240  
ATTTAATGAT TAAAGACTGT GATTGCCACC AAA 273

SEQ ID NO:2345

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02707

SEQUENCE DESCRIPTION:

GATCCATGAA GCTGCCCTGC CCACGCCTCC CCTCCCTGTA GCAACACCTC TGGGTGTTTG 60  
GAGTTTAGCT TTTGTGGGTT TGCTCTCCCT ATCCCATCTC CTGTACTACA CAGTTCATGG 120  
CAGGGTGGGG AGNNGTGGGG TTGGTTCGGG TGGGTGAGGG TCTTTTCCT CTGTGTGCGA 180  
TGTTGTTATC TGACAGNTCT CCGTCCCTAC TGGCCTTTCT CCTCGTCTTC ATATTTGTAC 240  
GGTACAAGCA ATAAAGACAC TCATTTCAGA CCAGAAA 277

SEQ ID NO:2346

SEQUENCE LENGTH:431

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02708

SEQUENCE DESCRIPTION:

GATCTTNCTA GGAGGGAGAC ACTGGCCCCT CAAATCGTCC AGCGACCTTC CTCATCCACC 60  
CCATCCNTCC CCANTTCATT GCACTTTNAT TAGCAGCGGA ACAAGGAGTC AGACATTTNA 120  
AGATGGTGGC AGTAGAGGCT ATGGACAGGG CATGCCACGT GGGCTCATAT GGGGCTGGGA 180  
GTAGTTGTTT TTCCTGGCAC TAACGTTGAG CCCCTGGAGG CACTGAAGTG CTTAGTGTAC 240  
TTGGAGTATT GGGGTCTGAC CCCAAACACC TTCCAGCTCC TGTAACATAC TGGCCTGGAC 300  
TGTTTTNTCT CGGCTCCCCA TGTNGTCCTG GTNNCGGTTT TNTCCACCTA NGACTGTAAA 360  
CCTCTTCGAG GGCAAGGGAC CACACCCTGT AACTGTTCTG TGNCTTTTAA CAGGTTCTCN 420  
CCATTAATGC N 431

SEQ ID NO:2347

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02709

SEQUENCE DESCRIPTION:

GATCTTTTGT GTCTGGTTCC TTTCACGTTG AACGCTATTT TTAAGGTTCTG TGCCTGTTGT 60  
AGACCACAGT CACACACTGC TGTAGTCTTA CCCCATCCTC ATCCCAGCT GCCTCCTCCT 120  
ACTGTTTCCC TCTATCANNN NGCCTCCTTG GCGCAGGTTT CCTGAGCTGT GGGATTCTGC 180  
ACTGGTGCTT TGGATTCCCT GATATGTTCC TTCAAATCCA CTGAGNATTA AATAAACATC 240  
GNTAAAAGAA TGACCTTCCC AAGGNAAA 268

SEQ ID NO:2348

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02710

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCAGAAAC CAGTCTCCTT CCCCCTAGTC TGGACTGGGT ATCCCCTCTT AAATNTTTC 60  
 AAAGCAACAC AAATTTAATT CCGTCACAGA ACTTGCCACT CTGTGCTGTG TCCTCTGTTT 120  
 CTTTGCCATC TTCCTCAATN AGCTGGAAGC CCATTGGCAG CAGGGACTGT TTCTTGTTCA 180  
 CAGCTGCACC TCAGTGCTAA GCATAGTGCC TGGTAGGTAA TAGACTCCTT AAGTATTTGT 240  
 TGAATTAATA AAGGATGNNT TTTTAAAA 268

SEQ ID NO:2349  
 SEQUENCE LENGTH:268  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02711

SEQUENCE DESCRIPTION:  
 GATCAGAAGC CATTNNATTT GGTAGGTGTG TCAGAAGGGA GAATGATGGN AGACGAACTG 60  
 CTGGAAGAGG TCAGAAGATA GCCATGCTAA AATGCAATTA TATCCTCATG TTTATCCCAA 120  
 ACTAATCTTG GACTTTTCCA CTCATTAGCT TTGTNTGCC CTGTTTCCC TTGAAGGTTT 180  
 AAGTTCAACC ATATTCTGTC AACTGTTTCTG TTTTCTGGA ATCTTGTTAT TCTGGTTTCAT 240  
 TATAACAAAC TGTTCGCTTA AATCCAAA 268

SEQ ID NO:2350  
 SEQUENCE LENGTH:398  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02712

SEQUENCE DESCRIPTION:  
 GATCCGAGAA CGCTCTAAGC CTGTCCACGA GCTCAATAGG GAAGCCTGTA ATGACTACAG 60  
 ACTTTGCGAA CGCTACGCCA TGGTTTATGG ATACAATNCT GCCTATAATC GCTACTTCAG 120  
 GAAGCGCCGA GGGGCCAAAT NAGACTGAGG GAAGAAAAAA AATCTCTTTT TTTCTGGAGG 180  
 CTGGCACCTG ATTTTGTATC CCCCTGTAGC AGCATTACTG AAATACATAG GCTTATATAC 240  
 AATGCTTCTT TCCTGTATAT TCTCTGTCT GGCTGCACCC CTTTTTCCNG NCCCCAGATT 300  
 GNTAAGTAAT NGAAAGTGCA CTGCAGTGAG GGTCAAAGGN GAGGCAACAT ATNTNTNTT 360  
 TCCATAATAA AACTTTCTTG GGGGNNATAC TTTTCAAA 398

SEQ ID NO:2351  
 SEQUENCE LENGTH:381  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02713

SEQUENCE DESCRIPTION:  
 GATCTGCAAG CATTGCTCT TGTTCACACA TCACCTCTGG GATATTTTCTG CTGTTGTTTC 60  
 CAAATGGCAA ATCATCAACT AAANGCACTT GTTCAAGTT TTGTTCTGCA CTCCCACGAC 120  
 TGAAGTTGTA GATTGAGCTG AATAACCATG GGAAGTGANC AAGCAAAGAC ACTCGATTGG 180  
 AGTCAGTTGA ATATTTGTAC CCTCAGTGGA GCCCTTCTGG TCTTTTCTTC CACTTCTGCA 240  
 GAATTTCTC TAGCAAATAC TTCTTTCTCC TTGCTTGCC CTACCATGAT ATTTGAATAA 300  
 GAGATGGCCA GAGGATAACA CTGTCTCTT AAAAATAAG CTAATAAGGA CCTAGGAACC 360  
 TTCAATTTGA GCAGTTGGTT N 381

SEQ ID NO:2352

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02714

SEQUENCE DESCRIPTION:

GATCTGCCCC CCTTGGCCTC TCAAAGTGTT GGGATTGCAG GCGTGACACG TGCTCCTGGC 60  
 TTGAATTTTC TTATAATCCC ATGAAACCAT CATCAGAGTC ACAATAATNA ATTTATCTAA 120  
 TCTATCACCT TTGTATTAC CTGGAGCCTT TATAAAGTTT TTNTCTATGC AGACAACCAT 180  
 TGATTTACTC TGCTGTATAA TACTTTCCAT TTTCTAGAAT TTTCTGACTG ATGTAATAAA 240  
 GTGTTTCCTC TTATAATCCC TGAAG 265

SEQ ID NO:2353

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02715

SEQUENCE DESCRIPTION:

GATCGGGGGC TTGAACCCAG GTGGTCAGGC TCTGGAGCCC ACAATTGTNT TACCCACTAT 60  
 GCCCTCTCT AGTCATGGTC CCCAAGAGGG GCTTGGAGAC CCACTTAGCA GGTGAAAGCA 120  
 ATGGCAGCCT TCCTTATTG ATTATGCACC TAAGAATAAA TGGTATTTGG GCATGTATTC 180  
 CCAATATGTG TATATTTATT TATAAATATA TACAGATACT ATNATCTGTA TGTNAGTAAT 240  
 AAAGCTTAA TTATTCCATT TAAA 265

SEQ ID NO:2354

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02716

SEQUENCE DESCRIPTION:

GATCGGCGGA CGCCCATCAC CGTGGTGAAG CAAGGCTTTG AGCCTCCCTC CTTTGTGGGC 60  
 TGGTTCCTTG GCTGGGATGA TGATTACTGG TCTGTGGACC CTTGGACAG GGCCATGGCT 120  
 GAGCTGGCTG CCTGAGGAGG GGCAGGGCCC ACCCATGTCA CCGGTCAGTG CCTTTTGGA 180  
 CTGTCCTTCC CTCAAAGAGG CCTTAGAGCG AGCAGAGCAG CTCTGCTATG AGTGTGTGTG 240  
 TGTGTGTGTG TTGTTTCTTT TTTTNTTTN NNNAGTNTCC AAAANAGCC CTNAAAAAAT 300  
 TCAGGGNCCT TGAAAATTN TNTAAATGC CAGNNTTTGG GGAAATNAAA CCCANTAAAA 360  
 ACNTTTTGAG GGGTGNAAG 379

SEQ ID NO:2355

SEQUENCE LENGTH:261

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02717

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCACAAAA CAATTCTAAA ACCTAACTGT TTTTACCATT GAAATTTAAA TTGTGATAAT 60  
 AGGTTTTTAAA TGTCTAGAAT GCAACTGATA GGCTTTTCTT GAACTGTTAG TTTTTTTGAA 120  
 GTAGTTTTTT CATGTTTANN NNGTATTTGT AAAAAAACAA AAAGCAAAAA AATTCCCAAA 180  
 ACCCAGATAA CAACCAGAGC AAAACTGTTG TGCCTTCTAT TTATCTTTGA TTTCAGTCTT 240  
 GGCAATTGTT TAAAAA AAAA N 261

SEQ ID NO:2356

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02718

SEQUENCE DESCRIPTION:

GATCATTGGA GAGAGAATTG CACAGAAAAGT CCTGAAGTTT AAAACACTTT ATGACCAGCT 60  
 TTGGCTCGGG AGAGTGGGGC TGCTTGTAAGA ACTGGAAGTG AATAACTTTT TCAAGCAATA 120  
 TCAGTGAGTG GGTCCCATCG ACAGGGTTCC AGGACCTGGA ACACTTTAAC AGAAGGAAAT 180  
 GCCGAAGCAG CTGACACAGT NGCTTGACAG ACTTCCAAGN NGGCTGATTC TGGCTTCAAG 240  
 ATGGAGCCTT GGAGTTGGN 259

SEQ ID NO:2357

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02719

SEQUENCE DESCRIPTION:

GATCTGGGAG TACACCAGGC AGCAGCTGCT CTCGNACGGA GATACCAAGC CATGATGTGC 60  
 CNNNNTTAGT GAACTGCTGC TGCTGTTCAG ACTTTTTTAA AAAAAACTAT TTGGACTAAA 120  
 GAAACAGATT CTGAAATTTA TTGTGATAAT TTGTATTTCT TTTTCTTGC AATTTAATGC 180  
 CAAAAGTTTG CCATGTGCCT TAAACATATT ACTATATATT TNCCCCTTTA ATAAACACTT 240  
 TTNGTTAAAT TGTATTCTTC CTTTAATAAA ATATTTTAAAG CAATTGTGGA AATAAA 296

SEQ ID NO:2358

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02721

SEQUENCE DESCRIPTION:

GATCAGAATA CATGATGGAT GAAATTCTTT ACATGTTTTA GCAGAATNAA TTTGTTTAAAT 60  
 ATAATAAAGT TTGCTACTTA TCTGTATGTA GGTGCTAAA AANGATTTTC TTAAGTCTAGA 120  
 TTTTAAGCCA AATAACCATT TAACACTAGT ATTTGTAAA TGGGTTATTT TNCTGTATTT 180  
 GTATGTTTCA CTATAATAAG GGAATTAAGG ATAATGTGCA TTGAGAATAT TTTGAAAANT 240  
 AATTGACTCA AATN 254

SEQ ID NO:2359

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02722

SEQUENCE DESCRIPTION:

5 GATCAGTTAT AAGTAGCAGG CCAAGTCAGG CCCTTATTTT CAAGAACTG AGGAATTTTC 60  
 TTTGTGTAGC TTTGCTCTTT GGTAGAAAAG GCTAGGTACA CAGCTCTAGA CACTGCCACA 120  
 CAGGGTCTGC AAGGTCTTTG GTTCAGCTAA GCTAGGAATG AAATCCTGCT TCAGTGTATG 180  
 GNAATAAATG TATCATAGNA ATGTAACCTT TTGTAAGNCA AAGGTTTTC TCTTCTATTT 240  
 10 TGTAACCTCA AAN 253

SEQ ID NO:2360

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS02723

SEQUENCE DESCRIPTION:

20 GATCAATCCC AAGAATCCAT CAGCAACCTC AGACCAACCC AAGAAGATAA TTAAATCTA 60  
 TACTGCTTAT TGGTCAATAT ATTTGGTTCT AGTATTAATA AAGAAAAATG TTATTAAAAAT 120  
 AGCATACATA GTAGTAAAAT AAANTACANA AAGTGTGTTG ATTTATAGCT GTTTGAGATG 180  
 AAAAAAGTGN AGCAAAGCCT GTTAAATCAT TGGAAGACTT GGANANTTAT TTAAATAAN 240  
 CAATTACATG TAN 253

25 SEQ ID NO:2361

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02724

30 SEQUENCE DESCRIPTION:

GATCTGCATA AACAGGGTTC CTGACCTCAC CGAAAAGACT AATGTGCCTT AGAACAAGCA 60  
 TTTGCTGTGT TTTGTTAGCA CCTGGTTCCA GGACAGACCC TCAGCTTCCC AAGAGGATAC 120  
 TGCTGCCAAG AAGTTGCTCT GAAGTCAGTT TCTATCGTTC TGCTCTTTGA TTCAAAGCAC 180  
 35 TGTTTCTNTC ACTGGGCCTC CAACCATGTT CCCTTCTTCT TAGCACCACA AATAATCAAA 240  
 ACCCNACATA AA 252

SEQ ID NO:2362

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02725

SEQUENCE DESCRIPTION:

45 GATCTTCTCA GCCAGGAGAA GAGGGTGGTG TTTTCACGCG GGCAACTGCT CGCCGGCCTA 60  
 CATGGGGTTA ATTCAGTCT GCTGCGAGCA CGACTCCGCC CTTGGCACTG GCCTCCAGCA 120  
 AGCCCTGTTC TCTTTGGGGT ACAGGGGAAC GGGATGGTTT AGACTTTCCT GCTCAGTGTG 180  
 TAAAAAATGT AGCTAAAGCC ACTATTTTGT CTCTCCTTAA GCTGTTCAAT AAACCGGTTT 240  
 50 CTCATTTTAA A 251

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SEQ ID NO:2363

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02727

SEQUENCE DESCRIPTION:

GATCTGGAAC ACTCCCCTGA CCCCTTCACA CCTGGCCCTC CCTGGGCTTA AAGCTCCTGA 60  
TATTCCTCAT CCCCTTCCTT GTTTTCCAGA ATCGGTCGAG GTGGACGGTT TGGCCGTAAA 120  
GGTGTGGCTA TTAACATGGT GACAGAAGAA GACAAGAGGA CTCTCGAGA CATTGAGACC 180  
TTCTACAACA CCTCCATTGA GGAAATGCCC CTCAATGTTG CTGACCTCAT CTGAGGGGCT 240  
GTNCTGCCAC CNAGCCNCAG NCAGGGCTCA ATCTCTGGGG GGCTGAGGGA GCAGCAGGGA 300  
GGGGTGGN 308

SEQ ID NO:2364

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02728

SEQUENCE DESCRIPTION:

GATCGTAGAT TTTTAAACAAT CTGTATCTTT AACAACTCTG GGTGCNAGTG TNAGAGTGTG 60  
AGCAGGGCTT GCTCCTGCCA ACCACAATTC AATGAATCCC CGACCCCCCT ACCCCATGCT 120  
GTAATTGTGG TTCTCTTTT GTATTTTGCA TCTNACCCCG GGGGGCTGGG ACAGATTGGC 180  
AATGGGCCGT CCCCTCTCCC CTTGGTTCTG CACTGTTGCC AATAAAAAGC TCTTAAAAAC 240  
GCAAA 245

SEQ ID NO:2365

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02729

SEQUENCE DESCRIPTION:

GATCTAACCA ACTCAACTGA TAGAAAGCTG AATTGTTCCC AGTGGACAAG TGGTATTTGA 60  
TGTTTAGCAG GTTTTTTTGT TGTTATTTTT TTGGTAAACT CTGTGGTAAA ATCTAAAATA 120  
ATGTTAAAAC CCTAAAAGTA ACTATTGANT ATNCTGTAAT CTTAGACATG TATTTTTCAA 180  
GCTAACCCCT TGAAGAAATG TGTCAAGGT AGGAAAATAT AAAATTTTTT GGTATTTTGT 240  
AAATTTAAA 249

SEQ ID NO:2366

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02730

SEQUENCE DESCRIPTION:

GATCATGCAT TGTTGAGGTG GTCTGAATGT TCTGACATTA ACAGTTTCC ATGAAAACGT 60  
TTTATTGTGT TTTTAATTTA TTTATTAAGA TGGATTCTCA GATATTTATA TTTTAATTTN 120



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ATTTTTTCT ACCTTGAGGT CTTTGTGACAT GTGGAAAGTG AATTTGAATG AAAAATTTAA 180  
GCATTGTTTG CTTATTGTTT CAAGACATTG TCAATAAAAG CATTTAAGTT GAATGCGAAA 240

5 SEQ ID NO:2367  
SEQUENCE LENGTH:251  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02731  
10 SEQUENCE DESCRIPTION:  
GATCTATACT GTGTGGTCAT GAGTTGTGTA TAGTTCCATA ACACTGTATT TTNCTNCTGT 60  
CAGTACCCTT AGGATACACT NTAAACACC TTAAGGTCTG ATGTTATGGC AACAACTAC 120  
TTNTTCAAACT CTAATAGGA ACCATGTAAT TNCTCAAAAG TGATTGAACA GTTTGCCAC 180  
15 ACTTAGTTTG TTGGTCTTAT GTAAACATT GGCTCAAAAT AAAGNNCACA CTGATTTATT 240  
TNACTGNNA A 251

20 SEQ ID NO:2368  
SEQUENCE LENGTH:239  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02732  
SEQUENCE DESCRIPTION:  
25 GATCTGAAAA TTTATTTTAC CCAGCTTTCA CAATTAAGTC TGTATAAAAT GTGGTACCTT 60  
TTNGTACCTA TCCAGAGAAA CCTGTACATA TTCAATGTGA TCTAGATGTG ATTGGATAAT 120  
GGAGAAAAATN TATTTATAAT GATTTTNCAA TGGCATCAAT AACATTTAAA TGATTTTGAA 180  
GAAGTATTAT TTTACTACCC TATAAAATGA ATCGAAAATA ATAAAGTTCT TAACATAAA 239

30 SEQ ID NO:2369  
SEQUENCE LENGTH:239  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02733  
35 SEQUENCE DESCRIPTION:  
GATCAAAATTA TCTTCAGCAT GTATATCTGG GGAAAAAAGG TCCGAATTTT CACATTTATA 60  
TTTAAANTTC AATTTTTTAT ATTTAAANTT CAATTTTITA GCAACAGCTG AATAGCTTTG 120  
CGGAGGAGTT TAATAGTTAC ACATTCATGC TAATATACAT TNCCTTTAAA CATCCACAAA 180  
40 TTCTTAAAAA GATTGAATCA GTANATTTC TTTTCAAGTAA AAATGGAGTC TAATATATN 239

45 SEQ ID NO:2370  
SEQUENCE LENGTH:237  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02734  
SEQUENCE DESCRIPTION:  
50 GATCCACCCG CCTTGGCCTC CCAGAGTGCT GTGATTACAG CTGTGAGCCT CCGTGCCACG 60  
GCCAGTGTTT TCTCTTAAAT GTGTTTCAAT ATGGTGGACA TTTATTGAGC ACTTGTGTTG 120

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GGCGTTTCAA CAGGAGGCAC TGGTACGAAA AGTAGCTTGT TCTAGTTCAT ATATCATTTG 180  
CACTTTGCTT AACTTGTATA AGTACTTTTT ACTGTTTAAT AAATATTTTA TTAGAAA 237

5 SEQ ID NO:2371  
SEQUENCE LENGTH:236  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02735

10 SEQUENCE DESCRIPTION:  
GATCAAAAGA GCAAACAATA CTTTCTATGG CTTATCAGCA GGAGTGTTTA CCAAAGACAT 60  
TGATAAANCC ATAACAATCT CCTCTGCTCT GCAGGCAGGA ACANTNTGGG NGAATTGCTA 120  
TGCGGTGGTA AGTNCCCAGT GCCCCTTTGG TGGATTCAAG ATGTCTGGAA ATGGNAGAGA 180  
15 ACTGGGAGAG TACGGTTTCC ATGAATATAC AGNGGTCAA ACAGTCACAG TGAAAN 236

SEQ ID NO:2372  
SEQUENCE LENGTH:236  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS02736

SEQUENCE DESCRIPTION:  
GATCCNATTC CCGTTGCCTC AAAGCACCAG CTCTCTCGCT CCATCCTCCC AAGAGCCTCC 60  
25 AAGGCGCCAT TGGCTTCCTG GGACTCTGAG TCTGCCGCC TCTTTTCCTG ACTCCAGTTT 120  
CTTCTGGCCT GAGCCAATGG GGCATGTTCT GTGACTGCAT TTGCATCTCG GATTGTGTTT 180  
TTAAACCCAT TTTCTCCCAT ATTTGCCTGA AAAATATATA GAAACTGATA TACAAA 236

SEQ ID NO:2373  
30 SEQUENCE LENGTH:245  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02737

35 SEQUENCE DESCRIPTION:  
GATCAGGCTG GTACAGGATG CCTTAAGGTG ATGAGAGGTG AGGGTGCATG AAGAATAATG 60  
AGCACAGGGA AGAGAGAAGC AGGACAAAGT AGCAGATAAA ATGCCGGCAA AGCACAGATG 120  
ANTGTTTTCA AGAAGCTCTT GTATTNTNT GCACAGTGTA AATATCCTTG CTATTTTCAGG 180  
ATGGCGGCTG GCCTGCTCAG TAACATACAT GTTCAAATA AAGATTTTGC ATGAAAGTAC 240  
40 CTAAA 245

SEQ ID NO:2374  
SEQUENCE LENGTH:231  
45 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02738

SEQUENCE DESCRIPTION:  
GATCTGACTG CCTCCTTTCT CTGGCCTCTN CCCCCTNCCC TCTTCTCTTC AGCTAGGCTA 60  
50 GCTGGTTTGG AGTAGAATGG-CAACTAATTC TAATTTTAAT TTATTAAATA TTTGGGGTTT 120

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# EP 0 679 716 A1

TGGTTTTAAA GCCAGAATTA CGGCTAGCAC CTAGCATTTT AGCAGAGGGA CCATTTTAGA 180  
CCAAAATGTA CTGTAAATGG GTTTTTTTTT AAAATTAAAN GATTAAATAA A 231

5 SEQ ID NO:2375  
SEQUENCE LENGTH:236  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02739  
10 SEQUENCE DESCRIPTION:  
GATCCACTGT GAGCACCAAC CTGCTGCAGT CTCTTGGGCC CCTGCTGGCA GCTCTGCCAC 60  
GTCACCGNCT GCCTGGCTCC CACACAGCCA TGCATTGTCA CTCTGCCTCC GGGACCCNAG 120  
CTTNGGAGCN NNTGGGTCTG CCAGGTCCCA CCTCCTCTGT CCCCNATGCC ACAACCTGGG 180  
15 CTCCTGGCTA CAGCAGGGNT CCAGGGACTN CAAATAAATG TTCAGTGACT GGCAAA 236

SEQ ID NO:2376  
SEQUENCE LENGTH:235  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS02740  
SEQUENCE DESCRIPTION:  
GATCGGTAC ACAGCTGTT CCACGATAAT TTTGTNTCA NAAGGGGAGN CTGACTACCA 60  
25 GGACCACTGG CCCCCTTCC AGCCCCTCCA TTCTNAGTAC ACTTCAGAGG GCTCTGGCAG 120  
GGTGAGGGGG TCTTGNCCGT GCCACAGAGA GTAAAGGTCT AGCACACCCA TTGTGGAGAT 180  
ATTTTCATGGG GACANCCAG TGACTTCACT TTGAAGTAA GTGGGATTTT CCAA 235

SEQ ID NO:2377  
30 SEQUENCE LENGTH:253  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02741  
35 SEQUENCE DESCRIPTION:  
GATCGNAGGC TACCCTGGCT CAGTNACCAG CTGCTCACTG TGTCTTCTG TGGTCTCAGG 60  
AGCTGCAGTT GTTGCTGTTG TATGAATAGA CGATAGTNAA TTAGACTGGA TGTGTCTGTA 120  
CTGGCAGTNA TTTTCCAAC NCCTCTGTAT AAGCAATACA TTTGTAAATC ATGGGAATGT 180  
40 ATTTAATGGT AATTGCCTGT GGTGGTTGTA TCATGATTTA NTNNTATNAT GAGCTTTTGG 240  
CTTTNTNTAT NTN 253

SEQ ID NO:2378  
45 SEQUENCE LENGTH:232  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02742  
SEQUENCE DESCRIPTION:  
50 GATCTGGGGT CCCAGTGTCA TTGGTGAAGG CCTTGGGATT CGAGGCAGCT GAGTCCTCAC 60  
TGACCAAGGA TGCCCTGTG CTTACTCCAG CCTCCTTGTG GAAACCCAGC TCTCCTGTCT 120

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# EP 0 679 716 A1

CCCAGTGAAG ACTTGGATGG CAGCCATCAG GGAAGGCTGG GTCCCAGCTG GGAGTATGGG 180  
TGTGAGCTCT ATAGACCATC CCTCTCTGCA ATCAATAAAC ACTTGCCTGA AA 232

5 SEQ ID NO:2379  
SEQUENCE LENGTH:232  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02743

10 SEQUENCE DESCRIPTION:  
GATCTCTGAA AAGNAGGTTT CAGCCACGAG GCAGCTGNTC CCAGGACACT GAGGCCAAGA 60  
GAAATGTAAC AGAGCCACAG CTCCACAGGC CTGCACTCGG AGTCTGGGGC CTCTGCAGAG 120  
CCAGCAAGGG GAAAAGTATA ATCTGGGGGA CCTTCAACCA CTAAGCCTCT TGTGAGAGCC 180  
15 CTCAGGCAGG CAGATGTGTC ACCCAAATAA ACAGTGATAT TGTCTCCAGA AA 232

SEQ ID NO:2380  
SEQUENCE LENGTH:232  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS02744  
SEQUENCE DESCRIPTION:  
GATCTNAGCT GGACAGAGGA GGAGGAAGAG GAGGAAGCAA TGGGGGAATA GTGACACCAG 60  
25 ACAGTTGATG TCTAGATAGG ACCTCAATNA TTCCNTTAGA ATCTNAGATA CCAGGATATT 120  
GTTGGCCATG TGGCATCATT GAGCAGCAGG AGGCTGAAGG AGGNGAGAAC AAAATTGTCC 180  
AAACCATGCT GTTTTTTTCC CTAAATAAA TCTTGATTTC TTCAGTTTCA AA 232

SEQ ID NO:2381  
30 SEQUENCE LENGTH:236  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02745  
35 SEQUENCE DESCRIPTION:  
GATCTANGGA ACCAAACGGA AGGTTTTGAG GTGATGTAGG TCTTTCACAG TTAGCTTTGG 60  
GGAATACAGA ATACTCAAAT AAAGTGCTTT GTTATTATTT CAGAGGGAAT GGCGATTGAA 120  
ATGTTACAAC AGAGATTTCT TGGTGGTAGC TATTNNGTA AAGGGTATAT GGNTATTTTT 180  
40 CTGTACATGT GAAATTATAT AGANNTAAAA GTTATATANA TTACATTGGC CAGAAA 236

SEQ ID NO:2382  
SEQUENCE LENGTH:229  
SEQUENCE TYPE:nucleic acid  
45 TOPOLOGY:linear  
CLONE:HUMGS02746  
SEQUENCE DESCRIPTION:  
GATCAAGTTT AAGTCAGTCA GTTAAGGGGA GGAGAAGGAG AGGTTATACN TTCAGGGGGC 60  
TACCAGACAG TGTTCTCAAC TTGGTTAAGG AGGAAGAAAA CCCAGTCAAT GAAATTCAAT 120  
50 GAAATTCTTG GAAACTTCCA TTAAGTGTGT AGATTGAGCA GGTAGTAATT GCATGCAGTT 180

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TGTACATTAG TGCATTAAAA GATGAATTAT TGAGTNCTTA AAGATTAAA 229

SEQ ID NO:2383

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02747

SEQUENCE DESCRIPTION:

GATCTGATTT CAGATTTTTC CTGTATCTTT TTTACATACA TCAGAAAAAG AAATGTTTAC 60  
TATATTTTGG GTTCCATTNA TGATTGTTTT AAGCATTTGA CGNATAAGGA AACTAACAA 120  
TTAANTCAAT TAGAAAAGCA ACATAAAATT AANTGATATT TAGGAAATCA GTTATATGTG 180  
AGCTTGGGTA TTCAAATGTC ACAANTAAAA GGCNTANACC CATNAAA 227

SEQ ID NO:2384

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02749

SEQUENCE DESCRIPTION:

GATCAAAATNA CCTGTGAAGG AATATTTTGC CTTTCATCCTA GCTGCTGGGG AAGCGGGGAG 60  
AGGGGTCAGG NAGGCTAATG GTTGCTTTCC TGAATGTTTC TGGGGTACCA ATACGAGTNC 120  
CCATAGGGNC TGCTCCCTCA AAAAGGGAGG GGACAGATGG GNAGCTTTN TNACCTATTC 180  
AAGGAATACG TGCCTTTTCC TTAAANNCTT TCATTGATTG AAA 223

SEQ ID NO:2385

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02750

SEQUENCE DESCRIPTION:

GATCAGGGTT TNGGGTCTGT GTTCTTTCTA CCGTCAGCAC CTGTGTGGTC AATTCTGGAC 60  
ACTTCCCAGA GAAGTCTTTG AGTAGAGAAT CCTACTCAAA TTTCAGTGA TATNTTAAGC 120  
ATTCCTCTCC TNTCCNTTG CCTNCCCTGT TGCTTNTCT TCCCCTGATT TCTCCTCTGG 180  
TCATCTNCTC TCCCTNCTGC GTGTAAGCCA TGGGAAAGGG N 221

SEQ ID NO:2386

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02751

SEQUENCE DESCRIPTION:

GATCATGAAA ACAATGTAGG TAAAGTAAAG TATGTATTTG TCTGTGCTTG AAAAATATTG 60  
TAAATGTGA TGTATTTGGA ATATATTTTG TGGTTTGTCT AATATTTATA AACACAACCTC 120  
GGGGTGAATT CACANTGAGT TTATTTTCAAT GAAATACTAG AGATATGGGG GCCATGTTAC 180  
TGTGCTTGGN GCCTTACCNT TTGTATAGTG AAATTTGCAN 220

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SEQ ID NO:2387

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02752

SEQUENCE DESCRIPTION:

GATCCGCCTG CCTTGGCCTC CCGAAGTGCT GGAATTACAG GCATGAGCCA CTGCTCCTGG 60  
 CCTAAGATGT TTTTAAATA ATGTTTTTAA CTAAATTTTA AGAATGTTTT TAACTAAAGT 120  
 TATTTATATT TGGAAATAAT CGTTAATGAT TTGTGTCATT TCCCCAACC CTTTTTAAAT 180  
 TTGTGAATTT GAGGACTGGA TTTAAAGATA AAAAGTTAAA 220

SEQ ID NO:2388

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02753

SEQUENCE DESCRIPTION:

GATCTAATTA ATAGCTGACC TCCCAAATCT GACAGGATAG ACACTGCCAC GTGCAAGGCC 60  
 TGCCAGCCCC TCAGACGCAC AAAATGCGTA AAACAAATGC ATCCTTTCCT GGCTAAGCGA 120  
 GTATTACTCT CTTAGCCCTG CACCAAACCT CCAATCTAGC CACATTTAAC TNTTCATTTT 180  
 TTAGACCCGC AGAGTGTCTT CCTGCCTCTG AGCTGTGAGT GTTGTTCCCT TTGCCCCGGA 240  
 TGCTCTTGTT TTTAATACCA GTTCAAGTCC CACTCTCTCA GTGAAGCACT CCCTTCCCCA 300  
 CTNATAGCCT TTAGTGAACC CTCGTTTCTT GCTTCTTTN 339

SEQ ID NO:2389

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02754

SEQUENCE DESCRIPTION:

GATCCATGTG CAGTAATGCC TGGTGGCTCC AGGTCTGCCC CGCCGTCCTG TGGGGCTGTG 60  
 AGCTTTCCCA GCCTCCTGCC CGTGTTTG TGATATCATTC TGTCTCAGC TGCATTTCCA 120  
 GCCCAGGCTG TTTGGCGCTG CCCAGGAATG GTATNAATTC CCCTGTTTCT CTTGTAGCCA 180  
 GTTACTAGAA TAAATCATC TACTTTAAAA TCTTTCAAA 219

SEQ ID NO:2390

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02755

SEQUENCE DESCRIPTION:

GATCTTGACC GGGAAAAGGG ACTTGAGAGA ACCTTCTAGG ATAATTTNAT TTCTTGATTA 60  
 GGTGGTGGTT ACATTTGTAA AAATCATCGA CCTCTAAATT TAGGGTTTGT GCCCTTCACA 120  
 TACCTTGTG TATGCATTTT GCCACTTGT TTTTCAAAGC AATGAAAAAG TATCACTGCA 180

ATTAGGTTTT AAATAAATTT GTTCGTAA CATGTCAAA

219

SEQ ID NO:2391

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02756

SEQUENCE DESCRIPTION:

GATCTGGAAT CGGGGTCAGC GGGGCTACAG TCCTTCCAGG GGCTNTGGGG CAGCTCCCAG 60  
 CCTCTTCCCA TGCTGGTGGC CACCGTGTCC CTTGCTGCGG CTGCATCTTC CAGTCTCTCC 120  
 TCCGTCTTCC AGTGGCCGCT CTCTTTATAA GAACCCTGGT CATTGAATTT AAGGCCACC 180  
 CCAAGTCCAG AATGACCTCG CAAGACCCTT AACTCAAA 218

SEQ ID NO:2392

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02758

SEQUENCE DESCRIPTION:

GATCCATTTT TAATGGTTCA TTTCTTTAT GGTCAATATA CTGCACAGCT GAAGATGAAA 60  
 GGGGAAAATA AATGAAAATT TTACTTTTCG ATGCCAATGA TACATTGCAC TAACTGATG 120  
 GAAGAAGTTA TCCAAAGTAC TGTATAACAT CTTGTTTATT ATTTAATGTT TTCTAAAATA 180  
 AAAAATGTGA GTGGTTTTC AAATGGCCTA ATAAAAAN 217

SEQ ID NO:2393

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02760

SEQUENCE DESCRIPTION:

GATCAGAGGA ACTTNAGGT GTCTGCCGGC TAACATTGTG TCATTCCTGG AGTCCACAGT 60  
 ACACGTCCCC TGCCTCAACA GGCACAGCTC TCACAAAGCT CTTCAAGCAT GGAAGTGGGA 120  
 GTTGTGTTGT ACTTCATGGC ACTCTGATGC CTGCTGTCTC AGTGTGTTGGT TATTATGCAA 180  
 ACAAGTAATG TTTGAAATAT ATAATAGCAC TGGAAA 216

SEQ ID NO:2394

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02761

SEQUENCE DESCRIPTION:

GATCCATTTC TACCTGCATT TCCCAGAGGA CTAGCAGGAG GCAGCCTTGA GAAACCGGCA 60  
 GTTCCCAAGC CAGCGCCTGG CTGTTCTCTC ATTGTCACTG CCCTCTCCCC AACCTCTCCT 120  
 CTAACCCACT AGAGATTGCC TGTGNCCTGC CTCTTGCCTC TTGTAGAATG CAGCTCTGGC 180  
 CCTCAATAAA TACTTCCTGC ATTCNNCTGN NAAAA 215

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SEQ ID NO:2395

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02762

SEQUENCE DESCRIPTION:

GATCTAAATG TAAAAGCAAA TGAAAAATGC ATGTNTTTTT NCCTGTCAAA CATGTATACC 60  
CTTATGTATA GAGACCAGTA GTCACGTATG GTGACTGAAA CAGGATTATG TAATCCCTAA 120  
AAAGCAGAAAT ATGTAAAANT CACATGTATG CGTTTGGTTT AGGAATGTNC TTTTGTACTT 180  
CCACTTGAAT AAAGGTGTGT TTGGTATTCT GAAA 214

SEQ ID NO:2396

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02764

SEQUENCE DESCRIPTION:

GATCCAGAAA TTCAAACCTC GAGAGCAGAT GGAACGACAT CTAAATCTNT GAATAAAGCA 60  
GCAGGCCTGT CCTGGCCGGT TGGCTTGA CTCTCCTGTC AGAATGCAAC CTGGCTTTAT 120  
GCACCTAGAT GTCCCCAGCA CCCAGTTCTG AGCCAGGCAC ATCAAATGTC AAGGAATTGA 180  
CTGAACGAAC TAAGAGCTCC TGGATGGGTC CN 212

SEQ ID NO:2397

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02765

SEQUENCE DESCRIPTION:

GATCTATTAA AGTGTCAACT TTGCATTATA GAACTGAACA TGAAGTAAAT TGAGTGTTTC 60  
TGAGTTTNC ATAGAAAATT TATGCTACCT CTCATCTTTT CACATACAAA TAAGCAACTT 120  
TTAATGAAGG CTTAGGGTGN AAATTTTAAT TTTAGCACTT TACATTACAT GATGAATGGT 180  
GAATATTAAA GGACTTTGAA CATTTTAATA AA 212

SEQ ID NO:2398

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02767

SEQUENCE DESCRIPTION:

GATCGAGAAG CTGCTCAATT ATGCACCCCT GGAGAAGTGA CCACGCTGAA ACCCACCAC 60  
CCGCTGTGCT GACCATGGGC CCTGAGCGTC CTACCCCGAA TTCACGAGGC TGAGGCATCC 120  
GGGAGCTGGC GTAATGCCTG GCCGCAGTGT GTGTGTATCC CATACCCAC TCTGGAAGGA 180  
ACCATCCAGT AAAGGTCTTT CAGAACCACT AAA 213



SEQ ID NO:2399

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02768

SEQUENCE DESCRIPTION:

GATCAGAGAT GCACCACCAA GCCAAGGGAA CCTGTGTCCG GTATTCGATA CTGCGACTTT 60  
 CTGCCTGGAG TGTATGACTG CACATGACTC GGGGGTGGGG AAAGGGGTCG GCTGACCATG 120  
 CTCATCTGCT GGTCCGTGGG ACGGTGCCCA AAGCCAGAGG CTGGGTTCAT TTGTGTAACG 180  
 ACAATAAACG GTACTTGTC A TTTCGGGCAA A 211

SEQ ID NO:2400

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02769

SEQUENCE DESCRIPTION:

GATCAGACAC CCCTTCACGT GTATCCCCAC ACAAATGCAA GCTCACCAAG GTCCCCTCTC 60  
 AGTCCCCTTC CCTACACCCT GACCTGGCCA CTGCCGNACA CCCACCCAGA GCACGCCACC 120  
 CGCCATGGGA GTGTGCTCAG GAGTCGCGGG CAGCGTGGAC ATCTGTCCCA GAGGGGGCAG 180  
 AATCTCCAAT AGAGGACTGA GNACTGCTAA A 211

SEQ ID NO:2401

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02770

SEQUENCE DESCRIPTION:

GATCACCTAC TTA CTGTATT CTACATTATT ATATGNCATA GTATAATGAG ACAATATCAA 60  
 AAGTAAACAT GTAATGACAA TACATACTAA CATTCTTGTA GGAGTGGTTA GAGAAGCTGA 120  
 TGCCTNGNTT CTACATTCTG TCATTAGCTA TTATCNTCTA ACGGTTCACT GTATCCTTAC 180  
 AGGAATAAAA GCAGCATNTG GNTAAA 206

SEQ ID NO:2402

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02771

SEQUENCE DESCRIPTION:

GATCGAATGA AGGATTCAAA ATTAACCACT CCAAGGGGGG ATTGAAGGAA GAACCACTCT 60  
 TAATGGACAA AAAGAAAGAA AGGGGAGGGA GTAACAGGGA TATNAGCTCT AGCCGCCCAA 120  
 GCTAGCAATG GCAACCCTTC TGGGTCCCCT TCCAGCATGT GGAAGCTTTC CTTTCGCTTC 180  
 ATTCATAAAA CAGCTGCTGC TCAAA 205

SEQ ID NO:2403

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02772

SEQUENCE DESCRIPTION:

GATCTATAGA CATNAGGAAG GGAGTNAGAC GGCTCCTCCA CCATCCTCAG CCAGTGCAAC 60  
CCATTCCCTC TNCTTCTCTC TCTCTCTCTC TCTCTCCCTC CCTCTCCTTC CCTACCTCT 120  
CACCATCTTT NTTGGCCTCT CTNAGGGTCT CTCTGTGCAT CTNTTTAGGA ATCTNGCTCT 180  
CACTCTCTAC GTAGCCACTC TCCTTCCCN ATTNTGNGT CCACCCNN 228

SEQ ID NO:2404

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02773

SEQUENCE DESCRIPTION:

GATCTAGCTA GGGCTTTGTC TTTTCATCTT TGTGCATAAC TTACCTGTTA CCAGTATAGG 60  
TGGGATATAC ATNTATCTTG CAGGAAATTC CCCAAAGCTC AGAGTCCAGT TCCTTCCATA 120  
AAACAGGCTG GACAAATGAC CACTATGTGA GACCCCCCGG NTCGACTTCA GGGGTCAGTG 180  
TTCCTGTCCC AAACCCNCAC ACAGAAATNCT CTGNCTGNGG TTCATGTNGA AACTGAGCAA 240  
AAACTANAGT ATCTNTCAAN ANGTGTAACN TGN 273

SEQ ID NO:2405

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02774

SEQUENCE DESCRIPTION:

GATCCACCTC ATATGTGAGT CCGTCCAAAA GATGTTACTG CTCTGGGTGG GCCAGTGTTT 60  
TATATCGGTT ATACTAAGT TCATTTAAAG TATTTATTCT AAAATGCCTC TGAGAAACAG 120  
TAAAAAATAA AAACAACAAG TTGTCTAAAA TGCAACAGCT TTTATAGTAA ATGTACATTT 180  
ATAAATAAAA TACTCAAATC AAA 203

SEQ ID NO:2406

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02775

SEQUENCE DESCRIPTION:

GATCTCTGAT GGATTGTG ACTCCTCTGT GGGAGAAAGG CTTGGTCTAC TGCAGGTGTT 60  
AACGCTAAGC CAGGCTGGAG CTGCGGACGT NAGTTTCCTC AGCNCCCCGC TGTTGCTTTC 120  
GAACGTNACC TCGACGTCTG CTCTCCCTT CCCTTTAGCT GACAATGTGA CAGTNCTTGA 180  
ATAAAAGTNA GTCTGACAGG AAA 203

SEQ ID NO:2407

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02776

SEQUENCE DESCRIPTION:

GATCTGAATG TGAATTTCTA ATTGTATCAG ACGTTAATGT TTAAAGCTA TAACAAAGTT 60  
 TAAAATTTCT ACTTTTGTG TTTNATTTAT TTAACTGTT CTTTATCTA TTAAATTGTT 120  
 GTATGTGGAT GGGGAAGTTT TGTTTCTCCT CTTAGCATTT GTTCTATAA CCAGAAATAA 180  
 AATTCTATAT TAAAGAAATG ACAA 205

SEQ ID NO:2408

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02777

SEQUENCE DESCRIPTION:

GATCCCAATC TGAGAAAAGG CAAAAGAATG GCTACTTTT TCTATGCTGG NGTATTTTCT 60  
 AATAATCCTG CTTGACCCTT ATCTGACCTC TTTGGAACT ATAACATAGC TGTCACAGTA 120  
 TAGTCACAAT CCACAAATGA TGCAGGTGCA AATGGTTTAT AGCCCTGTGA AGTTCTTAAA 180  
 GTTTAGAGGC TAACTTACAG N 201

SEQ ID NO:2409

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02778

SEQUENCE DESCRIPTION:

GATCTTTAAC TGCCTGCTGA TAAGATATTG GGCCAACTGA AAATAGAAAT TGTTCCTTCT 60  
 TAGAAATATT TTAATGCTAA CTTGTTAGTT TTCCTCAGAA AGCTAGTATT TGAAGCCATT 120  
 CGAGTTTAAG ATNCTCTAAT TTCAATAAAA TAGCTTCCAA ATATTTAAAA TGTAATAAAA 180  
 TATATGTTTG ACACTCTAAA 200

SEQ ID NO:2410

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02779

SEQUENCE DESCRIPTION:

GATCAAAACG CTCCATCTTT TTACAGTGGC ATAGGAAGAC GGCAAAAATT TCCTAAAGTG 60  
 CAATAGATTT TCAAGTGTAT TGTGCCTTGT TCTAAAACCT TTATTAAGTA GGTGCACTTG 120  
 ACAGTATTGA GGTCAANNNN TATGGTGCTA TTTCANTNAG TCTAGGTTTA GGCCCTTGTA 180  
 CATNTTGCCC ATAACNN 198

SEQ ID NO:2411

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02780

SEQUENCE DESCRIPTION:

GATCTGCCCCA TTGCTGAAAC TTCAGTACTT AAGTCCCCTA TTATNATTGT ATGGCAATCT 60  
ATCTGTCCAC TCAGAAGTTA TTATATTTGT TTTATATGAT TGAGCACTTC TGTTTTGGGT 120  
ATATATGTAT TTACAATNAC TATAACCTCT TGCTGAATTA ACCCCTNTTA CCATTATGTA 180  
ATAAACTTAT TTCCCAA 198

SEQ ID NO:2412

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02781

SEQUENCE DESCRIPTION:

GATCTTGAAT CACTTGACAG TGTTTGTNG AATTGTGTTN GTTTTNCCT TTGATGGGCT 60  
TAAAAGAAAT NATCCAAAGG GAGAAAGAGC AGTATGCCAC TTCTTAAAC AGAACAAAAC 120  
AAAAAAGAA AATTGGGCTC TNTTCTAATC CAAAGGGTAT ATTNACAGCA TGCTTGACTT 180  
TACCAATNCT GATGACAN 198

SEQ ID NO:2413

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02782

SEQUENCE DESCRIPTION:

GATCCAAAGT AACTAAACAG GAGCCCACAA GACGGTCTGC CAGATTGTCA GCGAAACCTG 60  
CTCCACCAAA ACCTGAACCC AAACCAAGAA AAACATCTGC TAAGAAAGAA CCTGGAGCAA 120  
AGATTAGCAG AGGTGCTAAA GGGAAGAAGG AGGAAAAGCA GGAAGCTGGA AAGGANGGCA 180  
CAGAAAAC TG NTCTGTAGA TAACGTGGGA GAATGAN TTG TCATGAAAAT TTGGTGGTTG 240  
ATTTTTTTGT NTGCTTGGG ACAACTTTTA AANGCTATTT TTNCCANGTN TTTTNGTNN 300  
TTGGTTTTTT TTTTAGGGNT CTNCTTGTG GCATNCGGNA GTTTTTTANG GTTTGGNCN 359

SEQ ID NO:2414

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02783

SEQUENCE DESCRIPTION:

GATCCCAGGG GTGCACATGG GCCCCTTGGG TGTCTGAACA GAAGGGCATG GNAGGAAGGG 60  
CTGCACCCCT GCAGTCTTAC TCTGCTGGTG TAGCGGGCAG CTGCCCACTC CCACCCACC 120  
CTGCACCGCG GGCTCCTNAG TCGGCAGATT AAGCATTTNA TAAATTGTAT TTAAATACA 180  
TGTTTAAAC TTGTCAA 198

SEQ ID NO:2415

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02785

SEQUENCE DESCRIPTION:

GATCCCATCC ATCAGCTCCC TTTTCTTTT CCCTTGAAC GTTCTGGCCT CAGACCAACT 60  
CTCTCCNNNN NTAATCTCTC TCCTGTATAA CCCCACCTTG CCAAGCTTTC TTCTACAACC 120  
AGAGCCCCC ACAATGATGA TTAAACACCT GACACATCTT GCANAAA 167

SEQ ID NO:2416

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02786

SEQUENCE DESCRIPTION:

GATCTGTGAT TGGNTGGTTA ATGGGAAACG GTTTTTNNCT TTGGCTGCAG GTGTTCTGCT 60  
GATATCAACA GCTTCCCTAT TTTNAATGCA GAAAACAGGG TCTGGGACAT TAGTCGTTAT 120  
ATTNACTTG AAAAGAAAGA AACCAAGTGC GCTTTGCAAT ATTTATTACA CAAAGAACTT 180  
GCTGCTGCAT TCTAAA 196

SEQ ID NO:2417

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02787

SEQUENCE DESCRIPTION:

GATCACAGAT TTCCCTGCCA GGGTGTCTGT GGTTATCAGC TGCAGGCTCA GCTNGGGTCG 60  
GCCGNTTCAC ACAAGCCACT CTGTACCAGG TGCCCTACCT TAGTGACGGG AGTAAGGAGC 120  
TTCCTTCCCC TCCATGTCAT TCCTNCCTGT TCCNTNCATT CCCCAACAGC AAATAAACT 180  
GTTGAATGCT CAAA 194

SEQ ID NO:2418

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02788

SEQUENCE DESCRIPTION:

GATCTTCCTA CGCACAACAC AAACGTCAGT TAATGTTCCA TCCATGCTGC TTAAAGAGCA 60  
TTCCTGTCCT AGTAAATGG GCAAGTCCCT CTACCCCCCA CCCTCACCTG GTATGCTTAC 120  
ATTAATAGCT AAAGTCAATC CTGTAATGAA ATAAAGCAAG TGGTAGCTGT CTGGTAGCCT 180  
CCACTACTGC AAA 193

SEQ ID NO:2419

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02789

SEQUENCE DESCRIPTION:

5 GATCAAAACC CAGCAGAGTG CAAGCAGCAG TGAAGCAGGA TGTATGTGGA CTTGAGGATA 60  
 ACCTGCACTG GTCTACCTTC TGCTTCCCTG GAAAGGATGA ATTTACATCA TTTGACAAGC 120  
 CTATTTTCAA GTTATTTGTT GTTTGTTCG TTGTTTTNT TTTGCAGCT AAAATAAAAA 180  
 TTTCAAATAC AAA 193

10 SEQ ID NO:2420

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS02790

SEQUENCE DESCRIPTION:

GATCAGACCT CAATAATTTT ATACTGTAAT AAGCTCTTTG AATGTNTATA TTATTATTTT 60  
 TNACAATCAT TTCATTTTGT ATTTAATATC AATGGACTGA GTCTGATTCA GAAAATAATT 120  
 20 GTAATGTTCA TATTCAATAT CTTACAGTGA TACAGTTTTG TATTACATA TAAATATACC 180  
 GACATGACCA AA 192

SEQ ID NO:2421

SEQUENCE LENGTH:276

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02791

SEQUENCE DESCRIPTION:

30 GATCAGGGTT TCAAGAATGA CTGCAGTGGG TTTTGGAAAC AGACTTATCA TTATTGATTT 60  
 GAGGTTTCCC AGAGATATAG TTCACAGTTA ATTGTTGCGC TCTAATACAA CTGACCATT 120  
 AAAATTGAAC AAGTTTATTG TTTTGTAACA ATGTCAGTTG TTAAACCTTG NCATTTCAAT 180  
 TAAAACATGA NTTGTAGTTA TAACTCANTG CAANTNCAAC AGTTGTATTT GNGGTTAANT 240  
 TATTTTCACA CGTNNCTTTN TTTTCATGGAN NNCCCN 276

35 SEQ ID NO:2422

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS02792

SEQUENCE DESCRIPTION:

GATCTTTTAT TTTCTCATTA TTTATAACTT CAGACTTGGG CCCCCTGTTT TTTCTTTCCC 60  
 ATTAACCTGA GTGACCTGTG TGAGAGACAG ACAGATGCCC CACGAGGATG GCTGGACAAG 120  
 45 GACTTTTACT TTTTATTACA TAAAAATATT AAAAAATAAA TAAAAAAAAT AAAATTTTAA 180  
 ACTAACTTAA A 191

SEQ ID NO:2423

SEQUENCE LENGTH:189

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02793

SEQUENCE DESCRIPTION:

5 GATCGGAATG CGGGGTCGAG AGCTGATGGG CGGCATTGGG AAAACCATGA TGCAGAGTGG 60  
CGGCACCTTT GGCACATTCA TGGCCATTGG GATGGGCATC CGATGCTAAC CATGGTTGCC 120  
AACTACATCT GTCCCTNCCC ATCAATCCCA GCCCATGTAC TAATAAAAGA AAGTCTTTGA 180  
GTAGTCAAA 189

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SEQ ID NO:2424

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS02794

SEQUENCE DESCRIPTION:

20 GATCGAGACC ATCCTGGCTA AAACGCCTGG AATGCAGTGG CACAATCACT GCTCACTGCA 60  
GCCTTGACCG TNTGGACTCA AGTAATTCTC TACTTCAAC CTCCAAGTA GCTGGGACTA 120  
CAGTCATGCA CCATCATGCC TATAAAGATA ATTTAATTTA TAATAAATNA TTTATACAAA 180  
CAATAAA 187

25

SEQ ID NO:2425

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02795

SEQUENCE DESCRIPTION:

30 GATCAATCGT GCATCCTNAG TGAACCTCTG TTGTCCTCAA GCATGGTCTN NNTACTTGTG 60  
AACTATGGTG TTCAGTTTGG CCTCTGTTAG AAATTCACAC TGTTGTTGTA ATNATGTGGA 120  
ACTCCTCTAA AANTTACAGT ATTGTCTGTG AAGGTATCTA TACTAATAAA AAAGCATGTG 180  
TAGNAAA 187

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SEQ ID NO:2426

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS02796

SEQUENCE DESCRIPTION:

45 GATCNCGTTT TNAACCCGNT CCTGCCCCAC CTGCCCTATA GTTATGGCCT GTGTTCTGCT 60  
CTCCTGGTCC CAGTGCACCG TCTGCTCTGT GAACTCCTCC CACCAGGCCC TTCTTACCCC 120  
ACGCGTGTCT GTCCCCNTCG TTCTGTAGCG GGNGGTACAT AATAAAACAA TGGNGTGGNG 180  
ACAAA 185

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SEQ ID NO:2427

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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# EP 0 679 716 A1

CLONE:HUMGS02797

SEQUENCE DESCRIPTION:

5 GATCTATGTT TTCTGAAAAT AATTGGTTAA TGGAAGTTAT CTAATATATT TNAACTGTTC 60  
CTGTAAAAA CAATAGGCTT CAAGATGACA TAACACCAA TCAAAAATNA CCAAAGGAAT 120  
CATTTTGTTC GTTAGATTG TAATTTAGCA TCATTGGCAA TAAATCTACT CAAACGTAA 180  
A 181

SEQ ID NO:2428

10 SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02798

15 SEQUENCE DESCRIPTION:

GATCCCAAAG GGGTTGGAGG CAGGGAATAT TTGAAAATTC AGACTGGAAT TCCAGGCCAA 60  
AAGCTCAAGA CCACCAGCCT CTCCTCCTGC CTGGAAAAAT AAGCCTTGT GAAAGACTGA 120  
TTTACCATGT ACAATTGTGA TTGTGAACGT TGTGAGTAA ACCTCCAGAC TTTCTCTAAA 180

20 SEQ ID NO:2429

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS02799

SEQUENCE DESCRIPTION:

30 GATCATAAGT NAAAAATGTA TTTAATATAC CTAACCTACC AAACATCATA GCTTAGCCTA 60  
GCCTGCCTTA AACATGCTCA GAACACTTAC ATTAGCCTAC AGTGGGCAAA ACTATCCAAC 120  
ACAAAATCTA TATTGTAATA AAGTTATAAA GANTTTTGAA TAAAANTTCA ATATTTGANG 180  
TACAAA 186

SEQ ID NO:2430

35 SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02800

SEQUENCE DESCRIPTION:

40 GATCTGGTGG AGGGAAGTGA AGATGAAGGC CTCTCAGGCA CCATGGATGG NATGGGTGTG 60  
TGTNAAGGGG GCAGGGTCCC CAGGAGCTGC CCCAGGTCTG GCTNGACAGT TGCACGGNAA 120  
GTCCTGTTTG TAAACTCAAC GTTCCACGN CTTTCCATT AAACTTTACC CCAAATCAAA 180

SEQ ID NO:2431

45 SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02801

SEQUENCE DESCRIPTION:

50 GATCTATTTT TCCTAAAAA- TTCCCCTCCC-CACTCCTCTC CCACAGAGTG CTNNNTGTT 60

55



EP 0 679 716 A1

CCAGGCCCTC CAGTGGGCTG ATGCTGGGAC CCTTAGGATG GGGCTCCCAG CTCCTTTCTC 120  
CTGTGAATNG AGGCAGAGAC CTCCAATAAA GTGCCTTCTG GGCTTTTNCT AACCTTTAAA 180

5

SEQ ID NO:2432  
SEQUENCE LENGTH:179  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02802

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SEQUENCE DESCRIPTION:  
GATCTTACC AATGGCAAGT GGAATGACAG GGCTTGTGGA GAAAAGCANN TTGTGGTCTG 60  
CGAGTTCTGA GCCAACTGGG GTGGGTGGGG CAGTGCTTGG CCCAGGAGTT TGGCCAGAAG 120  
TCAAGGCTTA GACCCTCATG CTGCCAATAT CCTAATAAAA AGGTGACCAT CTGTGCAA 179

15

SEQ ID NO:2433  
SEQUENCE LENGTH:273  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02803

20

SEQUENCE DESCRIPTION:  
GATCTAAAAA TTCAATGCAA ATATCTTTTA TTTGGTAGTT TTGTCTACAT ATTTNATGCT 60  
CTAGCATGTG CAATATATCT TTGTAAAGCA CGATGATACA AATCTGGTGC CAGTGTTATA 120  
TTTNGCATAA CATATTTGTA ACAGCATAAA ATATTGTTT ATGATTTTCA TGGGATTTTG 180  
TCTATAATGT TTTCTTATGT AAATNGGAGT TGAATGACTC TGGTAAATGT CATGACTGTA 240  
AAANTGGGGA AANTGACTTT NAGTTCAGTG AAN 273

25

SEQ ID NO:2434  
SEQUENCE LENGTH:178  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02804

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SEQUENCE DESCRIPTION:  
GATCCAAACT AATTTTACAT TTAAAAAAA AGTTAAACTA AACTTCTTTA CTGCTGATAT 60  
GTTTCCTGTA TTCTAGAAAA ATTTTNACAC TTTCACATTA TTTTGTACA CTTTCCCAT 120  
GTAAAGGGAT GATGGCTTTT ATAAATNTGT ATTCATTAAA TGTTACTTTA AAAATAAA 178

35

SEQ ID NO:2435  
SEQUENCE LENGTH:176  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02805

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SEQUENCE DESCRIPTION:  
GATCTAAAAT AAATATTGTT AAAAGCATTG CCTCTAGGGA ATGGGATTTA GATTTAAAAA 60  
GGGTGGGATG GGAACTGTG TTTTTCATTT TAAGTCCTTC TGTACTANNT AATTTGTNAC 120  
CTTGTGCATG TATTACTTTG AAAAAATTTT TAATAAACCC AAATAAAANT CTAAAA 176

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# EP 0 679 716 A1

SEQ ID NO:2436

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02806

SEQUENCE DESCRIPTION:

GATCANCCCT CAAGGGCACA TGCCAAGGGC AGAGCAGCCC ATNTAGACAG CTCGNAGGG 60

CATGGGGGTG TAGGGAGTTC GGGGTAGCTC CTCATTAAC TTTGTNGGN TGAGTAAAG 120

GGTGAGGCTC AGTGGCAGGT ACCTCTNCAA TNACAAGCTG CCNCCCCTCT ATGTN 175

SEQ ID NO:2437

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02807

SEQUENCE DESCRIPTION:

GATCGGCAGC AAGAGTAAAG ACACAGCTCC AGAGGCCAC ACTGTGGGGT CTGGGCCCTG 60

CCTTAGGCAG CCCCCCTCT TGGCCCCCTC CTGTCAGGCC CAGGGCTTGG AGTGAAAGTN 120

ACTCTCAGGT GGTGGGGTGG GGAATGTGAA TAAACATGAT TTCTTGCCGG GCAA 175

SEQ ID NO:2438

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02808

SEQUENCE DESCRIPTION:

GATCCCTTCA CTGGCCCCCT CGGGAGNCCT GGGTTGGA CT CAGGGNCTCC NCCAGCTGGG 60

GNGGNGGACC GCAGCACCTA TCTGAGCAGT TAGAGCGTCT TTTTTCAG ATTGTGTACA 120

GTAGATTATT TATTTGTNA TTTTGAATA AAATTTATT TATGGCTTAG GAAA 174

SEQ ID NO:2439

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02809

SEQUENCE DESCRIPTION:

GATCTTGCT GAAATGCTAG TTTCTGACTA CAAAACTAC AGGACATAGT AGATATGCTC 60

AGTAGAGCTG CTAAATAA TTCCCTTTT TTTTCTGTTG AATTCTGTTA CAAAACCAGG 120

TCTGTGTTAT AATAGAAANC AACTTATGA ATAAAAATCT TAAAAATTA AA 172

SEQ ID NO:2440

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02810

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCAATGTC CCTGGTTACC TATGTGTTTG AATTATCTTC GTGTTACAGG TGTTTAATGA 60  
 TTTTNCCTCT TCTAGCTTAT TTGTATTTCA CCTGTTTTTC TTTAAATNAA CATGGTTACA 120  
 CTNTGTTTCA GCAACTGTAT AAATTAAACA CAGATNATTA CTACTGCTAA A 171

SEQ ID NO:2441

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02811

## SEQUENCE DESCRIPTION:

GATCGTAAAA TTTTAAGCAC TAAAAATTTT TTCATAACCT TTCATAATAA AGTTTAATAA 60  
 TAGGTTTATT AACTGAATTT CATTAGTTTT TTTAAAGTGT TTTTGGTTTG TGTATATATA 120  
 CATATACAAA TACAACATTT ACAATAAATA AAATACTTGA AATTCTCAAA 170

SEQ ID NO:2442

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02812

## SEQUENCE DESCRIPTION:

GATCTACTTT GAATTCACACA CTCTCATTA TAAATTGANT AAAAGGGAAT ATTTTGGCAC 60  
 CTGATATAAT CTGCCAGGCT ATGTGACAGT AGGAAGGAAT GGTTCCTCCCT AACANGCCCA 120  
 ATGCACTGGT CTGACTTTAT AAATNATTTA ATAAAATGAA CTATTATCAA ATAAAACGTA 180  
 TGATTCAGTC CTAAA 196

SEQ ID NO:2443

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02813

## SEQUENCE DESCRIPTION:

GATCAAATTT TTTCTTGCA ATNATGTGAT GAGTTGCCAA ATAATTGANA TTATTTTAAA 60  
 ATGTTTTGTT CATATTCTTG TTTTATAATT AAAATTTACA TTCAGTGTGT ATGGGTTTTT 120  
 TTTTNATTTT NACTCTTAAT GTAAGGTGGA TATTNCTGTN ATTTTACATG GTTTCTTACT 180  
 GAGATTTTAT ATATAANTNA TAAAANGTTT ACCAAA 216

SEQ ID NO:2444

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02814

## SEQUENCE DESCRIPTION:

GATCGTTAAT GCCCTTGAAG TGGTTTTTGT GGGTGTGAAC AAATGGTGAG AATTTGAATT 60  
 GGTCCCTCCT ATNATAGTAT TGAAATAAAG TCTACTTAAT TTATCAAGTC ATGTTTCATGC 120

CCTGATTTTA TATACTTGTA TCTATCAATA AACATTGTGA TACTTGATGT AAA 173

SEQ ID NO:2445

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02815

SEQUENCE DESCRIPTION:

GATCAGCTCC GTGGGGCTGG TTTTGGTCCA CAGCATAACA GGCAGTGCCT CCTTACCTGT 60  
GAGGAATGCA AAATAAAGCA TGGATTAAGT GAGAAGGGAG ACTCTCAGCC TTCAGCTTCC 120  
TAAATTCTGT GTCTGTGACT TTCGAAGTTT TTAAACCTC TGAATTGTA CACATTTAAA 180  
ATTTCAAGTG TACTTTAAAA TAAAATACTT CTAATGGAAC AAA 223

SEQ ID NO:2446

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02816

SEQUENCE DESCRIPTION:

GATCTGTCAC TTTGTATAAA AACAAGAAAC GATTAGTTCA TTAACTTTT TCTTTACCTT 60  
CTGGTAGTAA AAATAGATAA AATAATTCCG TNTCAACTAC TGTGTGTAAG AAGCCTGTAT 120  
CATATGTAAC TGGGACTTTT GTAAATAAAT NTTTTGCGC TCTGCAAA 168

SEQ ID NO:2447

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02817

SEQUENCE DESCRIPTION:

GATCATAAAA TGTATCTTTT CCATGGCCAA CAAGGNGCAT CTNTTATAAA TGCATAATAA 60  
CCGAGTTNGT ATCAAAGGGT ATCGACTTAA GTGAAATTC AACATGCTGT TACTTTTTCC 120  
TTTAAATGTA ATNCTGTTTT CCAAATAAAT GGGGGAGACA AATGGAAA 168

SEQ ID NO:2448

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02818

SEQUENCE DESCRIPTION:

GATCTGTGCA ATAAAGTGTT TGCAGTCTTA TTATTCTCTA AGAAATTCCT TATGGACGTC 60  
ATAATTGTTG TATATTGAAC AAAATATTTA TACTTATGCA GTTGCAATAC ATTGAAATAA 120  
AAATTTAGCA TGAAA 135

SEQ ID NO:2449

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02819

5 SEQUENCE DESCRIPTION:

GATCCTGCCA GAAAATTTCA AAGACAGTAG ATTGAAAAGG AAAGGCTTGG TAAAAAAGGT 60  
TCAGGCATTC CTAGCCGAGT GTGACACAGT GGAGCAGAAC ATCTGCCAGG AGACTGNGCG 120  
GCTGCAGTCT ACAAACTTTG CCCTGGCCGA GTGAGGTGTA GCAGCAN 167

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SEQ ID NO:2450

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS02820

SEQUENCE DESCRIPTION:

GATCAGNAGG CATCACTGAG GCCAGGAGCT CTGCCCATGA ACCTGTATCC CACGTACTCC 60  
AACTTCCATT CCTCGCCCTG CCCCCGGAGC CGAGTCCTGT ATCAGCCCTT TATCCTACA 120  
CGCTTTTCTA CAATGGCATT CAATAAAGTG CACGTGTTTC TGGTAAA 167

20

SEQ ID NO:2451

SEQUENCE LENGTH:413

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS02821

SEQUENCE DESCRIPTION:

GATCCGGTTT CTTTTTGCTC GCCCCTGTTT TTTGTAGAAT CTCTTCATGC TTGACATACC 60  
TACCAGTATT ATTCCCGACG ACACATATAC ATATGAGAAT ATACCTTATT TATTTTTGTG 120  
TAGGTGTCTG CCTTCACAAA TGTCATTGTC TACTCCTAGA AGAACCAAAT ACCTCAATTT 180  
TTGTTTTTGA GTACTGTACT ATCCTGTAAA TATATCTTAA GCAGGTTTGT TTTCAGCACT 240  
GATGGAAAAT ACCAGTGTTG GGTTTTTTTT TAGTTGCCAA CAGTTGTATG TTGCTGATT 300  
ATTTATGACC TGAAATAATA TATTTNGTNC TTCTAAGANG ACATTTTGTT ACATAAGGGG 360  
ATGGCCTTTT TTATACAANG GGAATAANAT TNTGGGCATT TCCTATGGAGGGCATT TCCTATGGAA AAA 413

35

SEQ ID NO:2452

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS02822

SEQUENCE DESCRIPTION:

GATCTGTNAT TGGCATCTTG GTTCTACCTT TTATCAGATG TTGTTGCCTT GTGCAAATNA 60  
CATTTTCTCT GAGTCTCCAT TTTCTCATTT ATAACATGCG GAGAATAATA CTTATATTTG 120  
TGGTAGTAGT GTGAACATTA AAAAGATAAT GTATGTGAAG TACAAA 166

45

SEQ ID NO:2453

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

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# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS02823

SEQUENCE DESCRIPTION:

5 GATCCATGCT AATATTGTAT TTTTNTTAA AACATAGCTT TCCTGTAATT TAAAGTGCTT 60  
TTATGAAAAT ATTTGTAATT AATTATATAT AGTTGGAAAT AGCAGTAAGC TTTCCCATT 120  
TAATATATTT TGNTATACAA ATAAAATTTG AACTGAAGTC TGAAA 165

SEQ ID NO:2454

10 SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02824

15 SEQUENCE DESCRIPTION:

GATCTTGTTA GAAGGCAGTA GGTCTGGGGT GGGGCCTGAG ATTCTGCATT TCTAACCAGG 60  
TCCTGGGAGA TGCTGATGCT ATCGAGCCAC AACCACACTT TGAGTAGCAA GCCTCTGGCC 120  
TATCCTTANN NNTTGAATA TAAAATGCT GCCTCTCAGT CAAA 164

20 SEQ ID NO:2455

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS02825

SEQUENCE DESCRIPTION:

GATCAATGCC AGATTTTNTT NTTGGGGTAA GTTAGCTGAA GTCATTTAAA GATGGAAAGG 60  
TGGGAAAATN CTTTGATATT TGATGTCATT GTATCCACAT TTNTTGAAG ACATATTGCA 120  
TACCANTTAT AATNATATCA ATTAAAGTTG ATAAAAGCTT CAAA 164

30 SEQ ID NO:2456

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS02826

SEQUENCE DESCRIPTION:

GATCCCTTCT GCCCTGGCAG AATGGCAGGG GTAATCTNAG CCTTCTNCAN TCCTTTACCC 60  
TAGCTGACCC CTTACCTCT CCCCCTCCCT TTNCCTTTGT NTTGGGATTC AGAAAAGTGC 120  
40 TTGTAAGAGA CTGTTTATNT TTAATNAAAA ATATAAGGCT TAAA 164

SEQ ID NO:2457

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02827

SEQUENCE DESCRIPTION:

GATCCAGAAT ATTTTCATTT AAAGCTCAAC CATTAATTGG AACATGGTGA AACATTGTAC 60  
50 ACATTGTAAA AGTAGGGAAC AGTACAAAAG AATGGAATCA AATACTATAT TATGTGAATA 120

55

ANCTAGAGTG ATTTTGAAT TTCACTCTCT TCACCCCTTA AA

162

SEQ ID NO:2458

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02828

SEQUENCE DESCRIPTION:

GATCAAAAAC CTCTATAGTA GCCACTAGGG CAAAAACTGT GTGTATGTGT GTGTGTAAGT 60  
 GTGTGTACAC TGTTCATAT GGTTCATAT GGTACCAATA GCCACATGTG ACTATTTAAA 120  
 TTCATTGCAA TGNAATAAAA TTAAAGGTAT ACTAGCTCAA A 161

SEQ ID NO:2459

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02829

SEQUENCE DESCRIPTION:

GATCTTCACC TCTCTGCCTC CCTACTGCCC CAACATAGCC TTGAGGAGGN TTCTCAGCCA 60  
 CCAAAGGGTT CTGGCCCTT CTCACTCTCC TCTCCTCTCA GATGGAATC TGGTTATAAT 120  
 GGTGTTAGTT ATCGAATAAA AACGACTTCA GAATGCAAA 159

SEQ ID NO:2460

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02830

SEQUENCE DESCRIPTION:

GATCAATTTA AAATATTTNA TTTCTTAAAA GCCTTTTTTG CCTGTTGTAA TGTGCAGGAC 60  
 CCTTCTCCTT TCATGGGAGA GACAGGTAGT TACCTGAATA TAGGTTGAAA AGGTTATGTA 120  
 AAAAGAAATT ATAATAAAAG GGATACTTTG CTTTTCAAA 159

SEQ ID NO:2461

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02831

SEQUENCE DESCRIPTION:

GATCTATTTA ATTTGAGGTT GATGTTCTAT CCAATGGCCG AAGATAGCAG CAGGTTTTTT 60  
 TTTTCATATG TTGATTTGTT TCATTTGGAT TTTTTTTTNA TNATNCTTNA TTGTCTTTTT 120  
 TTTNCCCAT CCCTGTCTTG NGATTTNCNG GCATGTTN 158

SEQ ID NO:2462

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02832

SEQUENCE DESCRIPTION:

5 GATCTGAAAT GTGATGATTA TTGGAATGCA TAAACATTGA CGTATTTTGG AATGTATTAA 60  
AACTGAAATG GATAAAAATT AGTATATATG TTTATTTTGT TCTATCTCCT TTGGTTGTAT 120  
TTTTCTCTGC AGTATTAAAC ATTTGGAAGA GACTAAAGGT ATGCAAAANT AATGTCTTAT 180  
TTTCATTATG TGTGCTTCCA TTTGACACAT GGGAAATTAG ATTAATTTC A TATTAANTA 240  
10 GNACTTTATA CAGAAA 256

SEQ ID NO:2463

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS02833

SEQUENCE DESCRIPTION:

20 GATCTTGTGT CTA CTCTAGG ACTGGGCCCG AGGGTGGTTT ACCTGCACCG TTGACTCAGT 60  
ATAGTTTAAA AATCTGCCAC CTGCACAGGT ATTTTGA AAA GCAAAATAAG GTTTTCTTTT 120  
TTCCCTTTC TTGTAATAAA TGATAAAATT CCGAAA 156

SEQ ID NO:2464

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS02834

SEQUENCE DESCRIPTION:

30 GATCTTCTCC TTTGTGAAGC ATCCCTCACC ACTACTACTG TGATGGGTCG GGGCCTTTCA 60  
TCTGTTTTTC CACAGCATCT ATGCTTCTNT NCACTGTATC ATTTATCAAA TTGATNNTN 120  
CTGCGTCCTG TAAAAAACAN NGAGTACCTT AAGAAA 156

SEQ ID NO:2465

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02835

SEQUENCE DESCRIPTION:

40 GATCTGCATT TATCATGAGT TCCTTTTTTT TTTAACTTT ATTTTGGGA AAGTAACACA 60  
TGANGTAGTT CAGTCATGTC AGGTTTGTCT GGGGTGGANT GGACCAGTCA GGTAGTTGAA 120  
AGTTTTTTTT TAGNGATGAA AAGCTTGTGA NCNCCTGTAA ANCATGCTGN ATTTGAAATN 180  
CATCTGTTNA N 191

45 SEQ ID NO:2466

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS02836



## SEQUENCE DESCRIPTION:

GATCCACCCC CTGCCCACAA AAAATTGCTC CTAAGTCCAC CGCCTATCCC AACCTACAA 60  
 GAACTAATGA TAATCCCACC ACCCTTTGCT GACTCTTTTT GGACTCAGCC CACCTGCACC 120  
 CAGGTGATTA AAAAGCTTTA TTGTTACAC ANAAA 155

SEQ ID NO:2467

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02837

## SEQUENCE DESCRIPTION:

GATCCTAGCA AATTTGCCCA ACCANCTTTA CTAAAGGGGG AGGAAGGGAG GGCAAAGGGA 60  
 TGAGAAGACA AGTTTCCAG AGTGCCTGG TTCTTTTAC TTTCCCTTT GTTGTGTTN 120  
 TTGTAGTTAA AGGAATTTAA TTTTAAAAA GAAA 154

SEQ ID NO:2468

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02838

## SEQUENCE DESCRIPTION:

GATCGGGCCT AGCCCGGCAA CACTAATGTA GAAACCTTTT TTTACAGAG CCTAATTAAT 60  
 AACTTAATGA CTGTNTACAT AGCAATGTGT GTGTATGTAT ATGTCTGTGA GCTATTAATG 120  
 TTATTAATTT TCATAAAAGC TGGAAAGCAG CAAA 154

SEQ ID NO:2469

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02839

## SEQUENCE DESCRIPTION:

GATCACCCGG GGCTGTCTGC ATACAGACTT CTCAGGGGAG TTCTCAGCTT GGACCCCTTAT 60  
 CTCCCAGAA TCCTGGAACC TGCTCCTTCT GCTCTCGTGA CTGACTGTGT TCTCTATGCA 120  
 ACTTCCAATA AACCTCTTC ATTTGAAAGG AAA 153

SEQ ID NO:2470

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02840

## SEQUENCE DESCRIPTION:

GATCTTAAGC CCAGCTCTGT TCTGCCCCG CTTTCCTCTG TTTGATACTA TAAATTTTCT 60  
 GGTTCCTTG GATTTAGGGA TAGTGTCCCT CTCCATGTCC AGGAAACTTG TAACCACCCT 120  
 TTTCTAACAG CAATAAAGAG GTGTNCTTGT CAAA 154

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SEQ ID NO:2471

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02843

SEQUENCE DESCRIPTION:

GATCACAGGC CTTGCTTTTG TAACAATGAT GACCCCGGCC TGTCTCATAT TCTGAAGAGG 60  
 AAAAGTCAAA GTGTTGCTGN GGCTCCATAT TTCAACTAAA AATATATCTG TTGGAGAAAAG 120  
 AAATTAACAA TAAAGAATTT TCATAGGTTA AA 152

SEQ ID NO:2472

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02844

SEQUENCE DESCRIPTION:

GATCGTATTC CCTGCTTTAA GGAACGTGNTA GNCTTGTTTG GGTGATGAGA CAAAGTTCTT 60  
 GAGACATTTA AACTGTATTT ACCAGTGTGA AAAATGTCAT TTATGGAGAT TAATTCATTA 120  
 TGGAAATAAA ACATTGCCTA AGCCCTTGAA A 151

SEQ ID NO:2473

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02845

SEQUENCE DESCRIPTION:

GATCCAATCA GCTGTAAGTN TTAAGCACAG GGCTGAGGCT CCCTCCAAGT ACCCACTGGG 60  
 AACAGCAGCT TCAACCTGAG CCCTGNGTCC CAGCCAGCCC CCACAATCAC CTATGCCCCAT 120  
 TCTTCAGAAT ACATTGGATG CATGTGCAAA 150

SEQ ID NO:2474

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02846

SEQUENCE DESCRIPTION:

GATCCAGAGA GTCTGAAGAC ATTTCTNATG CCTTTATATA TTGGAGAACC CTTCCCCATT 60  
 TTNATATCCT TTCTTCAAAA ATCTAAATNA TGTGCCTAAA AATAAGACAT GGCATAATAA 120  
 GGTATAATTA AAGAGATAAT AGAATGAAA 149

SEQ ID NO:2475

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02847

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## SEQUENCE DESCRIPTION:

GATCCAGTAC CTGAAAGATT TGATAGAAGA GGTCCGCAAG GCAAGGGGGA AGAAAAGGGT 60  
 CCCCTAGTTG AGGATAGTCA GGAGCGTCAA TGTGCTTGTA CATAGAGTGC TGTAGCTGTG 120  
 TGTTCOAATA AATTATTTTG TAGGGAAAGT AAA 153

SEQ ID NO:2476

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02848

## SEQUENCE DESCRIPTION:

GATCCTTTTG GAGTCAGACA GATGTGGTTG CATCCTAACT CCATGTCTCT GAGCATTAGA 60  
 TTTCTCATTT GCCAATAATA ATACCTCCCT TAGAAGTTG TTGTGAGGAT TAAATAATGT 120  
 AAATAAAGAA CTAGCATAAC ACTCAA 147

SEQ ID NO:2477

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02849

## SEQUENCE DESCRIPTION:

GATCTCCAGT GATTGGCGAT TTGACCTGGT TTCTNCCTGG ACTATTTGAA TGGGTGGATT 60  
 TGTGGGTGCA TCTCTGTCT TCTTTCCTTT TCCATTCTCC TNTATTNTN TATTACATA 120  
 CTTGTATGCA ACTNTGTAAT CTGATTNCCC CATGTAACAT TNTAATTGA NGGGTGGTCT 180  
 GCGTGTNCAC TGGAAAACAT ATNTATN 207

SEQ ID NO:2478

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02850

## SEQUENCE DESCRIPTION:

GATCGAGCTC ACAGGGGGCA CCCATCCTGN TAGTCAACAG AGTCTGAAGC AGTCAGGGTG 60  
 TTGGATTCTT CTGTTGTTGT CATCAATTCC TGCTGAGGGG TTTCTGGGGT TTTGTTTTTA 120  
 ATAAATAACT CCTTTGTAGC CTAAAA 146

SEQ ID NO:2479

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02851

## SEQUENCE DESCRIPTION:

GATCCCGGCC AGCCAGGTGA CCCCCACGCT CTGGATGTCT CTGCTCTGTT CCTTCCCCGA 60  
 GCCCCTGCC CGGCTCCCCG CCAAAGCACC CCTGCCACT CGGGCTTCAT CCTGCACAAT 120  
 AAACTCCGGA AGCAAGTCAG TAAA 144

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SEQ ID NO:2480

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02852

SEQUENCE DESCRIPTION:

GATCCAGGCA AATTCATGTT CTTTCTTTGT AACTCACTTT CTTCGTCAAC ATTTCTGTGA 60  
CTCAATGGAT AGCATATTTT CATCAAGTAG CACGTATAAC GTGATGCTTT CATGTTTCTG 120  
CCTTAAATAA AATAACCCTC AAA 143

SEQ ID NO:2481

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02853

SEQUENCE DESCRIPTION:

GATCTCTTTG ACTGCTGTAG TACTAAAGTG TACTTAATGT TACTANGTTN AATGCCTGGC 60  
CATTTTCCAT TTATATATAT TTTTAAAGAG GCTAGAGTGC TTTTAGCCTT TTTTAAAAAC 120  
TCCATTATA TTACATTTGT AACCATGATA CTTTAATCAG AAGCTTAGCC TTGAAATTGT 180  
GAACTCTTGG AAATGTTATT AGTGAAGTTC GCAACTAAAC TAAACCTGTA AAATTATGAT 240  
GATTGTATTC AAAAGNTTAA TGAAAANTAN ACATTTCTGT CCCCTGAAA 290

SEQ ID NO:2482

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02854

SEQUENCE DESCRIPTION:

GATCTGATTG AGATGTACAT AGTTTTTTTT TTTACCATAA CTGAATTATT TNATCTCTTA 60  
TGTTAACATG AGAAATGTAT GCCAAATNAT TAGTTGATGT ATGTTTTTNA ATTAAATATT 120  
TAAATAAAAT ATTTGGAAGG AAA 143

SEQ ID NO:2483

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02855

SEQUENCE DESCRIPTION:

GATCCTTATC AGGGAGAGCA GGAATCCTTA TTCCCGGTGT CGCTAGTACT CATCTCTGCC 60  
GCCTCCTGTC TGCCCCCAGG CTGCTGCTNC TGCTGCCCTG TGGGTTGTGC CAAGTGTGCC 120  
CAGGGCTGCA TCTGCAAAGG GCGCTCGGAC AAGTGCAGCT GCTGCGCCTG ATGCTGGGAC 180  
AGCNCGCTCC NAGATGTAAA GAACGCGACT TCCACAAACC TGGNNTNNT TATGANCAAC 240  
CCTGACNGTN ACCGTTTGCN ATATTNCNN 269

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SEQ ID NO:2484  
 SEQUENCE LENGTH:140  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02856  
 SEQUENCE DESCRIPTION:  
 GATCATACAT TTTATATGGT TGGGACTTCT CTCTTCGGGA GATGATATCT TGTTTAAGGA 60  
 GACCTCTTTT CAGTTCATCA AGTTCATCAG ATATTGAGT GCCCACTCTG TGCCCAAATA 120  
 AATATGAGCT GGGGATTAAA 140

SEQ ID NO:2485  
 SEQUENCE LENGTH:139  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02857  
 SEQUENCE DESCRIPTION:  
 GATCCAACCC CACCCTCCTG GGTGCGGCCA GAGGCAAGGC AGTCGCCCCG GCTCCTGAAT 60  
 CCCAAGAATG GTTCTGGCAA GTACTGCTGT TTGTTGTAG GGGCAAAGAG TTAAAAATAA 120  
 ACGAGGTTCT GCCATGAAA 139

SEQ ID NO:2486  
 SEQUENCE LENGTH:139  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02858  
 SEQUENCE DESCRIPTION:  
 GATCTGCCGG CTCCCGTCCA GCCTGTGTGG AAAGGAGGCC CACGGGCACT AGGGANNCNG 60  
 AATTCTACAA TCCCGCTGGG GCGGCCGGGT CGGGAGAGAA AGGTGGTGCT NCAGTNGTGN 120  
 CCCTGGGGGG TCATTGAN 139

SEQ ID NO:2487  
 SEQUENCE LENGTH:138  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02859  
 SEQUENCE DESCRIPTION:  
 GATCTTCAAT GCCTCTGAGT CATTGTTATA AAAAATCAGT TATCACTATA CCATGCTATA 60  
 GGAGACTGGG CAAAACCTGT ACAATGACAA CCCTGGAAGT TGCTTTTTTT AAAAAATAA 120  
 TAAATTTCTT AAATCAAA 138

SEQ ID NO:2488  
 SEQUENCE LENGTH:231  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02860

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## SEQUENCE DESCRIPTION:

GATCATGGTT CTCTTTGTAC GATAGTTGGG CATCTGTATT TCCACTTGTG TGAATTTGCC 60  
 TTAAATTTT GGTTATGGGT TTCACCTTTT AAAATAATCA AACATATTTA TCTTTTCCTG 120  
 TGTGATAGGT TTTTNCCTGT ATCTTTTCCT GTTAAACACA CAGACCCCTC CCAATCTGG 180  
 ACATTGAATA CNTATTCATT TTCCTTTGCN NNAATANNCC NNANACANAC N 231

SEQ ID NO:2489

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02861

## SEQUENCE DESCRIPTION:

GATCTGCCCC TGCATTGTAG CTTGCTTAAC GGAGCACTTC TCCTTTTCC AAAGGTCTAC 60  
 ATTCTAGGGT GTGGGCTGAG TTCTTCTGTA AAGAGATGAA CGCAATGCCA ATAAAATTGA 120  
 ACAAGAACAA TGATAAA 137

SEQ ID NO:2490

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02862

## SEQUENCE DESCRIPTION:

GATCTTTAAA TTTTGAGACA GTATAAGGAA AATCTGGTTG GTGTCTTACA AGTGAGCTGA 60  
 CACCATTTTT TATTCTGTGT ATTTAGAATG AAGTCTTGAA AAAAAGTTTA TAAAGACATC 120  
 TTTAATCATT CCAA 135

SEQ ID NO:2491

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02863

## SEQUENCE DESCRIPTION:

GATCCAAATA TTTTCAAGCC ATGTAATCCA TTGGTTTTGT GGGCAGTTTA ATAAACCTGA 60  
 ACCTTTGTGT GTTTTCTAAT TGTACCTGAG TTGACCATCC TTTCTTTTA NAGTATATTT 120  
 CTNGTATGAT ATTNTGTAAA GCTCTCACCT GGTCTTTTA TGGGGACTTT TCGTTTTTGG 180  
 GCAACTGCAG TGTATTTATG TGAANCTTTA TANGAGAATT ANTTTTTCCA TGTGCATATT 240  
 AATATGGTNC CTCCACACAT GGNNAGGGCA CAGTGGCTTC GTGTTN 286

SEQ ID NO:2492

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02864

## SEQUENCE DESCRIPTION:

GATCATGCCT CTTTCCAACA CGTGTTTACA ATCTCAAAG-GGACTGTATT TNTNCTCTGT 60

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GCTTAATNTG ATTTGAAATA TGTGAATCA AAGTGAAATA TTTATNTTTT GAATAAAGGA 120  
GATAATAGCC TTAAG 135

5 SEQ ID NO:2493  
SEQUENCE LENGTH:135  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02865  
10 SEQUENCE DESCRIPTION:  
GATCGAAAAC AAACGNTAGA TAATNCCCAA GGAGCTTACC AAGAGGCATT TNATATAAGC 60  
AAGAAAGAGA TGCAACCCAC ACACCCAATC CGCCTGGGGN TTGCTCTTAA CTTTCCNGTA 120  
TTNACTATG AGATN 135

15 SEQ ID NO:2494  
SEQUENCE LENGTH:135  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS02866  
SEQUENCE DESCRIPTION:  
GATCATGCCA CTNCACTCAC ACTGACACTG CCTCGGACAA CAGAGCAANA CTNCATCTCA 60  
AAAACAAACA AAAAAAATCA CAGNCTCATT TTAAAGGAGC AGCAACCNA CCAAATACAA 120  
25 NCTTCATTG ACAAN 135

SEQ ID NO:2495  
SEQUENCE LENGTH:134  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS02867  
SEQUENCE DESCRIPTION:  
GATCATTAAAC ATGCCAGGGC AGTTCCCACT GATTTAGATG GTCCAAGATA ATCTCATTCA 60  
35 GGAGGCTTGA AACATTAATG GTTTAGTCTT GTGAATTTTA ACAGTTCTCT GTCATCGTTT 120  
AACAAAACCA ACAN 134

SEQ ID NO:2496  
SEQUENCE LENGTH:134  
40 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02868  
SEQUENCE DESCRIPTION:  
GATCATGCCA CTGGACTCTG TGCTGAGCAA CAGAGTTAGA CCCTGTCTCT AAATAAATAA 60  
45 ATAAACAAAT AAACAGTAAA AAAATGTATA GTTCAATCCT TATCTGTATT AAACCTCCTT 120  
TAACTTGTGT GAAA 134

50 SEQ ID NO:2497  
SEQUENCE LENGTH:133

55

SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02869  
5 SEQUENCE DESCRIPTION:  
GATCACATGT GGGCCCGTGT CTGGCCGCCG CCGCCCGGCC CCGTCCCTGC GGNCACCACC 60  
TAATTTATTG CCGTGCCTCC TGCTGCTGTG ACTGCTTTTG TACCTTTGCA ATAAAGAATT 120  
TTCTGGTTTC AAA 133

10  
SEQ ID NO:2498  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
15 CLONE:HUMGS02870  
SEQUENCE DESCRIPTION:  
GATCCTGGAC ATATTTTATA TTTATACCAA ATATTTTATA TATTNCTAC TGTTGTCAAT 60  
GGTAGTGGTT TTTAAATTTT CAAACATTCA TTACTAGTAT ATAGAAATAN AATCACTTTT 120  
20 TAAAAATGTA AA 132

SEQ ID NO:2499  
SEQUENCE LENGTH:131  
SEQUENCE TYPE:nucleic acid  
25 TOPOLOGY:linear  
CLONE:HUMGS02872  
SEQUENCE DESCRIPTION:  
GATCCTGTTT TTTCTTAACA AGTTGAGGCG TGGGTAGAGC AGGAATTGGT TTTCCAGCAT 60  
30 TGTGTCCGTA AACCTGAGTT AGAATAAGAT GTAACGGAAG CCACGATAAA GACTCGGTCA 120  
AATCCTGCAA A 131

SEQ ID NO:2500  
SEQUENCE LENGTH:133  
SEQUENCE TYPE:nucleic acid  
35 TOPOLOGY:linear  
CLONE:HUMGS02873  
SEQUENCE DESCRIPTION:  
GATCCTGGAT GGAAGTGGCT TCTTTATCGA GAAGAATATA ATTCTCCATG AGGACTTAAT 60  
40 GAATCCAAAC CTGTGTCATG CCTGGTTTGC ATACCCAATT AAACACTNGA AATAAAAATT 120  
NTTNGGGTNN AAA 133

SEQ ID NO:2501  
45 SEQUENCE LENGTH:130  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02874  
50 SEQUENCE DESCRIPTION:  
GATCTCTGCT CTTTGTGAGA GATTTGCAAA GACTCACGTT TTTNTTGTTC TCTCATCATT 60

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CCATTGTGAT ACTAAGAAAC TAAGAAGCTT AATGAAAAGA AATAAAATGC CTATGTTGTT 120  
GTTCTAGAAA 130

5 SEQ ID NO:2502  
SEQUENCE LENGTH:130  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02875  
10 SEQUENCE DESCRIPTION:  
GATCAAAAAA GGCAGATGNA ANTACTTAAN ACTCAGTGTT TTGGAGAGAT TTCCTTTNAG 60  
TTTGTGTTGTT GGCTGGTTTG AACGATAGAA ATATGCAGCA TGCAATATAT GCTTATATTT 120  
NATTTNAATN 130

15 SEQ ID NO:2503  
SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS02876  
SEQUENCE DESCRIPTION:  
GATCCCCCAG CTGGCAGAGG ACCCAGTACA AAATAGGCAC TCAATAGATG TTACACCAAC 60  
TTTGGAAGGG CAAACATATT TCTTAATGAG AGGCAGTCCT TCATGTTTTN CAATAAAATG 120  
25 ACTTTTAA 129

SEQ ID NO:2504  
SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS02877  
SEQUENCE DESCRIPTION:  
GATCTTCTCC GAGGCCACAC GAAGGTACTG AAGAGCCTCA CCTGGGGGCA TTTTGTGGGT 60  
35 GGAGGGCCAG AGTGTGTATA CCCAGGCTTG TCTGGAAGGA GAAGGCCTTT GCTGCCTGAA 120  
AGTCTCAAA 129

SEQ ID NO:2505  
SEQUENCE LENGTH:129  
40 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02878  
SEQUENCE DESCRIPTION:  
45 GATCTAAATA AGTGTTTTCAA GGAAAGTTTT CCTAAGCAAA TGTAATATTA CCTCATTTGG 60  
GCATCATTAC TCTGTTAATT CTATATCAAA GGAAATAAAC TTGCTACTTG CACTAAATGA 120  
AAAAACAAA 129

50 SEQ ID NO:2506  
SEQUENCE LENGTH:128

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02879

SEQUENCE DESCRIPTION:

GATCGTGCCC CGGGGCGCCG GCCCTGNAG GGGCTCACCT GGATGGGGCC TGCAGTGCGT 60  
TCCCGCTTTG CTCCTTCCC TGGACGGCCC GCTCCNGAA ACGCGCGCAA TAAAGTGATT 120  
CGCAGAAA 128

SEQ ID NO:2507

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02880

SEQUENCE DESCRIPTION:

GATCACTCTT GTGGTTTTGG GGGATGGCAT TATAAGAGAG GAGACTGGAN ACAGGGGGGC 60  
TATTGTNATG CAGATTTGTT GGATGTCCAC CCAGCATTCA CTTTNNCCAT CTTTGGCCAG 120  
GGGNNNN 127

SEQ ID NO:2508

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02881

SEQUENCE DESCRIPTION:

GATCCCACGC AGCGCTGAAC CGAACCGAGT AGGAAGCCTT TCTCCCCANG GCACGTGGCT 60  
TCAGGGCGTT TCCCATTTGAC CAAGTTTGAC CCGNTTTGA ATAAAGAGAA GTGCGTTTGG 120  
ATTAGAAA 128

SEQ ID NO:2509

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02882

SEQUENCE DESCRIPTION:

GATCGAGCTT CTCCTCTGAG TTCTAACAAA ATGGTGCTTT GAGGGTCAGC CNTTAGGAAG 60  
GTGCAGCTTT GTTGTCCTTT GAGCTTTCTG TTATGTGCCT ATCCTAATAA ACTCTTAAAC 120  
ACATTGAAA 129

SEQ ID NO:2510

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02883

SEQUENCE DESCRIPTION:

GATCTCTGAT TTAACCGTGT ACTATCCACA TGCATTACAA ACATTTTCGA GAGCTGCTTA 60

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GTATATAAGC GTACAATGTA TGTAATAACC ATCTCATATT TAATTAAATG GTATAGAAGA 120  
ACAAA 125

5 SEQ ID NO:2511  
SEQUENCE LENGTH:124  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02884

10 SEQUENCE DESCRIPTION:  
GATCTTCCAT CTCCTCAGCA AAAAAATAGG AGCCCTGGCC CCCCAACTTT TTNCANAGTA 60  
ATAGCCTTAN TTCCTTCCCT ATCTCCTTAC CAAAGTACAN GTNACATCTT TCCCACCTTT 120  
CNTN 124

15 SEQ ID NO:2512  
SEQUENCE LENGTH:124  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS02885

SEQUENCE DESCRIPTION:  
GATCTACAGA TTCAATGCAA TTNCTATTAA AATCTNATCT GGCTTTTTTT GCATAAGCAA 60  
CAAAGGAAAA ANTAAGACAT CAAAATTNA AGANCTTTTG TCCTACAAAC AATATCATGA 120  
25 NGAN 124

SEQ ID NO:2513  
SEQUENCE LENGTH:343  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS02886

SEQUENCE DESCRIPTION:  
GATCAGAAAA TTCATATTTA AGCAAAGTGA TACAAACACA GTGATTGTTGGG AATGCCTTCA 60  
35 TTTACAATGC AATACTTAAA TTTTAATACT CTTGTAGGAG AAAAAGCAAC TGTATAAATG 120  
AATGTAGAGT GACTTTCTGC AATATTTCAA ACCTATATCA GAGAATTACA CTGTGGGAAA 180  
NCTACCATTG TAATAAGTGT AGCAAAATCT CCTTAGATAT CTGAAAAGTC ATACTGGATG 240  
GAATCTGTAG GAAACGGTTC TATTTTGAGG GAAGGGGGAT TCCTTTTTGT TTTTAAAGTG 300  
AATTCAGAAA ATGTTATAAA TAANTCTTTT GGTTTATTAT AAA 343

40 SEQ ID NO:2514  
SEQUENCE LENGTH:123  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
45 CLONE:HUMGS02887

SEQUENCE DESCRIPTION:  
GATCTNTACC CCACCCCTAT CTAACACCAC CCTTGGNTCC CACTCCAGCT CCCTGTATTG 60  
50 ATATAACCTG TNAGGCTGGC TTGGTTAGGT TTNACTGGGG CAGAGGATAG GGAATCTNTN 120  
ATN 123

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SEQ ID NO:2515  
SEQUENCE LENGTH:121  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02888  
SEQUENCE DESCRIPTION:  
GATCCAAAAT TACCTTCCTA TTGCATTTCC TACTCCTTTG CTACGNGTAT TGGACCTCTG 60  
GCCAAATNAC AAAAGATGTA CTCTTTGTNC TCTAAAACCA CACTAAAGTT TTCTNACTNN 120  
N 121

SEQ ID NO:2516  
SEQUENCE LENGTH:122  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02889  
SEQUENCE DESCRIPTION:  
GATCAACCAA CCTTAAATAT ATGTATGTAT ATATGTATAT GTGAAAAACA GTTTGTATAG 60  
TTGGAATATT TGTNTTTGTA ATTACTTGTG ATGTTTTAAA ATAAAANTTT TATTCAGTTA 120  
AA 122

SEQ ID NO:2517  
SEQUENCE LENGTH:122  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02890  
SEQUENCE DESCRIPTION:  
GATCTGGCAC CCCCTGGGTG GAGTGTCCCT CGGGGGCTTT GGGAAAGCAT GGCACCCTCA 60  
GACCACACAG TAGCCAAGTT CTGGAGCAAA TAAAAGGCCT GTGTTATNTC TTGTNCTTGA 120  
AA 122

SEQ ID NO:2518  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02891  
SEQUENCE DESCRIPTION:  
GATCTCAAAG ATATGCACCA GTTTGAATAA ATGCTTGTTT AAAGATTAAA TTTTACAATT 60  
CATTTTAAAT TNTCATTTTG TGACAATATT TCTAAACAAC GNCCATTTTA ATNACCAAA 119

SEQ ID NO:2519  
SEQUENCE LENGTH:118  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02893

## SEQUENCE DESCRIPTION:

GATCATAGGA TAGCTGACTT TGACAGTCAC ATTTATAAAG TAATTCACCT AAAGATATAT 60  
ATTTTTTTCA AACAAGTTTT GCTACTTTTG AAAATAAATC TTTCTTTATA TTGCTAAA 118

SEQ ID NO:2520

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02894

## SEQUENCE DESCRIPTION:

GATCCAAACC CATCTTCCTG GACCTGAAGC TTATGCTTCC AGGCACCCCA CTCCTGAGCT 60  
GAATAAAGAT GATTTAAGCT TAATAAATCG TGAATGTGTT CACATGAGTT TCCATAAA 118

SEQ ID NO:2521

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02895

## SEQUENCE DESCRIPTION:

GATCTGCACA GTGTTATGGC ACCCTACTTC CTGCAGCAAC GGGACACNCT GCGGCGCCAT 60  
GTNCAGAAAC AGGAGGCCGA GANCCAGCAG CTGGCAGATG CCGTCCTNNC AGGGCGGN 118

SEQ ID NO:2522

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02896

## SEQUENCE DESCRIPTION:

GATCCTATCT TTNCTGGCAG GACTGGNAGC CATGGTGGGC TACGTTNTGN TCAGCGGCAT 60  
TNTTCCATC CAGCGGGCAA CGCTGCTCGG GCCCCAGGCA CCCGGACCCT GGGCATGN 118

SEQ ID NO:2523

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02897

## SEQUENCE DESCRIPTION:

GATCTAGTCC GGACTTGCTG TGTATATTGT AACGTAAAT GAAAAAAGAA CCCCCCTTTG 60  
TATTATAGTC ATGCGGTCTT ATGTATGATN AACAGTTGAA TAATTTGTCC TCAGAAA 117

SEQ ID NO:2524

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02898

## SEQUENCE DESCRIPTION:

GATCGTNATT NAGAATCCAT GTGAATAGAC CTGCGATGGC CAAGGCTGTT TAAGCNACAC 60  
TGGGTTGGAA ACACTTGGGC TCTCTCATNA TTATTAAT TCTATTCAA TCTAAA 116

5  
SEQ ID NO:2525

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10  
CLONE:HUMGS02899

## SEQUENCE DESCRIPTION:

GATCCTTTGC NTTCAAGACT AAGTTAATAG AGAAGATGTT TGTAACNTG GCCCAAGCTT 60  
GGNCTCCAG TGTATTGAAG CTAACCTCTT TNAGAAGCAC CACTCTCATA TATNAN 116

15  
SEQ ID NO:2526

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20  
CLONE:HUMGS02900

## SEQUENCE DESCRIPTION:

GATCTCTGGG TAAAGAGGCC GTTTATCTTT GTAAACACGA AACATTTTC CTTTCTCCAG 60  
TTTTCTGTTA ATGGCGAAAG AATGGAAGCG AATAAGTTT TACTGATTTT TGAGAAA 117

25  
SEQ ID NO:2527

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30  
CLONE:HUMGS02901

## SEQUENCE DESCRIPTION:

GATCTAGGAA GACTTTGGAA AGAGTAGGAA GACTTTGGAA AGACTTTTC AACCTCATC 60  
ACCAACGTCT GTGCCATTTT NTATTTTACT AATAAAATT AAAAGTNTG TGAATCAA 119

35  
SEQ ID NO:2528

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40  
CLONE:HUMGS02902

## SEQUENCE DESCRIPTION:

GATCCCCAGG AGGCCTGGNC CGCCCAGAGG CTCCTCTCAG GCTGGGCCCC GACGTTTGCG 60  
NCAGTGTTCC TTGTGCCCGT GGGGCCGGA GCNAGTAAAG TCTGGGCCAG GCAA 115

45  
SEQ ID NO:2529

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50  
CLONE:HUMGS02903

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## SEQUENCE DESCRIPTION:

GATCACGTTT CAGGGTCCTC CAAAANGCTA GCCCGGCACT AACTAGGGA ATTCNCCCT 60  
CTCCTGTCAC TTGTCATGGT CTCCTTGGT ATTAAAGGCC ACCATTGCA CAAACAAA 119

SEQ ID NO:2530

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02904

## SEQUENCE DESCRIPTION:

GATCCAGAA ATGTAGCTTG TTTCATATTT TAGTCTTCTT ATTTTGTAA AATGTGTAGA 60  
ATTTGCTGTT TTTNTTTTTC TTTTGACAAC TCAGGAAGAA ACTGACCTCA GAAA 114

SEQ ID NO:2531

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02905

## SEQUENCE DESCRIPTION:

GATCAGCCCC CAAAGAAATG GGGGTGCATG CTGGGCCTGG CCCCCTGGCC CACCCCACT 60  
TTCCAGGGCA AAAAGGGCCC AGGGTATAA TAAGTAAATA ACTGTNTGT ACAGCCAAA 119

SEQ ID NO:2532

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02906

## SEQUENCE DESCRIPTION:

GATCTTGGCT TCTCAACAGG GCAAAGATAC CAGGCCTNCT GCTGAGGTCA CTGCCACTTC 60  
TCACATNCTG CTTAAGGGAG CACAAATAAA GGTATTCCGAT TTTTAAAGAT AAA 113

SEQ ID NO:2533

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02907

## SEQUENCE DESCRIPTION:

GATCAAAATG TTTGAAGAAA GGAACCTTAT TTTTGCAAGT TACGTACAGT TTTTATGCTT 60  
GAGATATTTT AACATGTTAT GTATATTGGA ACTTCTACAG CTTGATGCCT CTGCTTTTA 120  
TAGCAGTTTA TGGGGAGCAC TTGAAAGAGC GTGTGTACAT GTATTTTTTT TCTAGGCAAA 180  
CATTGAATGC AAACGTGTAT TTTTTTAATA TAAATATATA ACTGTCTTTT TCATCCCATG 240  
TTGCCGCTAA GTGATATTTT ATATGTGTGG TTATACTCAT AATAATGGGC CTTGTAAGTC 300  
TTTTCAACAT TCATGAATAA TANTANATAT GTACTGCTGG CATGNAAA 348

SEQ ID NO:2534

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

5 CLONE:HUMGS02908

SEQUENCE DESCRIPTION:

GATCTGATGG TTTTAAAAAT GGGAGCTTCC CTNCACAGAC TCTNTCTCTC GTGCCGCTGC 60  
CATGGCCATG TAAGNAGTGC CTTNACCTT CCCCCGTGAT TGTNAGGCCT N 111

10

SEQ ID NO:2535

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS02909

SEQUENCE DESCRIPTION:

GATCCCAACA GGACAAATCT GTGTACCTAT CTTTCTATCC TCCCTGAGCC TGTACCAACT 60  
AGATTCTTCA TATGTATTTG TAACAGATTA AATTGGAAAG CAAACACAAA 110

20

SEQ ID NO:2536

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25

CLONE:HUMGS02910

SEQUENCE DESCRIPTION:

GATCCCAAC TGCTCCAGCC TCTGCCAAC TGAATCTTCA GCATGTTCTC ATCGGCGGAC 60  
TNTCTTGTGT AATGTAACT GTGCCATGTT ATTAATAAAT GTGAACTAAA 110

30

SEQ ID NO:2537

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35

CLONE:HUMGS02911

SEQUENCE DESCRIPTION:

GATCTGTTTG GAAAACATAG ATTGTTTTCC CCTCAAATAA GGGGAAAAAA AAANACCCCTT 60  
TNTNCAAATN GNTTCTTTTG TAAAAAATTA TTTTAAAGG AAATCACAAN 110

40

SEQ ID NO:2538

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45

CLONE:HUMGS02912

SEQUENCE DESCRIPTION:

GATCTTTTGA ACTCTACTGT GTCATTAAGA TGCTTTGTAC AATGCCAAAC CATAGTTGGA 60  
GAAACTAAGT TTAATAAATA TCAAATAGAT TTTCTGTATT AAAGTAAA 109

50

SEQ ID NO:2539

55



SEQUENCE LENGTH:109  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02913  
 SEQUENCE DESCRIPTION:  
 GATCTCCCCC ACCCTTGGAT TAGAGTTCCT GCTCTACCTT ACCCAGAT AACACATGTT 60  
 GTTTCTACTT GTAAATGTAA AGTNTTTAAA ATAACTATT ACAGATAAA 109

SEQ ID NO:2540  
 SEQUENCE LENGTH:109  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02914  
 SEQUENCE DESCRIPTION:  
 GATCTCCTNT CCCTCACTCA GTGCACGGGA CAGCTNCTCC TCCGTCACAG CTTTGGNATG 60  
 AAAGACAGAA GACAGCATGA TTGGCCTCAC CCACGTGCAG GNCAATNN 109

SEQ ID NO:2541  
 SEQUENCE LENGTH:107  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02915  
 SEQUENCE DESCRIPTION:  
 GATCTGTCAC TCAACTTGCT GCGTNACCTG AACACGTCAC TTTACCTCTC TGTGCCTCAG 60  
 TTTTCCCATG CATGAAAAAT AAAATAAAAT AAAACGGGGA TTCTAAA 107

SEQ ID NO:2542  
 SEQUENCE LENGTH:112  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02916  
 SEQUENCE DESCRIPTION:  
 GATCAGTAAG GATTTACCT CTGTTTGTA CTAAAACCAT CTACTATATG TTAGACATGA 60  
 CATTCTTTT CTCTCCTTCC TGAAAAATAA AGTGTGGGAA GAGACAAATA AA 112

SEQ ID NO:2543  
 SEQUENCE LENGTH:109  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02917  
 SEQUENCE DESCRIPTION:  
 GATCATAGAA GGTGGGGTT CCAGAAAGGC ATCTGTGTGA TGGTTCCATT GATGTGGGAT 60  
 TTCCCTACTT GCTGTATTCT CAGTTTCTAA TAAAAAGAAC CAAATNAAA 109

SEQ ID NO:2544

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02919

SEQUENCE DESCRIPTION:

GATCCAGGAG ATANTTTTTT CATTCATCCT GACCAAGACT GAGCCAGCTT AGCAACTNCT 60  
GGGGAGACAA ATNTNAGAAC CTTGTCCCAG CCAGTNAGGA TGACAGTN 108

SEQ ID NO:2545

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02920

SEQUENCE DESCRIPTION:

GATCGAGCCC AGCGTACAAC TTCCTCAAGT CGCCCAAAGA CAACGTGGAC GACCCACGG 60  
GGAACTTCCG CAGCGGGCCC CTGACGGGGT GGCGGGTGTT CCTGCTGCNN NNGTGCCTC 120  
TCCTGGGCAT CGTTGTCTGC GCCGTGGTGG GGGCCGTGGT GTTCCAGAAG CGGCAGGAGC 180  
GGAAACAAGCG CTTCTACTGA GTGGCGCCTC CGGCGGTGGC CTGTCCCTGG GCCCAGGAGC 240  
CAATGTGAAC TTTTGTGGNT ACCGGGATTA TAAANGAACA ACAAGATGAC CTTATTTCTT 300  
AACTGTTTCA AATAAAATGA TTAAGATAT TTTCAAAAAA AGN 343

SEQ ID NO:2546

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02921

SEQUENCE DESCRIPTION:

GATCCTGCCG TGCCCCATC CTGGCTGTTG GGGGTGTCCT GAGCCACCT NNNTNCGCCT 60  
GTTCCCTTCA GCCAACCCGT TTCTGCAGTA AAATTAAGCC TGTCAAA 107

SEQ ID NO:2547

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02922

SEQUENCE DESCRIPTION:

GATCACTGAA CCAGACACAG CATTGCTGAC ACATGAGACT AACACGTGCA ATTATTTAAA 60  
AAGATTTCAA TAAACTNCC TGGCTGGCTC CGGGCCGCC CTAAA 105

SEQ ID NO:2548

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02923

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCCTGTGG GTTAGTATC ATTATCTTCA GCTCTTTGAT ACNCTGTGTT AGAGTAATAG 60  
CTAAAGGAAG TTCATGTCAA TAAATTCATA CTTATATCAC AAA 103

5 SEQ ID NO:2549  
SEQUENCE LENGTH:104  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02924  
10 SEQUENCE DESCRIPTION:  
GATCCAGAGC TGGGGTGGAA GGAGAGCCAT TCTGAACGNC ACGNCTGGCC CGGTCAGTGC 60  
TGCATGCACT GCATATNAAA TAAATCTGC TACACGCCAG GAAA 104

15 SEQ ID NO:2550  
SEQUENCE LENGTH:103  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02925  
20 SEQUENCE DESCRIPTION:  
GATCCNAGG CTCTGTTCCA TGAGCCTGTT GCANGTTTGT GTACTTTAGA AATGTAACTT 60  
TTTGCTCTTA TAATTTTATT TTATTAAATT AAATTACTGC AAA 102

25 SEQ ID NO:2551  
SEQUENCE LENGTH:102  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02926  
30 SEQUENCE DESCRIPTION:  
GATCGATGAG GCAGGTCAGT TGTAAGTGAG TCACATTGTA GCATTAAATT CTAGTATTTT 60  
TGTAGTTTGA AACAGTAACT TAATAAAGA GCAAAAGCTA AA 102

35 SEQ ID NO:2552  
SEQUENCE LENGTH:102  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02927  
40 SEQUENCE DESCRIPTION:  
GATCATATCT AGTNTNAAA TCTCTAGGAA CAATAGAGAT TATATCATAA CTCTGAAGAT 60  
GGACTCTAAA CTTTGGTTTA CCTCCATGGA AAATAANCGN NN 102

45 SEQ ID NO:2553  
SEQUENCE LENGTH:101  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02928  
50 SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

GATCGAATGA GGGTTAAATG AATTATTTCA TGTAAAGCTC TTAGCCCTGT GCCTGGTACA 60  
TAGTAAATNC TAAATAAATA GTGGTATTCT TACTGTTTAA A 101

5 SEQ ID NO:2554  
SEQUENCE LENGTH:390  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02929  
10 SEQUENCE DESCRIPTION:  
GATCCAGCTT ATTCTTTTAT TTTCAAGTCC ATTCTTGGGG CTGGTGGGGA GGCAGGAGAA 60  
TACCCCTCCC TAAGCCCTTA GTGTGTGCCG AGCTTGCTTT NTGATGTTGG CAGGGGAGGG 120  
GAGACCTGGG TGGTGNCTGA GTTCCCTTTA TCAAACCCTT CAATGGGCAC AAAATTGAGT 180  
15 GCTTNNTTNN TAGGTTTTAT TTNNNNATGA ATGTCCAAAT CTGTGTTTCC CCCTGCCANA 240  
ACAGACTGTG TGGCCAGTTG AAAGTGTCTT GGTTTGTGGT TCATCTCTCC CTCATTTTCT 300  
TGGAGGCAGG GCCTGAGANC CCTGNCANAA TCTCCTATGG TTNTGAATCC ACGGCTTCTT 360  
TTTGGACATT AAAGGTTGAT TTGATGCAAA 390

20 SEQ ID NO:2555  
SEQUENCE LENGTH:227  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02930  
25 SEQUENCE DESCRIPTION:  
GATCTATCCT CAGCACTGCT GAGTGTGCAG TCACACTTTC CTACCAACCC NCTTCTTACC 60  
ATCTCTAGCT GCCATTTGTG GGGGGAACAA AACAAGGGAA TCCTGATTGT GTACAGTATA 120  
AATTGTATTA TATTTTTTGT ACTTATGTTT TATGTAAATA GTTTGTCTCA TTCAATTGTA 180  
30 TGTGAGCATT GAAATAAATC CTACCATTTA GGGGAAAAAA ATNNAAA 227

SEQ ID NO:2556  
SEQUENCE LENGTH:106  
35 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02931  
SEQUENCE DESCRIPTION:  
GATCTTCAAA AATAATGCCT CTGTCTAGCA TGCCAACAAG AATGCATTGA TATTGTGAAC 60  
40 ATTTGTGATA TATGTATTAA TAAATAGAGC AATTACAAGC AGCAAA 106

SEQ ID NO:2557  
SEQUENCE LENGTH:99  
45 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02932  
SEQUENCE DESCRIPTION:  
GATCTTTCTT ACACAGTGAT TCATTCTCT ATTTGTACAG TGGCTTTATG AAATATTGTG 60  
50 AATTGATACT GTAATCAATA AAGTGCTTTT AACCAGAAA 99

55

SEQ ID NO:2558

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02933

SEQUENCE DESCRIPTION:

GATCCTGGTT CCCTGTTTGG AAAATTCACC ACCTCTAGCT CCTCACTGTT CTTTGTAATT 60  
AACACGCTGT TGGTAATCTT ATTAATTATT TAACCAAA 98

SEQ ID NO:2559

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02934

SEQUENCE DESCRIPTION:

GATCTGGGGA CCCTGACTGC ACAGAACAGT GGGCGCNTTA CAGACCACCG ACCGCCCAGAG 60  
GGTGAATTAC ATCTTAATAA AGCTACTGTG AGAGAAA 97

SEQ ID NO:2560

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02935

SEQUENCE DESCRIPTION:

GATCGCCGCC AACATCCAGG CTGACTACTT GTATCGGTGA CGCCCCACCG GCCCGCAGCC 60  
CCTGCTGCCC AATAAAACCA CTCCGACCCC AAA 93

SEQ ID NO:2561

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02936

SEQUENCE DESCRIPTION:

GATCATCCCT TGACAGTAGT TTGCTTTCAT CTCACCTTTC ATTTGTCCA AANNCACCTA 60  
TATTTAATAA AGTCCCCCCC NGTNGTCTCA AA 92

SEQ ID NO:2562

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02937

SEQUENCE DESCRIPTION:

GATCCACAAA ATGAGACAAT GCATGTGAAA ATCCATGCTC ATGTTCTAAA CATGGAAACT 60  
AGGAGCCTAA TAACTTCCT AATTCAGTAA A 91

EP 0 679 716 A1

5 SEQ ID NO:2563  
SEQUENCE LENGTH:96  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02938  
SEQUENCE DESCRIPTION:  
10 GATCGTATTT TTATATCATA TTCACATATT TTTTTTTTA ATTGGTGTTA GATGACATGA 60  
TTAATAAAAA AGGCAAGATA TTTTCAGAAT TTGAAA 96

15 SEQ ID NO:2564  
SEQUENCE LENGTH:88  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02940  
SEQUENCE DESCRIPTION:  
20 GATCGCGCCA TCGCACTCTC AGCCTGGGCA ACAAGAGTGN AACTCCATCT CAAAAAATA 60  
AAAATAAAAT AAGTAAGNAA TACCTAAA 88

25 SEQ ID NO:2565  
SEQUENCE LENGTH:87  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02942  
SEQUENCE DESCRIPTION:  
30 GATCTAATAT ATATCATCAG AAAATATATA TTGTATGTTT ACTCTTATTT TCAGAAAGAG 60  
AAAATGAATA AAAATGATGA CATCAAA 87

35 SEQ ID NO:2566  
SEQUENCE LENGTH:87  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02944  
SEQUENCE DESCRIPTION:  
40 GATCGCTTGA NCCCAGGAGT TTAAAACCAG CCCGAGGAAC ATGGCGAAAC CCCATCTTTA 60  
CAAAAATAC AGAAATNAGC CAAGAAA 87

45 SEQ ID NO:2567  
SEQUENCE LENGTH:86  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02946  
SEQUENCE DESCRIPTION:  
50 GATCTAAGGG GTTGCCATGG TGTGAACAA TGCAACTTTT TATTTAAAAA AGCTCTGCAC 60  
TGCCATGTAT GAAAGTNTCT TTATGN 86

55

SEQ ID NO:2568

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02947

SEQUENCE DESCRIPTION:

GATCCNGGAT TGCTGGGAAT GGAAGCCAGG TGGGGTCATG GCACAAGTTC TGTAATCTTC 60

AAAATAAAAC TTTTTTTTGG TACAAA 86

SEQ ID NO:2569

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02948

SEQUENCE DESCRIPTION:

GATCCTGGCC ACTATGCCAG TTCTGACCTC GCATCCCCCT ACCCCGAGCC CATGCAGTCT 60

GGGAACATGC CGCCTTCTCT CCAAA 85

SEQ ID NO:2570

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02949

SEQUENCE DESCRIPTION:

GATCAAATTG TACTAGTGTC TGCAGGGTTT GTCAGTACTC GTCAAAGCCA AGTCCAATTA 60

AAAAAAAAAG TCTTTGCCCT CCAAA 85

SEQ ID NO:2571

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02950

SEQUENCE DESCRIPTION:

GATCTTTTCT TTAAAATTTC TCTGCACACA CAGGACTTCT CATTTTCCAA TAAATGGGTG 60

TACTCTGCCC CAATTCTAG GGAAA 85

SEQ ID NO:2572

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02951

SEQUENCE DESCRIPTION:

GATCTTTTAC CCCTTCACT CTTGGCTTTC TTATGTTGCT TTCATGAATG GAATNGAAAA 60

AAGATGACTC AGTTAAGGCA CCAAA 85

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SEQ ID NO:2573

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02953

SEQUENCE DESCRIPTION:

GATCTGCCTG ATGGGAGGGC TCCTGTCGAG GGAGACAGAC ATATCCCCAC TGAAAAATTA 60

ATAAAATTGG TTTTACATAT CAAA 84

SEQ ID NO:2574

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02955

SEQUENCE DESCRIPTION:

GATCTGACTG GAAAACAATC CTGTATCCCC TCCCAAAGAA TCATGGGCTT TTTTTTTNAN 60

TTAAAAAGCA GACAAATAGA CAAA 84

SEQ ID NO:2575

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02957

SEQUENCE DESCRIPTION:

GATCAAAAGA AACTTAAAAA GTGGAATGGG ATATGGCTTT TGGTACCTGA AAATAAATNC 60

TTTAATAATT GTAAGCCAGA AA 82

SEQ ID NO:2576

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02958

SEQUENCE DESCRIPTION:

GATCAAAAAT ATAGTTATAA TTTNTAAAT TTNAAAAATG TGATTGCNCT AATAAAGAAT 60

AAAANCTATG CTTTAAACA AA 82

SEQ ID NO:2577

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02959

SEQUENCE DESCRIPTION:

GATCACTGCA GNTTCTAGGA CCCGGTTTCT TTTACTGATT TAAAAACAAA ACAAAAAAAA 60

ATAAAAAAGT TGTGCTGNN ACAA 85



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5 SEQ ID NO:2578  
 SEQUENCE LENGTH:81  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02960  
 SEQUENCE DESCRIPTION:  
 GATCTCCCAT AATTTGAAAT TGAAATCGTA TTGTGTGGCT CTGTATATTC TGTTAAAAAA 60  
 10 TNAAAGGACA GAAACCTTAA A 81

15 SEQ ID NO:2579  
 SEQUENCE LENGTH:79  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02962  
 SEQUENCE DESCRIPTION:  
 GATCCACCAT CTTATCTTGG TGCCATCCCT GACTTGGCTT CTGTTCATAA ATGCCTATTA 60  
 20 AATGTTTCTT TCTGAGAAA 79

25 SEQ ID NO:2580  
 SEQUENCE LENGTH:79  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02963  
 SEQUENCE DESCRIPTION:  
 GATCCAATTG CTGGTTACAT TTTGGGAAGC TCTCATTTTA GTGCTATGTA GTTTCATTGA 60  
 30 ATAAACTGTT TAATATAAA 79

35 SEQ ID NO:2581  
 SEQUENCE LENGTH:75  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02964  
 SEQUENCE DESCRIPTION:  
 GATCTAAGAG GAAAGTGGTT ATCGGTTGCN NTTTATTTAT AAAGGATGCA AACATAAAAT 60  
 40 TAGATTTTGG GCAAA 75

45 SEQ ID NO:2582  
 SEQUENCE LENGTH:73  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02965  
 SEQUENCE DESCRIPTION:  
 GATCAGCCTT TTTGTTTCAA TGAGGTGTCC AACTGGCCCT ATTTAGATGA TAAAGAGACA 60  
 50 GTGATATTGG AAA 73

55

SEQ ID NO:2583

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02966

SEQUENCE DESCRIPTION:

GATCCCAGAG TGGCCTGCCT ATCACAACCA CATCCCTTCC CCCCACAAGG CAATAAATCT 60  
CATTTCTTTA AA 72

SEQ ID NO:2584

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02967

SEQUENCE DESCRIPTION:

GATCAACGAC AAAATGCACT TCTCCCTCAA GNAGTGAGGC TTGGTCCAAT ACATGGCTCT 60  
GCCCCCAGA AA 72

SEQ ID NO:2585

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02968

SEQUENCE DESCRIPTION:

GATCAATCTT GTATTTTCTG ACCACATAAA GGCTTCTTCT CTTTGTAATA AAGTAGAAAA 60  
GCTCTCCTCA AA 72

SEQ ID NO:2586

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02969

SEQUENCE DESCRIPTION:

GATCTTGTTT CTGAAGATGG TTAAAGTTAT AGCTTCTTAA ACGAAAGAAT AAAATACTGC 60  
AAAATGTTTT TATATTTGGC CTTCCACCC ATTTTAAATT GTGAGAGATT TGTCACCAAT 120  
CATCACTGGT TCCTCCTTAA AAATTAAAAA GTAACCTCTG TGTAAT 166

SEQ ID NO:2587

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02970

SEQUENCE DESCRIPTION:

GATCATAGGA GAGACCCATT NGCTAGCTAC TTCATTGTT CTGACCTAAT AATAAAAGTT 60

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AGAACCATAA A

71

SEQ ID NO:2588

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02971

SEQUENCE DESCRIPTION:

GATCTGACGT TCCTTGTGAC TTAAGGGTCC GGCTTGGGAA TTAAAGTTG TTTCTGGCCT 60

TTAGCCTACA AA 72

SEQ ID NO:2589

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02972

SEQUENCE DESCRIPTION:

GATCTGGCCA GTCAAGGGTC CACAGGGTGC CAGCCTCTCA CCCTCAGAAT AAAGACATCA 60

GCCATTCAAA 70

SEQ ID NO:2590

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02973

SEQUENCE DESCRIPTION:

GATCATCTAA ACTGAGTCCA GCTGCCTAAT TCTGAATATA TATATATATA TATATCTTTT 60

CACCATAAA 69

SEQ ID NO:2591

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02974

SEQUENCE DESCRIPTION:

GATCCTTATT ACAGGAAAAG CATGAGTGGT GGCTAACCTG ACCAATAAAG TTATTTTATG 60

ATTGCAAA 68

SEQ ID NO:2592

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02975

SEQUENCE DESCRIPTION:

GATCTTAGAT TTTATGTAGT ATTAAGTGAA AAAATACGAA AATAATAAAC ATTGAAGAAA 60

AAAATAAA

68

SEQ ID NO:2593

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02976

SEQUENCE DESCRIPTION:

GATCACATTT TCTGTTGGTT AACATTNTTC CTAGCTTATA TGATGGAATT AAATATATTC 60

TGTGTAAAAA GGAAA 75

SEQ ID NO:2594

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02978

SEQUENCE DESCRIPTION:

GATCCACCTA ACAAGAAACC TAAAGTGTAG AGATTGCCAT TTNATTTGT AATTTTTTTT 60

TTTTTTN 67

SEQ ID NO:2595

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02980

SEQUENCE DESCRIPTION:

GATCACACAC CGGCTGTATT TAATATGTAA CATTTTCACA NATATTAAAG ANACAGAAGT 60

ATTAAA 66

SEQ ID NO:2596

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02981

SEQUENCE DESCRIPTION:

GATCAGCATG GGCCACGTAG NCGNGACTCC ATCTCTACAC ATAAATAAAA AATTAGCTGG 60

GCAAA 65

SEQ ID NO:2597

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02982

SEQUENCE DESCRIPTION:

GATCCAATTT ATGTTTTTTT TTTNTTTATA TTTTGGGGAA AATTAAAATT TTTTAAAGGT 60

AAA

63

SEQ ID NO:2598

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02983

SEQUENCE DESCRIPTION:

GATCACGCAA TAATGACTAT GTAATCTCAA AAAACAAATA AAATATTCTT AACATGGCAA 60  
A 61

SEQ ID NO:2599

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02984

SEQUENCE DESCRIPTION:

GATCCAAGCA GTGTGCTACT ATATAACTGA TAAAAGCACT TGGTCTTNGA TTATCAGAAA 60

SEQ ID NO:2600

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02985

SEQUENCE DESCRIPTION:

GATCATTTTG CACATAGCTT TATCAACTTT TAAACATTAA TAAACTGATT TTTTAA 58

SEQ ID NO:2601

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02986

SEQUENCE DESCRIPTION:

GATCTTTGCA GTTTTGNGAC AATTACAAGT AAAGCTGCTA TAAACATTTG TATGCAAA 58

SEQ ID NO:2602

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS02987

SEQUENCE DESCRIPTION:

GATCGACACG CAGCTAGCCT CCTGCATTGT ATGGTTATAA ATAGCACCTT AGTGAGTNCT 60  
GTCGTCCAGT CAAA 74

SEQ ID NO:2603

# EP 0 679 716 A1

SEQUENCE LENGTH:58  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02988  
 SEQUENCE DESCRIPTION:  
 GATCCTGGGG CAACCCATCT GGTCTCTTGA ATAAAGGTCA AAGCTGGATT CTCGCAAA 58

SEQ ID NO:2604  
 SEQUENCE LENGTH:56  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02989  
 SEQUENCE DESCRIPTION:  
 GATCACGTTT CGTGTTTCATA CTCAACGTTA ATAAAAGGAG AGAGTTTGTA GTGAAA 56

SEQ ID NO:2605  
 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02990  
 SEQUENCE DESCRIPTION:  
 GATCGCTGTG CCTGGCATAT AGTAGGTGTT CAATAAATGC CCTGTGACTC TCAAA 55

SEQ ID NO:2606  
 SEQUENCE LENGTH:59  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02991  
 SEQUENCE DESCRIPTION:  
 GATCTATCCT CAACAACAAC AGAAAAAAGG AATAAAATAT CCTTTGTTTC CTAGTGAAA 59

SEQ ID NO:2607  
 SEQUENCE LENGTH:54  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02992  
 SEQUENCE DESCRIPTION:  
 GATCCATTTT AAAATTTGTA ATTCAATAAA GTTTTTTTTG TTGTAAACA TAAA 54

SEQ ID NO:2608  
 SEQUENCE LENGTH:53  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS02993  
 SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

GATCTTGTAT TCAGTCAGGT TAAAACAACG GACAATAAAA GAATGAACAC AAA 53

5 SEQ ID NO:2609  
SEQUENCE LENGTH:52  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02994

10 SEQUENCE DESCRIPTION:  
GATCTGGGGT GGGAGTAACA GGGCAGAAAT GATTAAAATG TTTGAGCACA AA 52

15 SEQ ID NO:2610  
SEQUENCE LENGTH:52  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02995

20 SEQUENCE DESCRIPTION:  
GATCCTTTTT TTTTCCACA AAATTTTAC AAATAAAAAA TGTCCCCTA AA 52

25 SEQ ID NO:2611  
SEQUENCE LENGTH:52  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02996

30 SEQUENCE DESCRIPTION:  
GATCTCAAAG TGCCTTCTGA AGCATCAGAG ATTAAATATT GTTCAAACCTA AA 52

35 SEQ ID NO:2612  
SEQUENCE LENGTH:53  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02997

SEQUENCE DESCRIPTION:  
GATCTGAATG GGGCTTNCCT GATGTTGGTA TCTAAGGCTT AGGCCTATAG ATN 53

40 SEQ ID NO:2613  
SEQUENCE LENGTH:50  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS02999

45 SEQUENCE DESCRIPTION:  
GATCTTGAAT GTATTTTCTT AAGTTTATTA ATAGACATTT TCACAATAAA 50

50 SEQ ID NO:2614  
SEQUENCE LENGTH:50  
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS03002

SEQUENCE DESCRIPTION:

GATCTATCTG GAAAATGNAG GACTCCGAAT AAAAAGCTAT TACTAATAAA 50

SEQ ID NO:2615

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03005

SEQUENCE DESCRIPTION:

GATCAGGGGA AATNTTTAAG CTAAATAAAT CTGGGGGGTT TTTTATTCAA A 51

SEQ ID NO:2616

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03028

SEQUENCE DESCRIPTION:

GATCGAATGG TATATATTAG AAATTACATC TGTGTGAATT AAAATTGTGT GAGCAATTAA 60

ACATGGTTGA NTTTTTCAAG CAAAAATCAG TTCATCTTTT GATGTAATTT TCTAGGCTAA 120

ATGGCAATCT CTGAAAGATG AATAAAGCTA TATTTATTTA GCAAA 165

SEQ ID NO:2617

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03030

SEQUENCE DESCRIPTION:

GATCACATTT TAAGCATCTN TCTCTCCTAC TCCATTTAGA AAAATAAGTA ACAGGTGAAA 60

TGTGGTCTCA GTGTAAACGG GATAATTCTG CTACCGGCTC CTCCTGATG ATTCTNAAAT 120

ACACTACTGA ACGAGCTCTG GCTGGTCCTT TCTATCCTGG ATGTGGTTCT TCTGTGTAGC 180

AATTCCTTGA NGTCCAGGTT GGAAAGATGT ACTCTTCTCA ACCAAGGAAA ACCTTAAATC 240

CCGTCGTGGC CAAA 254

SEQ ID NO:2618

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03031

SEQUENCE DESCRIPTION:

GATCAACCCC AGACTGGGCC AGAATGTTAG TGAAGGTTTT ATTGTGCCCG GTTGGAGGAT 60

AACGTTCTTT GGGTACTTTT TGTGGGTGTC AAATNAACTC AATTGCCACA AGTTTTAAAC 120

TGGTGTAAT CAAGCTTGAC TTAATGTGAT TGTNACTGTT ATATCCAGNC TATACTGCTA 180

GCAGCTGCTC ATACTGCAGT CAATTACTGG AAGCGGATAT ATTCCTATG CAAAAACTGT 240



TTAAACAATA AAATGAGCTA TGCTACAGAA A

271

SEQ ID NO:2619

SEQUENCE LENGTH:489

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03053

SEQUENCE DESCRIPTION:

GATCCACAGC TTAAAGATGG GAATTCAGGT ATGAAAGAAA ACAGGCAAGG AGGCACTGAG 60  
GGAGAAAGAC ACAGACTTTA TCGCTCTGTG GCTCATTGTT ACTGGAATAT NCTAAAACTC 120  
TTGTNCACAT GCTATTATGA CTTATAAAGC AGCAACAGCT GAGGCGCACC AGGACACAGC 180  
TTCCATTTCT TTAACGTCTG TNCCTTAAC ATCGCTGAAA TNATTACTG TTGAAGAGAT 240  
GCCTTGCGGT GTGGCCAGCT GTGAGGAGAA AGCAGCTGGC AGTGTTAGGA CATTAGTCCA 300  
CCTTCAGCGC AGGGTCTCTG GCCGGGCTCTG ACTCAGAAAC CTTGGTACTC GNCCCTTGGN 360  
CACAGTGCCC AGACCCATGT AACCNACTNG NTCCTGCATT AACCNAGAAA TACCTCGGTT 420  
CTATNTGTGC ACTTAGCTGG GGACTIONCC ACTGTAATCA CCTNAATNAA NGGGTTNTAA 480  
ACATGGAAA 489

SEQ ID NO:2620

SEQUENCE LENGTH:471

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03055

SEQUENCE DESCRIPTION:

GATCCAAAAC GCTTCGAGGC ACCCCAAATN ACCTGCCCAT TCGTNAGGAN GACCCACCCA 60  
CCCAGTGTTA TATTCTGCCT CGCCGGAGTG GGTGTNCCCG GGGGCACTG CCGACCAGCC 120  
CCTTGCGTCC CCAGGTTTGC AGCTCTCCCC TGGGCCACTA ACCATCCTGG CCCGGGCTGC 180  
CTGTNTGACC TCCGTGCCTA GTCGTGGCTC TCCATCTTGT CTCCTCCCCG TGTCCTCAAT 240  
GTNTTCAGTG GGGGGCCCCC TCTTGGGTCC CCTCCTCTGC CATCACCTGA AGACCNCAC 300  
GGCAAAANACT GAATGTAANC TGTGNCTGNN GNCTCGGTCC AACTTGCGGN CCGTGTNTNA 360  
CTNAACTNAG CTCCTTTAAC GGTAAATTTT CNGGGAAAAT CCCATGNTTG GGTGTTGGTC 420  
TTTAACCTTG GTAACGGTTG AAATCCAATT AAAGNTTTAA AAGTCATGAA A 471

SEQ ID NO:2621

SEQUENCE LENGTH:435

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03056

SEQUENCE DESCRIPTION:

GATCACCATT AAATCTGAAA GTACCTTTAA AAATACTGAG ATTNCTTCA TACTGGGCCA 60  
GGNATTTNAC GAAGNACCTG CAGATGACAG GAAAGTCAAG AGCACCATAA CCTTAGATGG 120  
GGGTGTCCTG GTACATGTNC AGAAATGGGA TGGAAAATCA ACCACCATAA AGAGAAAACG 180  
AGAGGNTGAT AAATGGTGG TGGAAATGCNT CATGAAAGGC GTCACTTCCA CGAGAGTTTA 240  
TGAGAGAGCA TAAGCCAAGG GACGTTGACC TGGACTGAAG TTCGCATTGA ACTCTACAAC 300  
ATTNTGTGGG NTATATTGTT CAAAAAGNTA TTGTNGTTTT CCATGGATT AGCAAGCAAC 360

TAATTTTNTC CCAAGCTNGN TTTTTTCAA TANTGGTNAC GTTGGNTAAA TAAANNTTTT 420  
TTTAGGNTTT TNAAA 435

5 SEQ ID NO:2622  
SEQUENCE LENGTH:411  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS03058  
SEQUENCE DESCRIPTION:  
GATCTCATCA GGGGAAGGCT CTGTGATGCT GCAGGTTGAT GTAGACACAG TAAAAGGAGG 60  
GCTGAAGTTG AACCCCAACT NNCTGGTGGA CTTCGGGAAG GAGCCCCTTG GCCCAGCCCT 120  
TGCCCATGAG CTCCGCTACC CTGGGGGCGA TTGTAGCTCT GACATCTGGA TTTGAACTCC 180  
15 ACCCTCATCA CCCACACTCC CTATTTTGGG CCCTCACTTC CTGGGGGACC TGGCTTCATT 240  
CTGTCTCTC TTGGCACCCG ACCCTTGGCA GCATGTACCA CACAGCCAAG CTGAGACTGT 300  
GGCAATGTGT TGAGTCATAT ACATTACTG ACCACTGTTG CTGTGTGCTC ACTGTGCTGC 360  
TTTTCCATGA GTCNNTTGA GCACCAAGAA ATAACTNGT AACCTGTAA A 411

20 SEQ ID NO:2623  
SEQUENCE LENGTH:410  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS03059  
SEQUENCE DESCRIPTION:  
GATCCAGGCG GGATGGAGTG TGGAGTGTGG GCACAGTGGC TTGTACAGGC CTGGNCTGGG 60  
CAGACTTGCC CCGGAGTCTC AGGCCACTGC GGAAGGAGGA CGCGTGGCCA GCAGGTGCCA 120  
CCAGGAGAGG AGAGGAGGGC CAGGCTGAGC TGCATCTNTG GACTCCAAGG AGAGCTTGGA 180  
30 GAGGTGACTG AAACCCTGCC CCACCCCGAG CCTGTNTCCA TCTGTGGGTC CTTGGGCAA 240  
TTGCCTCATC TCTCTNAGCC TCGAATGCGT AGTTTCAGGA CTAAGTAGGG TACTGTGTAC 300  
CAACTGCCTC TGCCAACGGC CCTGCACTGG GCANGCCTGG GGTACCTGGG CTTGGGGNA 360  
AGGAAGTAGG CCTTNGGNAG GAGGCTGGAT TGCTTACAAT TTTNTTTTN 410

35 SEQ ID NO:2624  
SEQUENCE LENGTH:408  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
40 CLONE:HUMGS03060  
SEQUENCE DESCRIPTION:  
GATCTGCGGC CCATCTACAT CTCTGTGCAG CCGCCTTCAC TGCACGTGCN GGAGCAGCGG 60  
CTGCGGCAGG CATACTGA AACCGAGGAG AGCCTGGTGA AGCGGCTNGC TGNTGCCAGG 120  
45 CCGACATGGA GAGCAGCAAG GAGCCCGGCC TGTTTGATGT GGTTCATCATT AACGACAGCC 180  
TGGACCAGGC CTACGCAGAG CTGAAGGAGG CGCTCTCTGA GGAAATCAAG AAAGCTCAAA 240  
GGACCGGCGC CTGAGGCTTG CTGTCTGTTT TCGGCACCCC GGGCCCATAC AGGACCAGGG 300  
CAGCAGCATT GAGCCACCCC CTTGGGAAGG CGATACGGCA GCTCTGTGCC CTTGGCCAGC 360  
50 ATGTTGGAGT TGGAGGAGAT NCTTGCCCT GTTGGTTTGG ACCATCCN 408

EP 0 679 716 A1

SEQ ID NO:2625

SEQUENCE LENGTH:398

SEQUENCE TYPE:nucleic acid

5

TOPOLOGY:linear

CLONE:HUMGS03061

SEQUENCE DESCRIPTION:

10

GATCTCAACG AGACAAACGA TGGGTGGACC CGAACTCCCC GGTGCTCTTN GAGGACCCAG 60  
TCCTTTNTGC CTTGGCAAAA AAGCACAAGC GAACCCAGC CCTGATTGCC CTGCGCTACC 120  
AGCTGCAGCG TGGGGTTGTG GTCCTGGCCA AGAGCTACAA TNAGCAGCGC ATCAGACAGA 180  
ACGTGCAGGT TTTNANTTC CAGTTGACTG CAGAGGACAT GAAAGCCATA GATGGCCTAG 240  
ACAGAAATCT CCACTATTTT AACAGTGATA GTTTTGCTAG CCACCCTAAT TATCCATATT 300  
CAGATGANTA TTANCATGGA GGGCTTTGCC TGATGGTNTA CCAGAAGCCC TGTGTGTGGN 360  
TGGGTGACGC AGAGGGACGT CTCTNTGCCG GTGACTGN 398

15

SEQ ID NO:2626

SEQUENCE LENGTH:394

SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear

CLONE:HUMGS03062

SEQUENCE DESCRIPTION:

25

GATCACAGCT GGGGGAAAAA AAGCTTTTTA ATTCTGTACC TTCCTAGTAG ATAAGTGAAG 60  
AGCAGGGAAA GAGACCTTTA AATATTTTNC TATAAAAAAA TTTGTGATAA GTTCTATCA 120  
AAATGGGGAG ATTGCAGAAA AGGCTTCCTT TGGNTCCCAA GGAGGTGTAG CAGGTGTGAG 180  
CAATATTAGT GCCATGTGCC TTTCACACAG GGTTCGATT TATCAGTCTG TTTCCGATG 240  
NNNNGGTACA TGAAAGAGTA CACCATGTGA AGAGAAGAGA GAATGATTGA AAATGTTTTA 300  
GTATAGACCT CTTCTTGCG TGGGTTGCTA TTTCTAGAT TTTACTTTTT AGGGACCAAA 360  
NTAAANTCCT TTGTAAACN TGGGTCAGNG NAAA 394

30

SEQ ID NO:2627

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS03063

SEQUENCE DESCRIPTION:

40

GATCGCACCA TTACACTCCA GCCTGGGTGA CAGAGAGAGA CCCTGTGCCN NTCAAAAAAA 60  
TGTTTTTTTT AAACAAGAAT CTCTCAGGCA TACTGAAATN TTGAAGAGGA AATNATATTA 120  
ATATCTGGGA CTTGTTTCCA AATTTGGAAT TGGGGCAGGG TGTAATNGT TGGCAATATC 180  
AAAGAAACGA GGAGTTGGAA TNATAATTGT AGAAGCTGCA TGATAGATAC ACATTCTTTA 240  
TACTTCTGTA TATGTNGAAA TTTTNNATCA AATTATAATN GTGTATAATG ACTAATTATG 300  
CTTNCATTGT CTATCCTGTG TGGTTATGTN ACTTGCTGAA ATNNATACAT AANGGGTCTT 360  
CAACCTTNAN NTGGTCTTAT CCANGGCATA NN 392

45

SEQ ID NO:2628

SEQUENCE LENGTH:385

SEQUENCE TYPE:nucleic acid

50

55

TOPOLOGY:linear

CLONE:HUMGS03064

SEQUENCE DESCRIPTION:

5 GATCTGTAAT NATCTCTATT GGCCTGGGGT GCCTGTGCTA TAAATAAGTT TCTTCACATG 60  
AAAAACACAG CCAGCCCAAG ATNACTTATC TGGGTTTAGG ATTCAATAGT ATTCACCTAAC 120  
TGCTTATNAC ATGAGCAATT TCATCAAATC TCCAAACTCT TAAAGNATGC TTTCGGAAAA 180  
CACGCTGTAT ACCTAGATGA TGACTAAATG CAAAATCCTT GGGCTTTGGT TTTTTCTAG 240  
TAAGGATTTT AAATAACTGC CGACTTCAAA AGTGTCTTA AAACGAAAGA TAATGTTAAG 300  
10 AAAAAATTGA AAGCTTTGGA AAACCAAATT TGTAATATCA TTGTATTTT NATTAAAAGT 360  
TTTGTAAATAA ATTTCTAAAT TTAAA 385

SEQ ID NO:2629

15 SEQUENCE LENGTH:385

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03065

SEQUENCE DESCRIPTION:

20 GATCGGGGCC CTGGGGCTGT NAGACCCCGA CCNTCTCGAG GAACCCTGCC TGAAACGCCT 60  
CCATTACCAC TGCGCAGTGA GATGAGGGGA CTCACAGTTG CCAAGAGGGG TCTTTGCCGT 120  
GGGNNGGNTC GCCAGCCACT CACCAGCTGC ACTGAGAGGG GAGGTTCGCA CACCCCTCCC 180  
CTGGGCCGCT GAGGCCCGCG CACCTGTGCC TTAATCTTCC CTCCCTGTG CTGCCCCGAGC 240  
25 ACCTNCCCCG CCCCTTTACT CCTGGGAAT TTGCAGCTGC CCTCCCTNC CCGTTTTTAA 300  
TGGCCTGCTG AAATATGTGT GTGAAGAATT ATTTATTTTC GNCAAAGCAC ATGTAATAAA 360  
TGCTGCAGNC CNGCCTNTGC CCAAA 385

SEQ ID NO:2630

30 SEQUENCE LENGTH:385

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03066

SEQUENCE DESCRIPTION:

35 GATCCCGGGN AGTNACAGGT GCCGACGTGA TGTCGCTTCT NTGGTGCCCA GCTCCCTTCC 60  
TGGTCTNANA CTAGCTCTGG GGGTGGCGGG GGCCCCACA CGCTGCTCCC GCTCCACCCT 120  
GCCCCTNCTG CTGCTCTGTG CCTGCTGTCA GAGCCCTGGT GGGGGAGGAT GTGGCCACCC 180  
TGAGACCCGG AGGAGACGGG CGTCTGCCTG GNTTTCGGA GAGCNGCTTA TGGGTGTGGT 240  
40 CCGTCCAGAC ACCTTGTTTC AAGGGGGATG GCGGTNANGG GCAAGCAGAG CATCCCCACC 300  
GNTGAGCAAG AACTTTTTCT TGTTTTTAAA CCATCACGTC CTCATTTTAC AATTGGAATA 360  
AAGTGAGTTT TTTGAAACC TGAAA 385

SEQ ID NO:2631

45 SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03067

SEQUENCE DESCRIPTION:

50 -----

EP 0 679 716 A1

GATCGCAAGG AACTGGGCGG CCTACTACCC CGACCTGCCC ACCCCAGAAC AGCAGCAAGA 60  
 CATGCCCCAG TTCATACATT TATTTTCTAA GTTTTACCCC TGTAAGGAGT GTGCTGAAGA 120  
 CCTAAGAAAA AGGTTGTGCA GGAACCACCC AGACACCCGC ACCCGGGCAT GCTTCACACA 180  
 GTGGCTGTGC CCCNTGCACA ATGAAGTGAA CCGCAAGCTG GGCAAGCCTG ACTTCGACTG 240  
 CTCAAAAGTG GATGAGCGCT GGC GCGACGG CTGGAAGGAT GGCTCCTGTG ACTAGAGGGT 300  
 GGTCAGCCAG AGCTCATGGG ACAGCTAGCC AGGCATGGTT GGATAGGGGC AGGGCACTCA 360  
 TTAAAGTGCA TCACAGCCAA A 381

SEQ ID NO:2632  
 SEQUENCE LENGTH:370  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03068

SEQUENCE DESCRIPTION:  
 GATCCGTAAG TCCATGACCA AGGAGGCCAT CCGAGAGCAC CANATGGCCC GCACTGGCGG 60  
 CACGAGACAG ACCTGTNCAC CTGCGGCAAG TGCAGGAAAA AGAACTGCAC CTACACACAG 120  
 GTGCGAGCCC GCAGCTCTGA TGAGCCCATG ACCACCTTTN TTGTCTGCAA CGAGTGTGGA 180  
 AACCGCTGGA AGTTCTGTCTG ACCCCTCGTG TAGATGTGCT GCAGCCTTGG GCCCTCCCCG 240  
 GCCACGTCC TCGTTGACA CAGCTTCTNT GGAGACCCTA GAAGGCGGCA TGTCTGCCCC 300  
 TCAACCTGCC TGCNTGGATT GCACCTTTCT GCCCTTTCCC CNTNATTATT AAATGTTTCT 360  
 TTTTGCCAAA 370

SEQ ID NO:2633  
 SEQUENCE LENGTH:344  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03069

SEQUENCE DESCRIPTION:  
 GATCTTCTTC AAGCCATTAT TTAACTCAA GAAAACTCTA GAGAAGAAAA GTGAAGAAGT 60  
 CATGTTGAAG AAGATGTAAG AATGTGTCAA GACCATCCAG AAATNATATG AGAAATACTG 120  
 ATATTTTAAA TGGTTGACAT CATCCAGCGA AATGAATCTA CATTAAATGT TGTTTTAACT 180  
 GCGCTATGAT TAAAACCAT CATATAGAGT TAGTNTTAC AACTACTATT CTGTTATTTT 240  
 TTTTTTAATC TGACAACATT TGTCTAAGT AAGATAAGCA AAAAAATTCT TCAACTCCTT 300  
 TTGGCAAGAA AACTGTAACA GAAAATAANT TTTGAATGTG TACN 344

SEQ ID NO:2634  
 SEQUENCE LENGTH:341  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03070

SEQUENCE DESCRIPTION:  
 GATCCCTGGT CCAGAATTCC ATTTACCTTC TGGGCCAGAT ACCACCAGAA TGCCCGCTCC 60  
 ANATTCCTC AGACCTTTGC CGGTCCCAT ATTGGTCCTG GTGGTACAGC CAGTGCCAAC 120  
 TTCGTGCCA ACTTTGGTGC CATTGGTTTC TTCTGGGTTG AGTGAGATGT TGGATATTGC 180  
 TATCAATCGC AGTAGTCTT CCCCTGTGTG AGGCTGAAGC CTCAGATTCC TTCTAAACAC 240

EP 0 679 716 A1

AGCTATCTAG AGAGCCACAT CCTGTTGACT GAAAGTGGCA TGCAAGATAA ATTTATTTGC 300  
TGTTCCCTTGG GCTACTGNTT TTTTCCCCT TGTGTGCTGT N 341

SEQ ID NO:2635

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03071

SEQUENCE DESCRIPTION:

GATCGNCAAG AAAATTNAGA TTGGCGATGG GGCAGAGCTG ACGGCAGAGT TCCTCTACGA 60  
CGAGGNGCAC CCCAAGCAAC ACGNCTTCAA GCAGGCCTTC GCCAAGCCCA AGGGCCCAGG 120  
GGGCAAGCGG GGCCATAAGC GCCTCATCCG NGGCCCGGGT GAAAATGGGG ATGACAGCTA 180  
GGAGGCTGGA GCATNNGNCG GCCACGTNTG GACTGTGGGG CTGCCCACCT TCCGCTCCCT 240  
GCCACCATCC TCCTTCCTGG GCTCCAGGAA AGTNTTCTG GGAGGTCAGG AGGGCTGGCA 300  
GCTTGAACGC ACTTGCAGCG TCCGANGGNC ACCGGGCTTN 340

SEQ ID NO:2636

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03072

SEQUENCE DESCRIPTION:

GATCTGTCTG CNTTCCTCAA GACCATTGCA CTGAATGGTG TGGAGGACGT GCGAACCGTG 60  
CTGGAGCACT ATGCCCTGGA GGATGACCCG CTGGCGGCTT TCAAACAGCG GCAAAGCCGG 120  
CTAGAGCAGG AGGAGCAGCA GCGCCTGGCC GAGCTCTCCA AGTCCAACAA GCAGAACCCTC 180  
TTCCTTGGCT CCCTCACCAG CCGCTTGTGG CCTCGCTCCA AACAGCCCTG AACTCTGGGC 240  
CTCCTCAAAC TCAGTGCCTG GGTCCAGGGC CCCAGTGCTT CCAGACCAAG ACTTGGGCCA 300  
CCACTTNTCC AATAAAGTAC ATCCGAGACG GCAAA 335

SEQ ID NO:2637

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03073

SEQUENCE DESCRIPTION:

GATCCAGTTG TGAACAAAGA GTCCTCTTNG TGGAAAAGAA AAAAATACAT NTCCCTTTAA 60  
ACGGTGGATT GAAAATAACT TTNATTATA AAGAGAAGAC TGAGGGCGGG GATACTGATT 120  
CANNAATCCT GTAGCGTGTA ATAAAAGAAG AGGAAATGGC ATGGAATCAC TGCCTCCTGT 180  
GATTTGAAGG CCATTGTGAA GGAAAAAAT GCAGTGAAAG AAAGTTCTTC ATATTAGGCC 240  
AGATATCATT GCATCACATT TATTTATCTT TCTGGNATTT TTATAGCCCT TAATAAAAAA 300  
TATTAATAA GCCTGTGCTA TTGTGTCTTA AA 332

SEQ ID NO:2638

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS03074

SEQUENCE DESCRIPTION:

5 GATCAAGAAT TTGGTGTGGA CGTTGGCCCT GTTTGCTTTT TATAAACCAA ACTCTATCTG 60  
 AAATCCCAAC AAAAAAATT TAACTCCATA TGTGTTCTC TTGTTCTAAT CTTGTCAACC 120  
 AGTGCAAGTG ACCGACAAAA TTCCAGTTAT TTATTTCCAA AATGTTTGA AACAGTATAA 180  
 TTTGACAAAG AAAAATGATA CTTCTCTTTT TTNGCTGTTT CACCAANTAC AATTCAAATG 240  
 CTTTNGTTT TATTTTTTTT ACCAATTCCA ATTTCAAAT GTCTCAATGG GGCTATAATA 300  
 10 AATAAACTTT CAACACTCTT TTATGGTNAA CCAA 335

SEQ ID NO:2639

SEQUENCE LENGTH:384

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03075

SEQUENCE DESCRIPTION:

20 GATCAAGCCT GCCTCAATCA GTATTCATAT TTATAGCCAG GTACCTTCTC ACCTGTNAGA 60  
 CCAAATTNAG CTAGGGGGGT CAGCCAGCCC TCTTCTGACA CTAAAACACC TCAGCTGCCT 120  
 CCCAGCTCT ATCCCAACCT CTCCCACTA TAAACTAGG TGCTGCAGCC CCTGGGACCA 180  
 GGCACCCCA GAATGACCTG GCCGCAGTGA GCGGATTGA GAAGGAGCTC CCAGNGGGG 240  
 CTTCTGGGA GACTCTGGTC AAGAAGCATC GTGTCTGGCG TTGTGGGGAT GAACTTTT 300  
 25 TTTGTTTCT TCCTTTTTTA GTTCTTCAA GATAGGGAGG GNAGGGGGGA ACCATGAGCC 360  
 TTTGTTGGCT AATCANTCCC AAGN 384

SEQ ID NO:2640

SEQUENCE LENGTH:352

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03077

SEQUENCE DESCRIPTION:

35 GATCAAAGGT TTAAAGTCTA ACTTCTAAGA TATATTTGCA GAAAGAAGCA ACATGACAAT 60  
 AGAGAGAGTT ATGCTACAAT NATTTCTTGG TTTCCACTTG CAATGGTTAA TTAAGTCCAA 120  
 AAACAGCTGT CAGAACCTCG AGAGCAGANC ATGAGAACT CAGAGCTCTG GACCGAAAGC 180  
 AGAAAGTTTG CCAGGNAAAA AANNGGCATC ATTATTACCA TCGATTCACT GCCTGGTTAA 240  
 NGNGGNAAGC TTAATTNGTT TNAGTGGCAG CCNCNTNGCA CGTGGTTTGC TATGNAGGTG 300  
 40 AANGGTTTCC CAATTCCTTC AGGCTTTTNN GGGGGTTTTC GGGCTCTNCC TN 352

SEQ ID NO:2641

SEQUENCE LENGTH:321

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03078

SEQUENCE DESCRIPTION:

50 GATCAAACAG CTCTAAGTAT GAAGCAAGAG TAAAGACTAA GGTTCGAGA NCATTCTTAC 60  
 TCACATAAGT GAAGAAATCT GTCAGATAGG AATCTAAATA TTTATAGTGA GATTGTGAAA 120

55

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GCAACCTTAA AGTTTTGAAG AAGACTGATG AGACTAGGTG CNNNGCTTCC TTTCATCAGG 180  
TATCTTTCTG TGGCATTGGA GAACAGAAAC CAAGAAACAT GGTAATTNCT AANTTATGAG 240  
GCTTTGCTTT TTGTTTGCTT TTAAGTAGAA AACCATGTTG GCAACATTGA GTTTTGGNGT 300  
TGATTGAGAT AATATGNCTT N 321

SEQ ID NO:2642  
SEQUENCE LENGTH:320  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03079

SEQUENCE DESCRIPTION:  
GATCTTTGGC TGGAAACTA GAATTTATAG CAGTTTATTA ATGATACCTT AAATNACTCA 60  
GGACTTAATG TAGCATTGCA CTTCTGTGTA CAGTAAACT GCTTTGTTT ACTAAAGAGA 120  
AAAATGTGAG TGGAAAAAT ATGTATGTGT TATATACTCA AATGTATATA ATNCTATCTA 180  
TAGATTTATA TATGTATACA TTCTGTACAG TAGTCCATC AAAATATGTA ATAATTCACA 240  
CCAATTTTAT TAAATGTATT TNCTTTTCA AAATTTAAAT TGAGCTGCTA TCAATATTAA 300  
ATGAAGTTAT GGCATCTAAA 320

SEQ ID NO:2643  
SEQUENCE LENGTH:303  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03080

SEQUENCE DESCRIPTION:  
GATCCCTTCG ATGTGGATTC AGGGAGAGAG TTTGGAAACC CCAACAGGCC TGTGGCATGC 60  
ACCCGGCTGC CCTCGGACAC TGATGACAGT GATGCGTCTG AGGACCCAGG GCCTGGCGCC 120  
GAGCGCGGAG GAGCCAGCAG CAGCTGCTGT GAAGAGGAGC AGACGCAGGG ACGGGGGGCT 180  
GAGGCCAGGG CCCCGGCTGA GGTTTGGAAA GGAATCAAGA AACGGCAGAG AGACTNAGGG 240  
TTGCAGACAC ATATATTTT GAGGCTGGGT GACGAGAAAA TCTAGAGACA TGAGGGACAT 300  
AAA 303

SEQ ID NO:2644  
SEQUENCE LENGTH:315  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03081

SEQUENCE DESCRIPTION:  
GATCCAGACG CAAGANGGCT GTCCTCTCTA AGGAATATGG TTTTNTCTT CTAAGTGGT 60  
CTGCCAGCTT TATAATGGTG GCCCACCTAG CCATCANTGT TTCCAAGGCC CGCAAGANGT 120  
ACAAAGTGGA GTATCCTATC ATGTACAGCA CGGACCCTGA AAATGGGCAC ATCTTCAACT 180  
GCATTCAGCG AGCCCACCAG AACACGTTGG AAGTGTATCC TCCCTTCTNA TTTTNTCTAG 240  
CTGTTGGAGG TGTTTACCAC CCGCNTATAG CTCTGGCCT GGGCTTGGCC TGGATTGTTT 300  
GGACGAGTTC TTTAN 315

SEQ ID NO:2645



SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03082

SEQUENCE DESCRIPTION:

GATCCTTCTT GGCCCCAGAA AGTCATTTGG CATGGCTCCA GCCCCCATGG CATCCGCTTN 60  
 TGGATAACTA CTGTGAAGCA TGGCGAACCG CGGACACAGC GGTACGCGGA CTTGCCTCCC 120  
 CGCTGAGCAC GGGGAAGATT CTGGACCAGA AAGCATACAG CTGTGCTAAT CGGGCTAATT 180  
 GTCCTATGTA TCGAAAACAG TTTCATGNCA GNCGTTAGGA AGTAATTGGC TTCTTNATGA 240  
 TTCTTAAAN NGTTTTCAA TTTTCCTAA TGNGAAGNGT TGNGACTGAA ATCTAAAATG 300  
 TTTANTTGTG NAAA 314

SEQ ID NO:2646

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03083

SEQUENCE DESCRIPTION:

GATCACTGTG GACAGGGTGC AGCTCTACCA GTTCCTGTTT CTNCTGAGCC AGACCCTCTT 60  
 CAGGGAAGGG ACCAATTAAT TTTAAACTC ACTTGAAGCA CAGCTGGTCA TGGGGCTTGG 120  
 TATAAAGTTC CTATTTCCAC CCTGATACTT CCAATTCCTG GAACCCACGC CCACTCCNCC 180  
 ATCCCTCCTC CCTATCAAAC TAGTATAATG ATTTTGAATC GGTACAGTGT GTTTAACTGT 240  
 AACTAAGTTC GACAGACTAT TATTATCTTT GTAATAAATT AACCTAGCAA TAAAAATTAT 300  
 TCTGTNTAAA 310

SEQ ID NO:2647

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03084

SEQUENCE DESCRIPTION:

GATCTATTAA GCTTGANACA TTANGTNTCA TCACGCACTG AAGACAGGAA GCAGTTCCTT 60  
 GAGTCAGCTG GTTCCCAAGC TCGCACAGAA GGTGATAAGT TACTATCAAA TGCCAGTNAG 120  
 AATCTNCTTA TAGAATAACC TGGGCCCAAG TNATTTTNGT AAAAACTTG CCCTTCTTTG 180  
 GTTTAATTTN CTATGTGCTT TTAGGTGTGA ATCCAGATAT GCGGTCTTAA TTCCTTTGGA 240  
 AATACACAGT TCGTTTAGTT ACTGTACACT CTGTTTGTTT AATAAACTGC ATATCANCTT 300  
 CCNACAAA 308

SEQ ID NO:2648

SEQUENCE LENGTH:302

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03085

SEQUENCE DESCRIPTION:

GATCAGCAGC CCCTGAGCGG AGAAGAGGAG CTAGAGCCTG AGGCCAGTGA TGGTTCAGGC 60

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TCCTGGGAAG ATGCAGCTTT GCTGACGGAG GCCAACCTGC CTGCTCCTGC TCCTGCTTCT 120  
GCTTCTGCCC CTGTCTAGA GACTCTGGGC AGCTCTGAAC CTGCTGGGGG TGCTCTCCGA 180  
CAGCGCCCCA CCTGTCTAG TTCCTGAAGA AAAGGGGCAG ACTCCTCACA TTCCAGCACT 240  
5 TTCCACCTG ACTCCTCTCC CCTCGTTTTT CTTCAATAA ACTATTTTGT GTCAGCTTCA 300  
AA 302

SEQ ID NO:2649

SEQUENCE LENGTH:302

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03086

SEQUENCE DESCRIPTION:

15 GATCAGCGAG CTACCANGAC CAGAGACCAA CTCAAGCTAC AGCAGAAGNA TTTTCCCAAG 60  
CCTGCTGACC ACAGTCACAT CACCCATCAG CACATGGAAG GCCCCTGGTA TGGACACTGA 120  
AAGGAAGGGC TGGTCCTGCC CCTTTGAGGG GGTGCAAACA TGAAGAGCCA 180  
GAGGCTGTGT AGAGGCTCCT GCTCCACCTG CCAGTCTCGT AAGANATGGG GTTGCTGCAG 240  
20 TGTGGAGTA GGGGCAGAGG GAGGGAGCCA AGGTCCTCC AATAAAACAA GCTCATGGCA 300  
AA 302

SEQ ID NO:2650

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03087

SEQUENCE DESCRIPTION:

30 GATCCCAGCT GATGTAGACC CTCTACCAT TACTTCATCC CTGTNATCTG ATGGGGTCCT 60  
CACTGTGAAT GGACCAAGGA AACAGGTCTN TGGCCCTGAG CGCACCATTG CCATCACCCG 120  
TGAAGAGAAG CCTGTGTCA CCGCAGCCCC CAAGAAATAG ATGCCCTTTC TTGAATTGCA 180  
TTTTTTAAAA CAAGAAAGTT TCCCCACCAG TGAATGAAAG TTTTGTGACT AGTGCTGAAG 240  
CTTATTAATG CTAAGGGCAG GCCCAAATTA TCAAGCTAAT AAANTATCAT TCAGCAACAG 300  
35 AAA 303

SEQ ID NO:2651

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03088

SEQUENCE DESCRIPTION:

45 GATCTCAGCT GGAAGTTCTG TTTGGAGCCC ATTTCTGTNA GACCCTGTAT TTCAAATNTG 60  
CAGCTGAAAG GTGCTTGTAC CTCTAATTC ACCCCANAGT TGGAGTTCTG CTCAAGGAAC 120  
GTGTGTAATG TGTACATCTG TGTCCATGTG TGACCATGTG TCTGTNAGGC AGGGAACATG 180  
TATTCTCTGC ATGCATGTAT GTAGGTGCCT GGGGAGTGTG TGTGGGTCCT TGGCTCTTGG 240  
CCTTTCCCCT TGCAGGGGTT GTGCAGGTGT GAATAAAGAG AATAAGGAAG TTCAAA 296

50 SEQ ID NO:2652

# EP 0 679 716 A1

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03089

SEQUENCE DESCRIPTION:

GATCTNACGG CCAGGCCTCT NTCCTGCTGC TGTTTTTAAT TTTCCCAGGT AGTGGGAGAG 60  
AGGAAAGGAG GGAAGGCAAG ATTCTTTCCC CCTCCCTGCT GAAGCATGTG GTACAGAGGC 120  
AAGAGCAGAG CCTGAGAAGC GTCAGGTCCT ACTTCTGCCA TGCAGCTACT ATGAGCCCTC 180  
GGGGCCTCCT CCTGGGCCTC AGCTTGCCCA GATACATACC TAAATATATA TATATATATA 240  
TGAGGGAGAA CGTNTCACCC AGNTTNNATC ATGCTGGAAA GAGTGTATGT N 291

SEQ ID NO:2653

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03090

SEQUENCE DESCRIPTION:

GATCTAAAGG GTGTAAAAAT ATTGATACTT CAATATTTCA CTTGCTGCCA GGAAAAACAA 60  
AATTCTCAAT CTTTGTAAA TGGGAGGAGG ACTTTTGCAT ACATTTTAC TCTTTAAATA 120  
ACGACAACGA CACTTATACT GTCATAATAA CAATNATGTA TTTCTTGTG GTTTTAATTT 180  
TTTTTGTAAAT TTTACATAAA ACAGTTATTT TCTATTTTNA CGCAGATAAA TATTTGTGCA 240  
TAAATGTAA AAATAGTAAA ATGAGAAAAA TAAACTATT ATACAGTAAA 290

SEQ ID NO:2654

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03091

SEQUENCE DESCRIPTION:

GATCTGTCCT CAGCTCTGGA CCAATTCCC CTTACTTCAT TTTGGCAAAC ACTAAGTCAA 60  
ATAGTGAAAT GCCTGTCACT ACATAGAACC TATTACCTGG GGCAAATACG AACAGATTGA 120  
GTTTCCTTCA TCTTGTGTAA ATATGATGAA ACAGAGACCT GGTAACCTGG TGACACTGTT 180  
AAACCCTTT NGGGATAAAG CCAAATGTAA ATGGAAACAT TAAACAGATA ANTTGTGGTG 240  
TTGAGACTTT TCTGAATTGA GAAAAATAAA TGTAATTTTG GAAGAAA 287

SEQ ID NO:2655

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03092

SEQUENCE DESCRIPTION:

GATCTGACCG GCTTCAAGCT CAAGCCCTAC GTGAGCTACC TCGCCCTTNA NGAGCGAGGA 60  
GACGCCCTG ACGGCCGCGC ACTCTTTCAG CGAANCNGTG GCGCCTGCCA TCGAAAAGNA 120  
CTTCAAGGAC GGTACCTTCG ACCCTGACAA CCTGGAAAAG TACGGCTTCG AGCCACACA 180  
GGAGGGAAAG CTCTCCAGC TCTACCCAG GAACTTCTG CGCTANTGGG CGGGGGAGGG 240

GCGGCCTGCC CTCATCTCAT TTCTATTAAA CGNCTTTGCC AGCTAAA

287

SEQ ID NO:2656

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03094

SEQUENCE DESCRIPTION:

5 GATCGTGGAG GAGGGACAAC GCTGCCACCG NTTCGNCTGC AACACGTGCC CCTACGTGCA 60  
CAACATCACC CGCAAGGTAA CAAATCGGAA GTACCCAAAA CTGAAAGAAG TGGATGATGT 120  
GCTTGGTGGA GCAGCTGCCT GGGAGANTGT TGA CTCTACT GCAGAGTCGT GTCCCAAATG 180  
CGAACATCCT CGTGCTTACT TCATGCAGCT TCAGACCCGC TCTGCAGATG AGCCGATGAC 240  
15 CACCTTCTAC AAGTGCTGCA ATGCTCAGTG TGGACACCGC TGGNGGGATT NGGNCAGGT 300  
NTGGCCAGC TGCCCTNGTG TGTGCTTGCC TTGTNCCTCN N 341

SEQ ID NO:2657

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03095

SEQUENCE DESCRIPTION:

25 GATCCACAAG GTTGTCTGCT AAACCTGCTC CTCCAAAGCC ACAGCCCAAG CCTAAAAAGG 60  
CCCCTGCAAA GAAGGGAGAG AAGATACCCA AAGGGAAAAA GGGAAAAGCT GATGCTGGCA 120  
AGGAGGGGAA TAACCCTGCA GAAAATGGAG ATGCCAAAAC AGACCAGGCA CAGAAAGCTG 180  
AAGGTGCTGG AGTTGCCAAG TGAAGTGTGT GCATTTTGA TAACTGTGTA CTTCTGGTGA 240  
CTGTACAATT TCAAATACTA TTTTATCA AGTTTAA 279

SEQ ID NO:2658

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03096

SEQUENCE DESCRIPTION:

35 GATCTGAATG TNCAGTTCTA GCCAAGGTAG ATTTTACTTT CAACTTTTTA ATCAGTATCA 60  
CTTTCTGTGC TTAATATTT GGTGTTACCT TGTCTGTTT CATTTGTCTA AAATNCTGTA 120  
40 GAGATGACTA AAATTTGACA TAATGGTGT AATGGATTGT NAAGGTAAT TTCAGTTGAN 180  
GATTAANGCA AGANGCCATT TTCCCATGA CTTTGGTTT GTTTACATT TNCCCTTCA 240  
GTTAGTATAC ACTACACGTA CTGTAATAAA GTNCAATAN 279

SEQ ID NO:2659

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03097

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTTTNCT AAAGCAAGGC CTTGAGCAAG TAGGTTGCTG TCTCTAAGCC CCCTTCCCTT 60  
 CCACTATNAG CTGCTGGCAG TGGGTTTNTA TTCGGTTCCC AGGGGTTGAG AGCATGCCTG 120  
 TGGGAGTCAT GGACATGAAG GGATGCTGCA ATGTAGGAAG GAGAGCTCTT TGTGAATGTA 180  
 AGGTGTTGCT AAATATGTTA TTGTGGAAAG ATGAATGCAA TAGTAGGACT GCTGACATTT 240  
 TGCAGAAAAT ACATTTTATT TAAAATCTCC TAAA 274

SEQ ID NO:2660

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03098

SEQUENCE DESCRIPTION:

GATCTGCCTG CNTTGGCCTC CCAAGGTGCT GGGATTACAG GTGTGAGCCA CCACCCCAG 60  
 CCGCCTCTAT GCTTTTGGNT TCTTTGATAT ATCTAAACTT AAGGTCAGAA CAGAAATTCA 120  
 TGTGCTGAAC AGAATGGATT CTTTTTGCAAG TACCAATCCA ATTGAATCCT CTTTTTATTT 180  
 TCCTGCGTCC TTACCAGTCA CTTTGATAGT GCTAACTAAC CTACACTATG GGGGTTATTC 240  
 ATGANTTAAG TATGATAAA 259

SEQ ID NO:2661

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03099

SEQUENCE DESCRIPTION:

GATCTGTGTT TGTAATACTG GTTGTAATTA ATTTTTTTAA TTCATGAACN AGCGGAAAAT 60  
 TTATTAAATT AACTATTAAC CACATTCACC TTGTAAATGA CTGTATAAAA CTNGTNGACA 120  
 ATGCACTGAC TTTAGAAAGA TGTTAATGTG CATAANTNGA GTGTAAATAA NATAGTGTG 180  
 ATGTACTGAN ATATGACCTG TATAANNNGT ATTAGTAATT GTNTATGGGG TGTACCTGTT 240  
 TATCTGTAAC TGTNATCCAA ACAAATNAAA TN 272

SEQ ID NO:2662

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03100

SEQUENCE DESCRIPTION:

GATCTATCTG GNNTGTGCNT TAGACTNGAT GAGAAGGTGT GAACTCTGCA GAAAGTCTCT 60  
 CCTTCATCAC TGAATTCAGT CACTTGGAGA TGACAACTTC AAATGCTAAC CCGATGACCC 120  
 CAGAAAACCG TGTGAGATTC GTACCGAAGA ACCTTGTTGGA ATCCCTTTNC TTAGGCCCAA 180  
 CCTGGTGCAT AGCTCGAGAA AGANTNTTIN CCAAGGAAAT GTCTCGGATA TGGGTACTGT 240  
 ATTTGAAAGC TGTTAGCTTT GTCAACACGN 270

SEQ ID NO:2663

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY: linear

CLONE: HUMGS03101

SEQUENCE DESCRIPTION:

5 GATCATGAAT CAAGCCCTGG AACAGATGAA GACAAAAGCG GATGAGTGAG TTATATAAAC 60  
TTACTTCCAT TCTGTTTCGG ATTTTAAGTT TGAGAGACTT GCTAATNAAT CTCCTTTATG 120  
TTGTTTTCTT TTTCAATTGT TTTGGATTGT TTTATGTTTG TCCTTTTTTT TCTTAATGTG 180  
GATTTTCATTG AGTTGATTTT TTGATAATCT GCAATCTGGA TAATTTGTAC TGCTAAAGTT 240  
TTAATAAACT CGACATGAGA AAAACAAA 268

SEQ ID NO: 2664

SEQUENCE LENGTH: 267

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

CLONE: HUMGS03102

SEQUENCE DESCRIPTION:

20 GATCAAAATA GTAATAAATC AACAAATAAT TTTTGATTGA CTGGTGGAAT TAGATTTACT 60  
AAATAAAAT GGCTTAAATT TTGACTGTAC TAACTATAAA TGTAATGAAT TATAATAATT 120  
ATAAATGGTA TAAATGCATT CTACAATGTG ATTATTTTCT GTATTTTAGT ATATAGTATA 180  
AAATGGAATT ATGGGGTTAA AGTACTTTTA TTACATTTCT TAATCCATTG TTTTACCTA 240  
ATAAAATTC CTCCTCTATA TTCCAAA 267

SEQ ID NO: 2665

SEQUENCE LENGTH: 266

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

CLONE: HUMGS03103

SEQUENCE DESCRIPTION:

30 GATCCGAATC TGTGCCCAGC GCTAAAGGCT CAGTGTTAGC ATGGCTTNNN CTGNCCGGTG 60  
TGCCATATTC TTGTTGGAGA TGAACCGTAG CACCAGAGCC CATTCTTCCT TGTCAGTCTT 120  
GGCCCAAAGA TGTCACCATT CCTAGTTATT TGTCACCACA TAATTGGTGT TGATTGGAAA 180  
35 CTTTTTCTGA GATGGGACAG AACTGCTGGG TTGTCTTTT CCATGTAACT TAAGCATAGT 240  
AATATAAATA AAGTAATAGT TGGAAA 266

SEQ ID NO: 2666

SEQUENCE LENGTH: 265

SEQUENCE TYPE: nucleic acid

TOPOLOGY: linear

CLONE: HUMGS03104

SEQUENCE DESCRIPTION:

45 GATCCTCCCT GTCATGCCAC ATTTCACTGA TTGGAATGTG GAAATGGAAA AGGAATTTAG 60  
GATGTGCATT TTCACCTGAG GTTTCCTGCG ATCCCTGCAG TGCCAAAGCC CCACCTTCAG 120  
GGACCACCTG GAATGTGTGA GGGGCTGACA GCACAGTAAC GTGCATACAT ATCTGCAGGG 180  
CTGGAATGGA AGCTTTAAAG GTGGTAGTGA TTTTNATTTT GGAAGAATCA TGTTACCTTT 240  
TTGTTAAATA AAATTTGTAC TCAAA 265

55

SEQ ID NO:2667

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03105

SEQUENCE DESCRIPTION:

GATCCAGTGT CCATGGAAAC ATTCCCACAT GCCGTGACTC TGGACTATAT CANTATTTGG 60  
 AAAGCAGGGT TCCTCTGCCT GCAAACAAGC CCACGTGGAC CAGTCTGAAT GTNTTTCCTT 120  
 TNCACCTATG TTTTAAAGTA GTCAAACCTC AAGAAACAAT CTAAACAAGT TTCTGTTGCA 180  
 TATGTGTTTG TAAACTTGTA TTTGTATTGA GTAGGCTTCT ATATTGCATT TANCCTTGTTT 240  
 TTGTAAGTCC TGATTCTCCC TTTNCGGATA CTATTGATGA ATAAAGGANT TAANGTGGAT 300  
 AAA 303

SEQ ID NO:2668

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03106

SEQUENCE DESCRIPTION:

GATCAACCAA GGCAGATGTG ACAGCAAGGG CCACGGACCC CATGGCAGGG GTGGCGTCTT 60  
 CATNAGGGAG GGGCCCAAAG CCCTTGTTGG CGGACCTCCC CTGAGCCTGT CTGAGGGGCC 120  
 AGCCCTTAGT GCATTCAGGC TAAGGCCCTT GGGCAGGGAT GCCACCNCTG CTCCTTCGGA 180  
 GGACGTGCC TCACCCCTCA CTGGTCCACT GGCTTGAGAC TCACCCCGTC TGCCAGTAA 240  
 AAGCCTTTCT GCAGCAGCTG AAA 263

SEQ ID NO:2669

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03108

SEQUENCE DESCRIPTION:

GATCTGGCCT AGGTCCCCC TTTNTNCTGT CCCCTGTNTT TAAGTCGGGA TTTTACAGA 60  
 GGGAGCTGTC TCCAGACAGC TCATCAGGAA CCAAGCAAAG GCCAGATAGC CTGACAGATA 120  
 GGCTAGTGGT ATTGTGTATA TGGGCGGGAC GTGTGTGTCA TTATNATTG AGTTATGCTG 180  
 TTGTTTAGGG GTAAATAACA GTAAATAATT AATAATAATA ATAATAATAN TAATAATAAN 240  
 GGNGCNGACG TTCTTAAA 258

SEQ ID NO:2670

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03109

SEQUENCE DESCRIPTION:

GATCCACCCG CCTCGGCCCT CCAAAGTGCT GGGATTACAG GCATGAGCCA TCACACCTGG 60  
 TCAACTTTCT TTTGATTAGT GTTTTGTGG TATATCTTTT TCCATCATGT TACTTTAAAT 120

# EP 0 679 716 A1

ATATCTATAT TATTGTATTT AAAATGTGTT TCTTACAGAC TGCATGTAGT TGGGTATAAT 180  
TTTNATCCAG TCTAAAAATA TCTGTCTTTT AATTGGNGTT TAGACAATTT ATATTTAATA 240  
AAATGGNNGA ATTTAAA 257

SEQ ID NO:2671  
SEQUENCE LENGTH:257  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03110  
SEQUENCE DESCRIPTION:

GATCAGATGT NGCTCAGAAA CTTTCATTGT TTACCTAATA ATTTAATATC ACTAGTTTCC 60  
TAGTGGGTCA AGCAGATGCA AAANCCAGCT TATTTCTCCTC TATGTNCTCT CAAGCTTATN 120  
GCTTATTINA AAGTAAAANC CTGAAAAAGG AAAATATTAG GTTGGTGCAA ACGTAATTNC 180  
GGTTTTGCCA TTGTNGAAAT TTGCCGTTTT ATATTGGAGT ACATTCTTAA NTAAATGTGG 240  
TTATGTTATA CATCAAA 257

SEQ ID NO:2672  
SEQUENCE LENGTH:256  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03111

SEQUENCE DESCRIPTION:  
GATCAATTAC TGCTCTCACT TAGAACAAAG CCTGAGTCCG AGAATATTTA TATTTTACCA 60  
ATATATGCCT GTTACAAGAG AAGGAAATAT GAGTTATTTA AGTTTAACTT TTTTATGTGA 120  
ATTCAGAGTT TATTTATCGA GGGAAATATG TACAAAGAAG CTTCAAATGG AATATTTACC 180  
GACATTCCTT ATACATGACA GACACTNGGC TACATGGGAA GATGATGTTA ATAATAANNT 240  
GATTTTAAAN TGGAAA 256

SEQ ID NO:2673  
SEQUENCE LENGTH:256  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03112  
SEQUENCE DESCRIPTION:

GATCTGGAGA GGATTAGGGA CGGCTCTTGT GGGCACATTT TNNCTCTAGT TTCATGGGTG 60  
GAGATGGCAT CTCCNGTGGT CTGCAGCATG CAAGTAAAGA CACCAGGTGG CACCATTNAT 120  
NAGCTTTCAA TCCCATGGAG AGGTCCCATC ATGTAAC TNC CAAGAGGTG AAGGAACCAA 180  
CTACCTCTTG CATATTGTNG CTAATGGTTC TNGCCTTCTC CTTCAGACT TGGGAAATAA 240  
NTTTNAAAAAT NGTAAA 256

SEQ ID NO:2674  
SEQUENCE LENGTH:433  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03115



## SEQUENCE DESCRIPTION:

GATCTACCTT GGTGATTGG ACCCTGGTTG CTTTGTGTCT AGTTTTCTAG ACCCTTCATC 60  
 TCTTACTTGA TAGACTTACT AATAAAATGT GAAGACTAGA CCAATTGTCA TGCTTGACAC 120  
 AACTGCTGTG GCTGGTTGGT GCTTTGTTTA TGGTAGTAGT TTTNCTGTAA CACAGAATAT 180  
 AGGATAAGAA ATAAGANTAA AGTACCTTGA CTTTGTTCAC AGCATGTAGG GTGATGAGCA 240  
 CTCACAATTG TNGACTAAAA TGCTGCTTTT AAAACATAGG AAAGTAGAAT GGTGAGTGC 300  
 AAATCCATAG CACAAGGTAA ATTGAGCTNG TTANGGCAAT CAGGTAAAAAT AGTCATGNTT 360  
 CTNTGTNATG TAANCCCGTA AATGANTGTT CCTGGTTTCN CGGTGGTTTT TTNANGGGNC 420  
 NCNTTNANNT TTN 433

SEQ ID NO:2675

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03116

## SEQUENCE DESCRIPTION:

GATCAGAAGA AAGAAAGACA ACTTTCCTCT GCGCGGAACA CTCACACGGA AGGGCTGGCC 60  
 GCCTCCCTGA GCCGGCTGGG AGTNGACGAC AGGACCTACC TCCCCAGAGC AAGGGCCTGG 120  
 GGCTTCCCGC CAAAGCTGCC GCGGAACCCC GCTAGTGC GA CCACCTCCC TCCGTCGGTA 180  
 TGTCTGCTT TCCAGCTGAA CCCAACTAC AAGTGGGTTT AAAAAAATAA ACACCACCAC 240  
 CAAAAACAAA 250

SEQ ID NO:2676

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03117

## SEQUENCE DESCRIPTION:

GATCTGAAAA AGATGGTCAT TCCGGACTCC TGACGCCGCC AGTCCCGCGG TGAGACGTGA 60  
 GCNCCATTGG GTCCAGTGGC CTCTNTTTC GTGGCAACCT AGTAACCATT AATTTTNAAT 120  
 TAAAGGAGAC AAAAAGCTCG ATGACAGCTC CAGGTCTGCT GAAGATGTCA AGAATCTGTA 180  
 TTAATATACA GCAAGAGAGC ATAATTGTNT GTCCATCTTC CAGAGCAGCG AAAAATGGAG 240  
 GGATAAN 247

SEQ ID NO:2677

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03118

## SEQUENCE DESCRIPTION:

GATCAAAACC ATCCTGGCCA AAATGGTGAA CCCTGTCTCT ACTAAAAATA CAAAAATTAG 60  
 CTGGGCATAG TGGCACGCGC CTGCAGTCCC AGCTACTCAG GAAGCTGAGG CAGGAGAATC 120  
 GCTTGAACCC AGGAGGCAGA GGTGCTGTG AGCCGAGATT GCACCACTGC ACTCCAGCCT 180  
 GGGCAACAGA GTGAGACTCC ATCTGAAAAA AAAAAANTNC AGGCNTGCAA GNTTGGCGTA 240  
 ATCAN 245

SEQ ID NO:2678

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03119

SEQUENCE DESCRIPTION:

GATCAGCAGG GCTACCATCT CACTCTTCTG TAATTTTACA ACATTCTAAA GGAAGTAAAT 60  
CACCAGATTT GCTGATGTAT CAGGGTCCAC CAGACACTGC AGAAATAATA AAAACATTAC 120  
CTCAGNAATA CAGNAGGAAA CTTGTGTCTC AAGAAGAAAT GGAATTTATC CAACGTGGAG 180  
GTCCTGAATA ACCATGGTGG CTGCTGTTTG TCATCAGACA NTAGAATTGT CTTTACAATA 240  
AAGGNCTTCC AAAATGGCAG ATGNGAAACT GTATATTAAA CACCTTTAGT AANTANTATG 300  
GANNAAGTGN NATNTAGGNN ATTTAGGTGG TCCCTNGGAT TNCCGNN 347

SEQ ID NO:2679

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03120

SEQUENCE DESCRIPTION:

GATCTGGCCT GGAGAGGCCA TCCTATACCC CTTATTAGAG CCATGACAGC CTACAGAGTG 60  
AGGTGAGGTG CTCCACCTT CCCAGATGGT TCCTTTCTGC CCCTTCCTGG AAGGAAAGGT 120  
GAGGCTGCCA ATAGCCTCCT GGCACCAGCC AGACCTCACC CTTGACCAAC CTCTCGGGGC 180  
TGGGGGTTCA TTCCTGGGGC ACTGTGGCCT GGTTTTGCTT TGAAACCAAG AAAGAGCAAA 240  
GN 242

SEQ ID NO:2680

SEQUENCE LENGTH:411

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03121

SEQUENCE DESCRIPTION:

GATCCCCAAC AATGTGAAAA CGGCTGTCTG TNACATCCCA CCTCGGGGGC TAAAAATNTC 60  
CGNCACCTTC ATTGGCAACA GCACGGCCAT CCAGGAGCTG TTCAAGCGCA TCTCCGAGCA 120  
GTTACGGGCC ATGTTCCGGC GNAAGGCCTT CCTGCACTGG TACACGGGCG AGGGNATGGA 180  
CGAGATGGAG TTCACCGAGG CCGAGAGCAN CATGAATGAC CTGGTGTCCG AGTACCAGCA 240  
GTACCAGGAT GCCACAGCCG AGNAGGAGGG CGAGTTCGAG GAGGAGGCTT AGGAGGAGGT 300  
TGGCCTAGAG CCTTCAANTC ACTGGGGAAA AGCAGGGGAA GCAGTGNGA ACTCTTTTAT 360  
TCACTTCCNA GNCTGGTCCN NGTNGGNCNT GTTCCCACTG TGTGCAATTG N 411

SEQ ID NO:2681

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03122

## SEQUENCE DESCRIPTION:

5 GATCTGCGCA CGGTGCACAG CCCACCAGAG CACTACAGCC TTTTATTGAG TGGGGTGGGG 60  
 CAAGTGCTGG GCTGTGGTCG TGCCCTGACA GCATCTTCCC CAGGCAGCGG CTCTGTGGAG 120  
 GAGGCCATAC TCCCCTAGTT GGCCACTGGG GCCACCACCC TGACCACCAC TGTGCCCTC 180  
 ATTGTTACTA CCTTGTGAGA TAAAACTGA TTAAACCTTT GTGGCTGTGG TTGGCTGAAA 240

SEQ ID NO:2682

10 SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03123

## SEQUENCE DESCRIPTION:

15 GATCACCTGG GGACAGAGGT GAAAGGCCTG CTGGGCCTGC TGGAGGAGCT GGCCTGGAAC 60  
 CTGCCCCCGG GACCCTTCAG CCCCCTCCC GACCTTNTCG GAGATGGCTT CTNAGCCCTG 120  
 GAGCTGGAGC CCAGCAGTTG GAGGTGGTGC ACCTGCCAGG CAGCGCCAC AGAACCAGCC 180  
 CTGTCCTCTC GACTTCCTTC CTTAGCTTCA TGTGAAATAA AAGCTATTCT GGTCAAA 237

20 SEQ ID NO:2683

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03124

## SEQUENCE DESCRIPTION:

25 GATCGGCATG GTCATTCACC AAGTGGAAGC CAAACCCTCT GTGTATTTCA TCAAGTTTGA 60  
 TGATGATTTC CATATCTATG TCTACGATTT GGTGAAAAAG TCCTAACTGT TAGGGTAAAA 120  
 TTTGGCACAT GTGTGGAAC AAATGTATAA TTTGTAGACA TGCAAAAAAT GTTGCTTTTC 180  
 30 AGTGTATTGA AAGCTTATGG AATCCCTGAT AACTAAACAT CTTTGCCAGC ATTAAA 236

35 SEQ ID NO:2684

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03125

## SEQUENCE DESCRIPTION:

40 GATCACACAT ATCCTTCCTG AGANGAGCAG TGAATAAAT GGAATATCTT TTAAAGANCA 60  
 GCTCCTCTTT AACAAAAAN CTAAAAAGAC AAATGTGAGA TGGGCTTAGA GTTAGTNCTC 120  
 TGGGAACCTG AAAGACATTT ATGCCATATT ATTTATNCAC GTGTTGTNC CTGGTGGGCA 180  
 AGATGCCATC TGAGGCTTCA GATGAGAAAT TGGGGTAANN TGGAATTTT NCACTN 236

45 SEQ ID NO:2685

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03126

## SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

GATCAATCCC TCAAGATTTT GAAATCCTGA AGAAATTGAG AAGTATGTTG CTGAAATTGA 60  
 AAANGAAAAA GAAGAAAACG AAAAGAAGAA ACAAAGAAA GCATCATGAT GAATAAAATG 120  
 TCTTTGCTTG TAATTTTAA ATTCATATCA ATCATGGATG AGTCTCGATG TGTAGGCCTT 180  
 TCCATTCCAT TTATTCACAC TGAGTGTCTT ACAATAAACT TCCGTATTTT TAAA 234

SEQ ID NO:2686

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03127

SEQUENCE DESCRIPTION:

GATCTAGGCC TGGCAAGANC TCTGGCCCCA AGGCCTCCTC TTCCCAGGGG CTGCCAAGTC 60  
 CTGGCCCTGG CCCTGGCATA TNACCCCGNA CTGTGGGGCC AGTCACCACT AGCCTGGCTC 120  
 AAATATTCCC CAGGGAGACT NCTGTGTGCT GCCCGGCTNC CTGCTGGCTC TCCCCAGNC 180  
 CCACATCCCN TCTNGAAGAG AATGTAAAAT AAACCTGGAC ACAAGGGAAA 230

SEQ ID NO:2687

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03128

SEQUENCE DESCRIPTION:

GATCCATGAG GTCCTAGCCC CTGGCTGCCT GGATGCNTTC CCCCTGCTCT CAGCATATNT 60  
 GGGGGCCTC ANTGCCCGGC CCAAGCTCAA GGCCTTCCTG GCCTCCCCTG AGTACGTNAA 120  
 CCTCCCCATC AATGGCAACG GGAAACAGTG AGGGTTGGGG GGACTCTNAG CGGGAGGCAG 180  
 AGTTTGCTTT CTTTCTCCA GGACCANTAA AATTTNTAAG NGAGNTACTA AA 232

SEQ ID NO:2688

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03129

SEQUENCE DESCRIPTION:

GATCACAAAA TGTNATAAAA CTTTAAATGT ATAAACTTT ATCAAATAAA GTTTTATTTT 60  
 CCCCTTTAAA ATGTATTTNT TTAGAGGCAT TACTTTTTTA AAAATATTGG TCAATTNCNG 120  
 ACATAAGATG TGAGGTTTAC AGTTGTATTC CAGTATTCAA GATAGATTCC TGATTTTCCA 180  
 ATTAGGAAAA GTAAATCCA AAATGTTAGC AAAACAAAGT GCAATATTN 229

SEQ ID NO:2689

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03131

SEQUENCE DESCRIPTION:

GATCCCATGC CCAGGTGTCC AGCAGACCTC AAGGCAGAAG GGTCACCTAA CCCAGGAGTC 60

EP 0 679 716 A1

CACAGACTGA TGTGACCTCA GGTTCACACA TCANTGGCCA CAGGGCAGGG CCCACCTGGT 120  
AGAAGTTTTC TGGATATGGC CAGGGTGGGT GTNTGGCTAA NTGGGCCTGA ACAGAGGGAA 180  
CCTAGGGCCC TTGGCCAATG TGATTAAAGC TGCCATCTTG AAA 223

5

SEQ ID NO:2690  
SEQUENCE LENGTH:222  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS03132

SEQUENCE DESCRIPTION:

15

GATCCGCCCT GGAGAAGTGA GTGGCTGAGA CCCGGGTGGG GCCCTCCTAA CTTGGNTCT 60  
GGGGGCTTCC NTTCTGGGTC TTGTCCGGGA TATGGCCTTC CTGAAGGTCT TACCTCCCCC 120  
AGCCGCCCTG CACTTGACCA CCAAAGCAAT CTCTAAGCTT ATAAAGGAGA AACATGTATA 180  
TATGGGGTTT TTTGGAGTAA AGGAAAATTC TAAGATATTA AA 222

SEQ ID NO:2691  
SEQUENCE LENGTH:222  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS03133

SEQUENCE DESCRIPTION:

25

GATCCACCTG CTTGGCCTT CCAAGGTGTT GGAATTACAG GCGTGAGCAA CCGCGCCTGG 60  
TCTATATGTN ATTTCAAATN AGGTGGCCTT ATAAATATAA GCAGATGGGT TTCTGGGCAA 120  
AATCAAATNA TTTCTGTCTC TATTTNNTTG AGTACCAATT GTAAAACTG AAATTAGGTT 180  
GAGGAAAGTN CTTTAGAAAT AATAAGATG TACAANTACA AA 222

30

SEQ ID NO:2692  
SEQUENCE LENGTH:220  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

35

CLONE:HUMGS03134

SEQUENCE DESCRIPTION:

40

GATCTGCCCC CCTCAGCCTC TTGAGTAGCT GGGACTACAG GTGCATACCA CCACACCTGG 60  
CTAATTTTTT AATTTTNATT TTTATTAAAG ACAAGGTCTC ACTATGCTGC CCAGGTTGGC 120  
CTCCCAAAGT GTTGGGATTA CAAGTGTGAG TCACCGTGCC TGGTCCCATG TACTTGANGT 180  
CATCACTANC AAAATGTATA GATATTGTAT AATGGCAACN 220

SEQ ID NO:2693  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

45

CLONE:HUMGS03135

SEQUENCE DESCRIPTION:

50

GATCTTTAAT AAAAATTGA TATGAAAAGC ACAATGTGCA GANGTTATGG AAAACCTATA 60  
GAGGATTACA ACAGGTAAAC GTTAAAGAGA ATACATTGCT GACTTATAGT GATGTGGCTA 120

55

# EP 0 679 716 A1

AGANGTACAT GCTTTGTTGT AAAATTNCTT GAAAGCCCAT TGAAAGATGT ATCTGTTTAT 180  
TTACAGTCTT TGAAGTAAAA GTTACCAATG TTTGCCAAA 219

SEQ ID NO:2694

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03136

SEQUENCE DESCRIPTION:

GATCTNGCCC CTGCGCTCTN GCCTGGGTGA CAGAGCAAGA NTCTATCTNA AAAATGTTTT 60  
TAAAAAATAC TTCTAGGGA AACACACATT TNGCCCTATT TGGAACCTTG AAAAGTGAGC 120  
CCTCCTCTGC CCATGGGCGG TGCTGCTCAG CCTGCCATAC TCGCTTGCTT TGCTGTTTGG 180  
NATTTGCCTC CAGAATAAAG GTCCTTTTTG TTGTTGAAA 219

SEQ ID NO:2695

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03138

SEQUENCE DESCRIPTION:

GATCCTAATC CCTTCCTCTC CCATTCACCC TGTGTAACAG NACCCCAAGG ACCTGCCTCC 60  
CCGGAAGTGC CTTAACCTAG AGGGTCGGGG AGGAGGTTGT GTCAGTACT CAGGCTGCTC 120  
CTTCTCTAGT TTCCCTCTC ATCTGACCTT AGTTTGCTGC CATNAGTCTA GTGGTTTCGT 180  
GGTTTCGTCT ATTTATTA AAATATTTGA GANCAAAAAA CAAA 224

SEQ ID NO:2696

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03139

SEQUENCE DESCRIPTION:

GATCAAAGTC TTAAGTGTGT TTGCAGCTCA AAAATAAAGA TGTATTAAGG AGGGGAAAAC 60  
CTGGTCTAAG TGCAAGGCAC ACTTACAGCG AGTTTACTT TCGGTTGTAT TTTCTTTGTA 120  
TATNATAAAC ATTTATTTAA CTTGTTGCCG TTTGAAGTAA AAAATTTCCA AAATGTATGC 180  
TCAACAATAA TCATTAAAT GTTTTCAGCG TACAAA 216

SEQ ID NO:2697

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03140

SEQUENCE DESCRIPTION:

GATCAAATTG TGTTTAGTAT CACTATCTTC TCTCCTCGTT TCTCTCTTAC TCCTCATCCT 60  
CCCAGAACTT ACCAGTTTAT GGTAGAAAGA TGGGAACCTT ATTTGAATGT GTTTTTTTT 120  
TCCATGATGT CCAATTTTGT NGTGGGAAAG GATTGGATA AAANTTTNGT TTAAATTNG 180

GTAGNTTTTN ATCTNTACAA NTTTAANTAA AATNAN 216

SEQ ID NO:2698

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03141

SEQUENCE DESCRIPTION:

GATCTCAAAA GTATTCCTCA GGGTAGTCTC CATTCTGTC ATTTNCCTC CTATTCATGA 60  
 GACGGAAAAA TTATGACCAT GGTACAGAGT TGTATCAAGG AAATGAAGAA CTAGAACATT 120  
 GAATTGAAAG GTTTTGAAAG GGTTCACAAT TTCTTTTCAT TTNCTATTAA TGTCTTCTTT 180  
 TAAATNCTCT TAAGAATAAA ACTTTTTTCT AATAAA 216

SEQ ID NO:2699

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03142

SEQUENCE DESCRIPTION:

GATCAGCAAA CAGGAATACG ATGAAGCCGG GCCTTCCATT GTCCACCGCA AATNCTTCTA 60  
 AAACACTTTC CTGCTCCTCT CTGTCTCTAG CACACAACCTG TGAATGTCCT GTGGAATTAT 120  
 GCCTTCAGTT CTTTTCCAAA TCATTCCTAG CCAAAGCTCT GACTCGTTAC CTATGTGTTT 180  
 TTTAATAAAT CTGAAATAGG CTACTGGTAA A 211

SEQ ID NO:2700

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03145

SEQUENCE DESCRIPTION:

GATCACGAAC ANTAGCTTGC GCTCTACTCT GTAGTTATGT GGATTGCCGA GCAATNACCC 60  
 TTTTCAATNT CTTATTTCTG TGTTACTGAG GACCCTAATC ACTTAGGGAT GTAATTTTAT 120  
 AGTATAAACT TTCTGNACAG TTTTNCCTNAT AGTCTAATAA GTAAAAAGTG TCCNNCAAAT 180  
 TATGATAATT GCCTATGGTA CATGGATAAN TTAANGCACT GCACACGGTG TAAANN 236

SEQ ID NO:2701

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03146

SEQUENCE DESCRIPTION:

GATCCATTTT TNACACACAC TGCCAGAGAT ACTCTAGGCA TGTAAGCAC AACATACAT 60  
 ATAAAANCTG CGGGCTTCAA AAAATATAAG TAGGATGTCA TCTATACTGT CATACACTTT 120  
 GTTTTTTATC ACTTACTTAA TGTTATATCT NGGATATTGT ATTACCCTGG GTATTAAAAA 180  
 GAACTCCTTT CACATTTTAA AATAAA 206

SEQ ID NO:2702

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03147

SEQUENCE DESCRIPTION:

GATCTAAAC TGGGGTTTGG GGGAGGGTTT CANCCTCTCC CCACTCCNCT TGCCCCACAC 60  
CCTTTACTCC CCAGCCCAGA GAGACGCTGC TTTTACCAGG AAAGACTATT GAAAGATGTT 120  
TTATATTATT TTNCTCTGAC CTTCCATCC TTGAAAAAAT GGGGAAAAAA GAAGAAAAAA 180  
GACAAAATCG ACCATAAAAG ACCAAA 206

SEQ ID NO:2703

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03148

SEQUENCE DESCRIPTION:

GATCTTGTTA ATGCATTTTT GATGGGAAGA AAAGGTACAT GTTTACAAAG AGGTTTTATG 60  
AAAAGAATAA AAATTGACTT CTTGCTTGTA CATATAGGNG CAATACTATT ATATTATGTA 120  
GTCCGTTAAC ACTACTTAAA AGTTTAGGGT TTTCTCTTGG TTGTAGAGTG GCCCAGAATT 180  
GCATTCTGAA TGAATAAAGG TTAAG 205

SEQ ID NO:2704

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03149

SEQUENCE DESCRIPTION:

GATCCTGAGG CTTTGATGCT ATTTNTTAA TCCAGCTGGT CTGTGGAGAA GCCTGGGACA 60  
GAAAGAAGCA GCCAGACTCC AGAATCCCCC ATTTTAATAG CTATNNNATG CTATGTCCCC 120  
GTCTTATTCC TGGCAACTTA CCTCTCAGCT CGTGCACTGT GACATTACAG CAAGAAGTAC 180  
TAATATAAAT GACACAAANG AAA 203

SEQ ID NO:2705

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03150

SEQUENCE DESCRIPTION:

GATCTGAAAA AAATACGGTT GAAAGTGGTG CAGGTAATTA CAATGTGTAG GCAAACCAGA 60  
AAACCATGGC TTAAACCAGC AGCTTTTGTN AGAAATNATT TCTCCAATGA NTGTAGAAAC 120  
GTTTGCNGCT GAATTGTGAC CTTNCCATTT NACCTGCTTT TCCTGCAAAG TATATTTNNC 180  
AGACCCAGGC AGTGCTGCTC GCN 203



# EP 0 679 716 A1

SEQ ID NO:2706

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03151

SEQUENCE DESCRIPTION:

GATCCAATGC TAAACTCCAA TGGTTCAGTG ACTGTGGTTG CTCTTCTTCA AGGCAGCTGA 60  
TACCTGTGCA TACTGCAGGC ATCTAAATTA GAAGACCTGC GAGTAAACT GAAGAAAGAA 120  
GGATATTCTA ATATTNTNA TATNGTTGTT AATCATCAAG GNATCTNTTC TCGATTAAAA 180  
TNCACACATC TTANGAAA 198

SEQ ID NO:2707

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03152

SEQUENCE DESCRIPTION:

GATCCATAAT TCCTATTCAA TGAACATCAT TGTTGGTGGC TGAATACATT TTGGAAGAGA 60  
GTTTTTCATC TTAGAGATTG GTGAACAAGT GTGAGGGTGT GAGAACTCA CAGAATACAA 120  
ATTTGCCTGT ATGTTTTGTG GGTTTTTTTT TTCCCCTTCA NGATGTTTNC TATTNCTAAN 180  
TTAANGTAAT TNCAAGGTAA A 201

SEQ ID NO:2708

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03153

SEQUENCE DESCRIPTION:

GATCTATTAG TTTAGTGTTC ATNAAAGAAT CAAATGTATA GAATTACCAA GCATTCGTGG 60  
GGAATNCTGT GTAGCAAATG TAAACTNAC CTGCTCGGAA GAAACGTAGG ANCGCTTCAA 120  
ACCCACTGTA ATGTTTGGTT TGANNTTATT TCCATTGCTT TNAGAGTGAN CTGCCTAAGN 180  
GTAGGCCTTA TAATAN 196

SEQ ID NO:2709

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03154

SEQUENCE DESCRIPTION:

GATCTACAAG NATTTTCTTT TAGTAGTTAT ACAAAGANT ATTACATTTA TTGGTCTGTA 60  
CAGTGTAATA AACCAGCAAT AGGGACAACA ACAAAGAGAA TCTAAGAAAG ANGACTATGC 120  
CTAANTATAG GGAAAGTTTA GAGAATCATT TTTAGACAGG ACACATTTTG CAGTAGTGAA 180  
TGTGGTAGGT TTN 193

SEQ ID NO:2710

# EP 0 679 716 A1

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03155

SEQUENCE DESCRIPTION:

GATCAGTGTT GCAACATANT GNAAGATG GCTACTGTGC CTTGTGTAC TTAATCATAC 60  
AGTAAGNTGA CCTGGAAATG AATGAACTA TTACTCCTAA GANTTACATT GTATAGCCCC 120  
ACAGATTAAN TTTAATTAAT TANTTCAAAA CATGTTANCC GCNACTTTCA TGTACTATGG 180  
AAAAGTACAN GTN 193

SEQ ID NO:2711

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03156

SEQUENCE DESCRIPTION:

GATCTCGAAC CCTGTCTAGA AGGAATGTAT TTGTTGCTAA ATTCGTCAGC ACTGTTTACA 60  
GTTTTCTCC ATGTTATTTA TGAATTTNAT ATTCCGTGAA TGTATATNGT CTTGTAATGT 120  
TGCATAATGT TCACTTTTAA TAGTGTGTCC TTTATNCTAA ACAGTAANGT GGTTTTATTN 180  
CTATCACACA AA 192

SEQ ID NO:2712

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03157

SEQUENCE DESCRIPTION:

GATCCAGAAT NGAGACTGGA CCTTCCAGAC CCTGGTAATG CTGGAAACAG TTCCTCGGAG 60  
TGGAGAGGTT TACACCTGCC AAGTGGAGCA TCCAAGCATG ATGAGCCCTC TNACGGTGCA 120  
ATGGAGTGCA CGGTCTGAAT CTGCACAGAG CAAGATGCTG AGTGGAGTCG GGGGCTTTGT 180  
GCTGGGCCTG CTCTTNCTTG GNACAGGGCT GTTCATCTAC TTCAGGANTC AGAAAGGNCA 240  
CTCTGGNCTT CAGCCANCAG GACTCTTTGN GCTGAAAGTGC AGGTGNCCAC GATTCAAGGG 300  
ANGAACCTTC TTGNCCCANG NTTTTCAAGA TGGAAAAGCT TTCCCCAACT TTGGNTTCTT 360  
NTTNTTCCC ACCAAAGAAN CTTNAN 386

SEQ ID NO:2713

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03159

SEQUENCE DESCRIPTION:

GATCTTCCGG AAAAATAAG CCCCTCCTTC ACCCCCGCAC ACCTGCATCC CTGCCGGAGT 60  
CNTGNTGAGG CACGAACCTT GCCTCCCTAG GCCGGACCTT GTGGACGACA GCCCCACCCA 120  
GTCTGTGCTC TCAGCCGCTG GCCGAAGGCC CAGCCTGCTC AGAATAAAGC ATGTCCTGCT 180  
GCCGGCAA 189

EP 0 679 716 A1

SEQ ID NO:2714  
SEQUENCE LENGTH:189  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03160  
SEQUENCE DESCRIPTION:  
GATCCCATAG TTTACATTT TNCCTGTTA TTTTGATTTT TTNCACTGCT TTATTTCTTA 60  
AAGTNCTAGC ACATCTGTNA CTCCTCCACT TCCACATTTT TNCCTGCTT ACACTTACGT 120  
GCAATCTTAT TCCTNGTCTG CACACACATG TGGAAAGCTA GAAATAAATG TTAAAACTNA 180  
CTTTTTAAA 189

SEQ ID NO:2715  
SEQUENCE LENGTH:187  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03162  
SEQUENCE DESCRIPTION:  
GATCAAACTCT CTCCTGGCTG TAGTAACCCA GTGGAATGAA TTTGGNCATG CCCCAATGCT 60  
TCTATATGCT AAGTGAAATC TGTGTCTGTA ATTTGTTGGG GGGTGGATAG GGTGGGGTCT 120  
CCATCTACTT TTTGTCACCA TCATCTGAAA TGGGGAAATA TGTAAATAAA TATATCAGCA 180  
AAGCAAAA 187

SEQ ID NO:2716  
SEQUENCE LENGTH:187  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03163  
SEQUENCE DESCRIPTION:  
GATCCAAGGG CACAAGGAGA TGAGCAAGGT GTGGAACGAC CTGAGGCCCA AGCTCAGCTG 60  
CCTCTTTGCG GGACCACACA GCACCCTGAC CCCACCGTGC TCCNNGNCGG AGGACGGCCT 120  
GTGTCCTCAN TAGCGCCTGA GGCTGNGGTG GTGCTCCCTG CGGNCGCACT AAAACCTCTT 180  
TNCNAAA 187

SEQ ID NO:2717  
SEQUENCE LENGTH:188  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03164  
SEQUENCE DESCRIPTION:  
GATCCTCCTG TTTACCCTGT ACCTCCAATG TCTGGCACTT GTAGGTGCTC AAATATTCGT 60  
TGAATGAATG AAAAATCCAT ATTGTAATTG ATGTCCTCTG GCCACATAGT TTTAAAATTA 120  
GGTGATTGAT TATATGACCG AATAGAACTA TCAAATGTTT TCCTAATAAA GTCAATATTT 180  
CAAACAAA 188

SEQ ID NO:2718

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03166

SEQUENCE DESCRIPTION:

GATCTGCCCC CCTCAGCCTC CCAAAGTGCT GGGNTTACAG GCATGAGCCN TCGCGCCCGG 60  
CCGGATTTTT TTTTTTTTG ATTCAGCTTA TACCAGGGCT GAAAACCTCA NTTTATGTC 120  
ATGACAGTNG GGATTTTTTT AAATGCCTAC ATTCTTTCTA ATAACTGTT GGAAGACNTT 180  
AAA 183

SEQ ID NO:2719

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03167

SEQUENCE DESCRIPTION:

GATCCAAGTG GCCCAGCAGA AACGGAATTN TNGTNAAAAT GACTGATTCT GGTGCATGTN 60  
AAAGGCTCTG GGGAAATNAAT ACCTGTTTGG TCCAACTTA CTGTATCATA ATGCTGTATA 120  
TGTINGAAAAC GTAATACCTG TNAATGTCCT AATGAATCAN GTTTTGCAGA AAACACCGTA 180  
AA 182

SEQ ID NO:2720

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03168

SEQUENCE DESCRIPTION:

GATCCTCCAT TGGAGTGGCC CAATCTTTCC TCTAGGGCAA TCCTGAAAGC CCAAGGCCCT 60  
TCNCACTCTG GCCTTGGCTT CAGCTGGAGA AGGTAACAT CAGTCATTGT CAAGGCACCN 120  
CCANCCNGA CAGACCGTGT CTCTGATAAA GGTTTGAAG TGATAAAGTT TAAAACTAA 180  
A 181

SEQ ID NO:2721

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03169

SEQUENCE DESCRIPTION:

GATCCTCACT CCACTGTCAT GTTTGAAAGA GGTATTGGTG TTCTGGAGTG GGGGTCAACC 60  
CCTCCCACT CTCTGTGCTA AGTTCACTTG GGAGGATGGC AGTAGGAGCC AGGGCTGGCC 120  
ATGGGTCCCC TACGCTTNCC NNTAGGATAT ACCCTGGAGA ATGGCAAAAT GATTTAA 178

SEQ ID NO:2722

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03170

SEQUENCE DESCRIPTION:

GATCCTAAGG CAAAGAGGTG TTTTTCCTTC TGGTTGATTC ATCCCAAAGC TTTCCACCCC 60  
AGGTTTTCTC TGAAAGCTTA GCCTTAAGAG AACACGCAGA GAGTTTCCTT AGATATACTC 120  
CTGCCCTCAG GTGCTGGGAC ACACCTTTCG AAAATGCTGT GGGAAAGCAGG AGCTGGGGAG 180  
CTGTNTTAAG TCAAAGTAGA AACCCTCCAG TNTNTGGTGT TGTGTAGAGA NTAGGNCATA 240  
GGGTAAAGNG GCCAAGCTGC CTGTAGTTAG TAGAGAAGAN TGGGGAN 287

SEQ ID NO:2723

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03171

SEQUENCE DESCRIPTION:

GATCACCATG ACTGCAACAT GGTTTATATT CATGCTGCCC TAGAACTTT TGTAATTATT 60  
TGGTGCAAT TTGTGACTGT CCTTATTAAC TTTCTTNAT GTAAGTAATT TGTAAGGTT 120  
TCTNAAAATT TTTGCTTTTG CTTATTTAAT TTTNAATAAA AGCTAAATTC CTAATAAA 178

SEQ ID NO:2724

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03172

SEQUENCE DESCRIPTION:

GATCCTGGAG CCCCCGTGTC GGGGGGCGAG GNGGGGCGG TGNCCGACGA GTTGANCTTC 60  
TNAACATGAG TGTCAACTTC AGGACTTGCT TCCAAGCCCT TCCCTCTGTT GGAAATTGGG 120  
TGTGCCATNN CTCCAAGGN AGGCCATGT GACTAATAAA AACTGTGAA CCCTGAAA 178

SEQ ID NO:2725

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03173

SEQUENCE DESCRIPTION:

GATCCTTTTG AATTTTGCAC AGCCCTAGAT ACAATCCCTT TTGATAAAAG GGTCTTTGCT 60  
TCTNATTACA GGAGCACTGT GGAACGTCTG TAAATATGTT TTTATAATTC CATGTATAGT 120  
TGGTGTACAC TCAAAACCTG TCCCCGGCAG CCAGTGCTCT CTGTATAGGG CCATAATGGA 180  
ATTCTGAAGA AATCTTGGGG AGGGAAGGGG AGTTNGAACA AATGTCTGTT CCCTGGGAGG 240  
CCAGTCCAGT GCTCAGACCT TTAGACTCAT TGTAAGTTGC CACTGTCAAC ATGGGACCAA 300  
AGGTGTGTGA CTAGTCAATG AAAGTGCGGN CANATTN 337

SEQ ID NO:2726

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03175

SEQUENCE DESCRIPTION:

GATCCAAAAC ACTCAATCCT CGTAAAAGGG TACAGGTCCT ATTGTATGTT AACACACGTG 60  
ATGATGTGAG CCATGTGAGA TGANCAATCA CCAGTTGTTA TGTTCTGAATC TCCTTTGTGT 120  
TGGGCCGCTT TAATGTCAGG GTTTCATAA ATAAATGAAT TTTTCATATC TGAAGTAAAA 180

SEQ ID NO:2727

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03176

SEQUENCE DESCRIPTION:

GATCTGAGCC AGGATGGGAG TGAATCCCAG GCGGAGGCCA GAGCTGGCAG CCAGCTCTGC 60  
CTTTCCACTG CCGGGAGTGC TGGGGGCCCA GCCTGGCCCC CNGAAGAGAC AGCCAAGTGT 120  
CGTCCACATA CTCCTCCCAG AGTGAGCTCT AACCAGGCTC ATTTGCTCTN TCCAN 175

SEQ ID NO:2728

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03177

SEQUENCE DESCRIPTION:

GATCCTGTTN CCNACCTCCT TCTCCTCCCC TGTACTCCCC AGTGCCTTCC ATTGTCCTGG 60  
TGGAGCTGGG GTTTCTCTCC TCCCAGTCC CACAACACTG CCAAAAATCT GTGTATGTNC 120  
CATTGGGTGG GGCAGCCCCA AGCCTCCTGG GGAGGCAGGG CAAAAACAGG TGCCN 175

SEQ ID NO:2729

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03178

SEQUENCE DESCRIPTION:

GATCAGAGGA AAGATGAGAA AGAGAACAAAG CATACCTATC TNACTCCTTC CAGTGGTCTC 60  
TGTTCCCTCC GTCTCCTGGA CCACGGCTAG AGTTCCCAGT TTGGCCTTTT GGGGCATTCA 120  
TCCCATCTAC TTTATTTTCA TCTGCTTGGG CAGTAATGTA AACAAATTAA AGGN 174

SEQ ID NO:2730

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03179

SEQUENCE DESCRIPTION:

GATCGTCTGG GAGCCCAGTG TCAAGTCTGC TGGAAATGCAG GAAGTAGAAC AGAATCGCCA 60

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5 CAGGACTGTT CTGGGGCCAG GTTCCCTTAA CTCTGTAGCC TGGCAGTCTG ACCCAAAGTT 120  
 GCCCTCACCC AAAGGTTCTG GCTCTTCCCT CCCTCACTTT TACTTTCCCT TCCCCATAA 180  
 GTTGGAGGAT AAAATGGGTA TCAATGNTAA TTTTCCAGG GNGNCCATGN NNACCAGCGG 240  
 TTTCTNNCTN TCTCTGTAAT CTGCTATGNA N 271

10 SEQ ID NO:2731  
 SEQUENCE LENGTH:178  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03180  
 SEQUENCE DESCRIPTION:  
 15 GATCTNCGGN CTGTCGTTAG CAGGCTTAAT NAAGAACACT TCTCAACAGT TTCCTTTTTN 60  
 TTTCTTTTA TAATCACTA AAATAAGCA TCTATTAGTG TCTGATTAG GAATGTAAAA 120  
 TAATTCTNTA TTAATGTAAA TAAGATTATC TATTGCAAAA NGATATTTC A NCCTAAA 178

20 SEQ ID NO:2732  
 SEQUENCE LENGTH:172  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03181  
 SEQUENCE DESCRIPTION:  
 25 GATCTTACCA AAGAGGTCAA CACATGGGAC CTTTGTGTCA CATGAACCAT TTTTTTTCCT 60  
 CTTCTATTAA GTGTATTNT GTTTAAGNTA CAGTTCTCTA AGAGAATTAC AATGTTTGTC 120  
 CCATTCTAA GGGCTTCTNT TCAACTCTAA TAACAGCATT ATTCACGTTA AA 172

30 SEQ ID NO:2733  
 SEQUENCE LENGTH:170  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03182  
 SEQUENCE DESCRIPTION:  
 35 GATCAGGAAA CGGCAACAAG CCTCCAGTA CTGACCTGAA AACTTGTGAC AAGAAGAACA 60  
 CCAACAAGTG CTCCCTGGGC TGAGGACCCT TTNTTGCCTC CCCACCCCGG AAGCTGNACC 120  
 TGAGGGAGAC AACGGCAGAG GGAGTNAGCA GGGGAGAAAT AGCAGAGGGN 170

40 SEQ ID NO:2734  
 SEQUENCE LENGTH:176  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03183  
 SEQUENCE DESCRIPTION:  
 45 GATCTGGATT TATGTATTTG TNAGATACAT ACGAATTGTT AAAATGGAAT GCAAGTTTTT 60  
 CAAAAGCCCA GGTCTAAATG TAATGGTTGG TTTATNGTNC TATAACCCCA GCCCATCATT 120  
 TCCTGTGTAA ATCATAAACA ATAAACAGAA TATACTCGGT GGCCATTCT AATAAA 176

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SEQ ID NO:2735

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS03185

SEQUENCE DESCRIPTION:

10 GATCCGCCCA CCTNGGCCTC CCAAAGTGCT GGGATTGCAG GCGTGAGCAN CCGCACCCGG 60  
CCTCCTGAAT TAACATTTTC TAAAGATGCC TCCGGCGTGC TATCCTGAAA GCTGCCAGAG 120  
GTGTCTTGGC TGCATTGGTG GTAATAAAAT TCATACTCAT AAA 163

SEQ ID NO:2736

SEQUENCE LENGTH:162

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03186

SEQUENCE DESCRIPTION:

20 GATCTCAACT ATGTNCCACT AAAGGCACAG GAATGGAAAA CTGAGAAAAG ATTTATTGGC 60  
CTCACCAATT CCTTGGTTT TGGTGGTACT AATGCAACAC TTTGTATTGC TGGNCTGTAG 120  
AACATATANT TNGTAATNAA ATACTGATTT TNAAATGTTA AA 162

SEQ ID NO:2737

25 SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03187

SEQUENCE DESCRIPTION:

30 GATCCTGCCA CCTGTAGCG CCAGTNTAAT CCCCAGGAG AACATCTTTG AACTCTGCA 60  
GACTGTAGT GTTCTGTCTA AAAACCAGAC AAGGAAATAC CCTTCTTTTA TGAGCAGAAG 120  
GAAACAAAAA AAAAAANGAG GCCCNTTNC CTGGANGAAA 160

SEQ ID NO:2738

35 SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS03188

SEQUENCE DESCRIPTION:

GATCTGCCTT ATTGCATATN CCATGCATCA GATAATGGAT GCATCAGATA ATGGNGTTAG 60  
ACAAAGCTTC ATTGTGAACA ACCTAATGCA TTTNNGAGAA ACANTCTCAT CACATTTTTC 120  
CTAGCCTTNC CTACATTTAA NCTTGCTGTT GCCCAAATN 159

SEQ ID NO:2739

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

CLONE:HUMGS03189



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## SEQUENCE DESCRIPTION:

GATCAGANGT TTCACTTGTT TCTCAGTTAT TGGATATGTA TCTTTGTGTA CATATCTTTG 60  
CAAAANTGGA TAAGTACAAA NCTTGATGTA AATNGTACCA ATGANTATGT AAACATACAG 120  
TGACANCATT AAACCTTAGAA AAGTTTTTAAA ACTTAAA 157

SEQ ID NO:2740

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03190

## SEQUENCE DESCRIPTION:

GATCCACTGG AATTAGCCAA TACACTATAT AACAATACTA TTAAAGTATT TTTTCCTGGA 60  
ATATAATTGG TATATGTCTT CCACTTTCCA TCATGTATGT AAAATTTTCAT AGTAAACTT 120  
CCTGATAGTT TCAATAAAGA AATNATCTGC AAA 153

SEQ ID NO:2741

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03192

## SEQUENCE DESCRIPTION:

GATCTTNAAT GCTTTGGAAA TCGGTGTAAC AGTACTGCAA TAATCACAGC TCTGGGAAAA 60  
ACAACGAAAC TTTCCCTTGT GGAGAGGAGG GATTTCCTG CTCTATATAA GCAACATATT 120  
TTNAGACATT AAAATATGGT ATNCNNNNCC N 151

SEQ ID NO:2742

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03193

## SEQUENCE DESCRIPTION:

GATCTTNCTN ATCCAAGCAA TAACGGGACG AGGGAGCCAG GGCCAAGGAC ACTCAGGGAC 60  
ACTGTTGGGG CAGCGGCCCC ACATGGTAAT GTTTTNTTTA GAGAGAAGAA AAAACAACCTG 120  
GCTGTAAACG TAAATNATAT TTNTTGAAAA 150

SEQ ID NO:2743

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03194

## SEQUENCE DESCRIPTION:

GATCGTNTTT TTNCTTGTTA AATAATTAAA ANTCATCTTA AAATTCATAC TTTGACTTTA 60  
ATTTAGACAC AAGGAGATGT AATCNCCTGTG TAACATCAGA GAAAGCTATA TGGATTATNG 120  
TCAGANGTAA ATGTTTCTAA CATTGACAAA 150

SEQ ID NO:2744

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03195

SEQUENCE DESCRIPTION:

GATCGAGTTG GCCGAGGATG GATGATTNTG NGCAGCAGAA GCCGTTGCAG CCCCACGTTG 60  
 TGCTCTAGGC AGGGACCTTT GGCCCTTTG GGGAGGGAGA GACAGACGGG CGGTTTGACT 120  
 TGGACACAAA GAAAGCCTTG GTTCTAAA 149

SEQ ID NO:2745

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03196

SEQUENCE DESCRIPTION:

GATCCCAGGT CTGGGGATGG GGGACACCTT NGGCCACAGG ATACTGGTTG CTTCAGGGGT 60  
 ACCCATGCCC NCTGCCCTNG CCTGGAATCA GTGTTACTGC ATCTGATTAA ATGTCTCCAG 120  
 AAATAAAGAA TAATTCTGCC AGAAA 145

SEQ ID NO:2746

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03197

SEQUENCE DESCRIPTION:

GATCACTCNT AGAGTNGCCA TTCTGCANCT TCCTAAAAAT ATTTAAAAA TACATTTATT 60  
 TTACTAAATA CTGACTACAT TTNTNTGTGA ATATTGAGCT AAATGTTAAA AAATGGCCAG 120  
 ATTAAAAGAT ATCAATTTGT AAA 143

SEQ ID NO:2747

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03198

SEQUENCE DESCRIPTION:

GATCCATAGT GTGCATGGGC AGACACATTT TGCCTCTATG TCTCTTAAAA TTTTAATTAA 60  
 AAATACTCTT TCCAGTAATC CTAATTTGCA CGAAGATATA ATGTCCACAT TACGTGCCTT 120  
 GCCTTGAAAT CTAAAAACA AA 142

SEQ ID NO:2748

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03200

## SEQUENCE DESCRIPTION:

GATCTCACAG GACTGAGAAC TCGTTCACCT CCAAGCATTT CATGAAAAAG CTGCTTCTTA 60  
 TTAATCATAC AAACCTCTCAC CATGATGTGA AGAGTTTCAC AAATCTTTCA AAATAAAAAAG 120  
 TAATGACTTA GAAACTGCCA AA 142

SEQ ID NO:2749

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03201

## SEQUENCE DESCRIPTION:

GATCTTTTCA TTTCTTACTA GCTTTTAAGA AATNAAATAC TTGCCTGAGA TAGAAATACT 60  
 TTATTTTTGT AACTTTAAGG TCTAAATNAC TAAACTTCAA AGTAAGATTT TNTCAGAATA 120  
 AATTGAGACC ATTAATCTAA A 141

SEQ ID NO:2750

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03202

## SEQUENCE DESCRIPTION:

GATCAGAAAA AGAAAGAAGC CAAAGAGAAA GGTACCTGGG TTCAACTANA ACGCCACCTT 60  
 GAGCTGCTGG AACCTATTCC CTATGAATTC ATGGCATAAT AGGTGTTAAA AAAAAAANA 120  
 AAGGACCTCT GGGNTACAAA 140

SEQ ID NO:2751

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03204

## SEQUENCE DESCRIPTION:

GATCCTATTT TCNTACAACC TTTCAGTGAC ATCGTTCAGG NTTCTTTCTT GGCCATTTAA 60  
 AAAAACAAAT TTTTTTTTNC TCACTTGTA GTCACCGCCA GTNCCTAAGT NAGGCTAACG 120  
 GNGACTTTGA CAGGN 135

SEQ ID NO:2752

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03205

## SEQUENCE DESCRIPTION:

GATCAGTAAT AGATNTAGAT ATACTATTTT NATATTGTAA GCAGTTACNT ACTCAGGATT 60  
 AGNATTTCGAA TTCATTTGAT TTAATATGTA ATAGGTAATA TAAAAANTAA AGATTTTATG 120  
 CTTTGAAACT CAAA 134

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5 SEQ ID NO:2753  
 SEQUENCE LENGTH:133  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03206  
 SEQUENCE DESCRIPTION:  
 10 GATCAGACGT CGCTGAGGGG CTGTNCACCA CCATCCTCGT TCTCCAGGGT CAAGGAAGTG 60  
 TTTTAACATG TCGTGTTC GACTTGACCT TGTGGTATTT TNCTNGGCCT AGTTGTGTGC 120  
 CATGGATATT AAA 133

15 SEQ ID NO:2754  
 SEQUENCE LENGTH:141  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03207  
 SEQUENCE DESCRIPTION:  
 20 GATCACTGTA GTTAGTTCT GTTGACCTGT GCACCTACCC CTTGGAAATG TCTGCTGGTA 60  
 TTTCTAATTC CACAGGTCAT NAGATGCCTG CTTGATAATA TATAACAAT AAAACAACCT 120  
 TTCATTCTT CCTATTGTAA A 141

25 SEQ ID NO:2755  
 SEQUENCE LENGTH:132  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03208  
 SEQUENCE DESCRIPTION:  
 30 GATCGTTATA TTNACATAA TATAAACAAA ATNACTAATG CATCTATATN CTTGGTTTCC 60  
 TTAACTACA ATNAACCACA GAATGGGTGA AAATGCAGGC ATGCACGCTT GGCCTAATCA 120  
 TGGATGNNGC TN 132

35 SEQ ID NO:2756  
 SEQUENCE LENGTH:131  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03212  
 SEQUENCE DESCRIPTION:  
 40 GATCCGNCCG CCTCAGCCTC CCTATATGTT TAAAAATATA ANTTTATTCT TATAAANTA 60  
 AATTNAANCT AGATTGAGGT AGTAATTACA ACAGTCCAGC ACATTATGGA TAATTAATAT 120  
 TNATATTAT N 131

45 SEQ ID NO:2757  
 SEQUENCE LENGTH:136  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 50 CLONE:HUMGS03213

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## SEQUENCE DESCRIPTION:

GATCTGATAT TTTAAGANTT TGGAGACCAT TTCCTGTGCC AGANTCACTG CTCTATTCCA 60  
 TACCGTGCCA TGGAGGCTGT TTTAGAAGTG GTTGGATAAC ATGTAAATA AAATATTAAG 120  
 TGTAAAAAAA AATAAA 136

SEQ ID NO:2758

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03214

## SEQUENCE DESCRIPTION:

GATCCACCCA CCTTGGCCTC CCAAAGTCCT GGGATTACAG GTGGGAACCA CAGCACCTNA 60  
 CCCAGAATAT AAAGACACTT TTNTAATGTG CAATGAAAAA TATGTAAATA AANTATTTTT 120  
 ATCTNTAAA 129

SEQ ID NO:2759

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03215

## SEQUENCE DESCRIPTION:

GATCCACCGT ACCAGGNAGC AGAAATATTT CTACAAAGGG GGCCTAGTTT GGAATGAGAA 60  
 CANNCTGAC GGCCGGTATG TGAAGGAGAA CTGCAAACCT CTGAAGAGTT ACATGCTCCA 120  
 AGACTCCCN 129

SEQ ID NO:2760

SEQUENCE LENGTH:408

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03216

## SEQUENCE DESCRIPTION:

GATCATGTTG GGATTAACCT GCCTTTTTCC CAAAAAANNA AACTCTCAGG CAAGCATTTT 60  
 TTAAAGCTA TTAAGGGNGT ATATACTGA GTACTTATTG AAATGGACAG TAATAAGCAA 120  
 ATGTTCTTAT AATGCTACCT GATTTCTATG AAATGTGTTT GACAAGCCAA AATTCNNGG 180  
 TGTAGANATC TGAAAGTTC ATTTCTGGG ATTCACTTCT CCAGGGATT TTTAAAGTTA 240  
 ATTTGGGAAA TTANCAGCAG TTCACCTTAT TGTGAGTCTT TGCNACATTT GACTGAATTT 300  
 AGCTGTCATT TGTNCATTTA AAGCAGCTGT TTTGGGGNCT GTGAGAGTCC ATGTATTATA 360  
 TCCAAGCCCA CCAGGGCTTN CCCTAAGGAN TTGCCATNGT AATACCCN 408

SEQ ID NO:2761

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03217

## SEQUENCE DESCRIPTION:

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GATCTAGGAA AGAAGGCAAC TGAAAAACCT GAAAGAAAA AAATNAAAGA TTAAAAGTAT 60  
ACGATATTCT ATTTTGATT AGCAATTACT TGTTTNCNAG TGTNCTGTNA ATTTTGGTN 120  
ACTTTAAN 128

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SEQ ID NO:2762  
SEQUENCE LENGTH:258  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS03218

SEQUENCE DESCRIPTION:

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GATCGGCAGG CTGAGGACCA GGTCTGAGG AAGCTGGTGG ATTTGGTCAA CCAGAGAGAT 60  
GCCCTCATCC GCTTCCAGGA GGAGCGCAGG CTCAGCGAGC TGGCCTTGGG GACAGGGGCC 120  
CAGGGCTAGA CGAGGGTGGG CCGTCTGCTT TCGTTCCAC AAAGAAAGCA CCTNACCCCA 180  
GCACAGTGCC ACCCNTGTTC ATCTGGGCTG NCTGGCAGAG AGCCTTGCTG TTTACAATTA 240  
AAATGTTTCT GCCACAAA 258

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SEQ ID NO:2763  
SEQUENCE LENGTH:128  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03219

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SEQUENCE DESCRIPTION:

GATCCTTGTT GGTCTAGCTA AATACTGTTA GGGGAGTGTG CCCCATCTCA TCATTTGAA 60  
GATAGCAGAG TCATAGTTGG GCACCCAGTG ATTGGGTTC AAAATAAAGC TGGTCTGCCT 120  
CTTCTAAA 128

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SEQ ID NO:2764  
SEQUENCE LENGTH:126  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS03220

SEQUENCE DESCRIPTION:

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GATCTNCCGC TCCCTCCCTG AAGGGCATGG GGCCAGGGNA GTCTGGACAG CCGCCCCCAG 60  
CCTGCTGACC CCCAGCTTTC TACAGACACC ANATTTGTAA ATAAAGTTGG GGAATGGACA 120  
GCCAAA 126

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SEQ ID NO:2765  
SEQUENCE LENGTH:126  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03221

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SEQUENCE DESCRIPTION:

GATCTTTTTA GGCCTTCATT TTATGTTTTT CCTTAACTGT TATATTATNA TTGTAACATA 60  
GATTATACTA CTACTAATTN NTGGATGTNT CAAAAGGTCA AGAAGTAAAA NATGTTAGAA 120  
AGCAAA- 126

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SEQ ID NO:2766  
SEQUENCE LENGTH:125  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03222  
SEQUENCE DESCRIPTION:  
GATCTCTGCA CAGTTTCTTG TTTAGTCTTA TGCCTTTTAG TTGAAAAACA AATTGTATTT 60  
TTTTCTNCT AAGTTTCATG GCCCTAGAGA AGAAGCCAAT NTNNNTAAAG ATGTTATCCC 120  
NGAAA 125

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20  
SEQ ID NO:2767  
SEQUENCE LENGTH:124  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03223  
SEQUENCE DESCRIPTION:  
GATCCTGGTT TCAATGACGG TTGGAAATAG AAATTNCCAG AGAAGAGAGT ATTGGGTAGA 60  
TATTTTCTCT GAATACAAAG TGATGTGTTT AAATACTGCA ATTAAAGTGA TACTGAAACA 120  
CAAA 124

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SEQ ID NO:2768  
SEQUENCE LENGTH:131  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03224  
SEQUENCE DESCRIPTION:  
GATCACTTAG CAACATGCTT GGNAATTTGG NATCTNTAAA GGTAGGAGAG TGGTGAACAG 60  
ATAATCTATG CATATATNAC TAGTGCCAAG ACATAAAGCG GGGGAAAATA TATTTTANCC 120  
CAAACATTAA A 131

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SEQ ID NO:2769  
SEQUENCE LENGTH:123  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03225  
SEQUENCE DESCRIPTION:  
GATCAATTAC CTAAGTGTTC CTTGGTCTAT TTATGTATAA GAATGCTTTT TAAAGCACAT 60  
GTCTCATTTT AAATNACGCA CAAACTGAAG ATGTTAATAA AATTTAAGAG TAATACAATG 120  
AAA 123

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SEQ ID NO:2770  
SEQUENCE LENGTH:388  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS03227

SEQUENCE DESCRIPTION:

5 GATCCATTG TCTGGCAGGA GGTTTTGTAT GATAAAGCAA CGCTTGC GCC AAGGCACAAT 60  
 AGTTGAAGNA TGGAAAGACA GCGCATATCC TGAGGAACTC AGTAGAGTCA CAGCATCTGG 120  
 CTCCTCTGTA ATCCTTTCTN CTCCTNGGTA CTTAGATTNG ATTAGCTATG GACAAGATTG 180  
 GAGGAAATAC TATAAAGTGG AACCTCTTGA TTTTGGCGGT ACTCAGAAAC AGAAACAAC 240  
 TTTCATTGGT GGAGAAGCTT GTCTATGGGG AGANNNTGTG GATGCAACTA ACCTCACTCC 300  
 10 AAGATTTATG GCCTCGGGCA AGTGCTGTTG GTGAGAGACT CTGGAGGTTT CAAAGATGTC 360  
 AGAGATATGN GATGACGCCT ATNACAGN 388

SEQ ID NO:2771

SEQUENCE LENGTH:219

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03229

SEQUENCE DESCRIPTION:

20 GATCGATGGA CCGTAAATAA GCTGCCATTA ACACATCTGG TTAGTCTGT AACATGACTA 60  
 ATAAAACCGA ACGCCTGTTC CCCTTACCCG TGTGGGGGAC ACGCAGATGA GTGAATTGGA 120  
 ATGTCCAGCA GAGTTACCCT CCCAATTATA TGTTCATTTT GTATATTTT TGGTCGGGGG 180  
 AAAAATTGAC CTGCAGTAAA AAAACCTTTG ACCATTAAA 219

25 SEQ ID NO:2772

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03230

SEQUENCE DESCRIPTION:

30 GATCAGCACA GGAAGAGCCT TCCTAAGCAT GTGGTCCCAG GGAAGGGTGA AAAGTAGGAG 60  
 TTATGAACGT AATCCACCTA CTACAATGTT GAATTAAAGT TATAATCTCA TAACTTCAA 120

35 SEQ ID NO:2773

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03231

SEQUENCE DESCRIPTION:

40 GATCCGCCCG CCTCGGCCTC CCAAAGTGCT TGGATTACAG GCATGAGCCA CCGCACCCAG 60  
 CAAGAGTTAT TTNNTTAACT TGAAATTTT TACTAGCCCT GGTGAACTTC TGTGCTTAAA 120

45 SEQ ID NO:2774

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03233

50 SEQUENCE DESCRIPTION:

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GATCCAAGGT GATACAGCTG GTAAGTGTG GAGATGTTGG TAGTGAAATN CATGTACTTT 60  
TAGTNCCTTC TATGGAATCT AGAGGNAGAA TACATGTACA AGAATATCGA CTACCGTCN 119

5 SEQ ID NO:2775  
SEQUENCE LENGTH:117  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS03234  
SEQUENCE DESCRIPTION:  
GATCCCAGCT GTGTGTCACC AGCAGCTTTC CCAGCTTCTC TGTGAGGGTC ACTGCTGCCC 60  
ACTGCAGGGT CCCTGAGGTG AAGTAAACGC CGGCGCTGGG CTTGGCCAGN CGGCAAA 117

15 SEQ ID NO:2776  
SEQUENCE LENGTH:115  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS03235  
SEQUENCE DESCRIPTION:  
GATCATTCCC ATTTTCATAGG TTTTATTGT GGAATAGTCA ACTTAATATA GATTCACTTT 60  
CAATTGTCAT GTATAANGTA ATACTCAATA AAATTTTTTC CATTNATTTT NCAAA 115

25 SEQ ID NO:2777  
SEQUENCE LENGTH:217  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
30 CLONE:HUMGS03236  
SEQUENCE DESCRIPTION:  
GATCCTGGGG TTGGTCTGCT TTGTGTATGG TACTTGAAAC CACGCTGTAA TTATTGTCCT 60  
GTTGCCAAAC AAAAGCCAGT CATGTAATC TAGAAGCAGT GACTGGTGGG GCTTCTGAC 120  
AGTTCCATGC TGATGTATCA GGCCATCTGT GTCATGCTTA TGTATTATGG CAAGAAGAGG 180  
35 AAAACTGGAT TAATAAATAC GTTTNNNNN NGTTAAA 217

SEQ ID NO:2778  
SEQUENCE LENGTH:114  
SEQUENCE TYPE:nucleic acid  
40 TOPOLOGY:linear  
CLONE:HUMGS03237  
SEQUENCE DESCRIPTION:  
GATCCTNAGC AACGAACACC TGCATTAGA AAAAGTGGAC AGCTTCTNCC AACCACACCC 60  
45 TACCCATGGN ACTGTATGCA ATTAACCTCT GGAACGCCC CGTAAATNCN AGTN 114

SEQ ID NO:2779  
SEQUENCE LENGTH:113  
SEQUENCE TYPE:nucleic acid  
50 TOPOLOGY:linear

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CLONE:HUMGS03239

SEQUENCE DESCRIPTION:

5 GATCCAAAAT TACCTTAAAT GGAGTTAAGT AGGCTTTGCA CTAAATGGAT ATAAAAGAGG 60  
CTGTCTGGNC TNCTATGAAA TNATGATTAA AATCCTTGT GTTGTCTTT AAA 113

SEQ ID NO:2780

SEQUENCE LENGTH:359

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03240

SEQUENCE DESCRIPTION:

15 GATCCTTAAA GAAGGTGTGG GGTCTTTCCC AACCTGAGGA TTTCTGAAAG GTTCACAGGT 60  
TCAATATTTA ATGCTTCAGA AGCATGTGAG GTTCCCAACA CTGTCAGCAA AAACCTTAGG 120  
AGAAAACTTA AAANTATATG ATTACATGCG CAATACACAG CTACAGACAC ACATTCTGTT 180  
GACAAGGGAA AACCTTCAAA GCATGTTTNT TTCCCTCACC ACAGCAGAGC ATGCAGTACT 240  
AANGCGATAT ATTTNTGATT CCCCATGTAA TTCTTCGGNG GNNGGNCAGT GCAGTNCTCT 300  
20 TTCGGAAGCT TAAGATGGCC NTGNGGCCTG NCCNNNNGGN CATATGCCCC TGAAGGGCN 359

SEQ ID NO:2781

SEQUENCE LENGTH:191

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03241

SEQUENCE DESCRIPTION:

30 GATCTAGGGC AGGCTGTCTT CCAGTCCATG TGTCTCGGT CGCCGTAGAC AGCGCTCTGG 60  
CTACCACCGT GAGGCTACTT GAACTGTCAG GGGCATCTGC CTAAACCAGA ATCTTTTGTC 120  
AGAAACCTTA ACCCAACAAA ACAAATCTTG AGTAGCTCAT GCCCGGCTCT TAGGAATTTT 180  
GTCTGTTTAA A 191

SEQ ID NO:2782

35 SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03242

SEQUENCE DESCRIPTION:

40 GATCACTCAA CAGCACTGTN ATGTATTATT TNNAATGAGG TGCCTTTTTT AACTGACCAA 60  
ATGCTGCCTT GTTTGGCCCC TAANTCAATA AAATATGTTA AAATTGTAA A 111

SEQ ID NO:2783

45 SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03243

SEQUENCE DESCRIPTION:

50 GATCTAAGAA ATAGAATTAG GGAGAGTTTA CACTTACTTA CCTATATAAA AGCAGATTTT 60

55

CNTGGAAGAA ACCCTTTTTT TTTTTTTTTT TAAAAAGNA NCANCCAGN

109

SEQ ID NO:2784

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03244

SEQUENCE DESCRIPTION:

GATCCAGAAG CTGGTGGACG TCACCACGGC ACAGGTGTAA CNTCCATGTN CCGTGTGAGC 60  
 AGAGTCCCTA CCAACGGGCA GGTCTGCATC CGGGGAGAAT GCAGCTGCTT CTGGCGACAA 120  
 TCCTGCTAGT AAACACTGGT CTTCCGTGAG CAACGAACAC TCGCCTGGGN TGGGAAACTG 180  
 CATGCCCACT TTNTGGGAGG GGTTAGTGCA GGTGCCGTGG ACAAAGGACA ACATTTCTNT 240  
 GGGGCTTTTT AACTTTTATT CCTAAGACTC TAAAGGCGTT GATTTCACC CTCCTTCACT 300  
 CTGGCTTCTT CAGGNAACCC ACGTGGTCTC CTGTNAGNTN 340

SEQ ID NO:2785

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03245

SEQUENCE DESCRIPTION:

GATCTTTAAG ACAACAAGTT AGGTTCTTAC TGGAGTTACC TGCCAGANTG GCCTCTTAAT 60  
 TAACTCAGGT AATGAAGAGC TAACTGTGTT ATAATCATCT NCCNNNTN 108

SEQ ID NO:2786

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03247

SEQUENCE DESCRIPTION:

GATCTGCTAA AAATGGCAAT TGTAAGATNA TGTTGTATGT AATGTACATA TGGAGAAAGA 60  
 ATGTATTTTN TCCATTTTCT TAATAAAATG TTATATATGG NTGCTAAA 108

SEQ ID NO:2787

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03248

SEQUENCE DESCRIPTION:

GATCTCTGAG GCTNCGGTCA CCACCCACAA GTTGTGGCCT TGGATACCAC ACTNCAGTTG 60  
 GGTGGTGATG GGGTNGTGCC TTCTAACTTT TNCCNTATCT TTACCGN 107

SEQ ID NO:2788

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS03249

SEQUENCE DESCRIPTION:

5 GATCAGTAAG GATGACTGGT GTTTTCTGAC TTTNACAAAA TTA CTGTGTTT GTTTTCATTA 60  
 AAAAAAAGC ATAANCTATG TTTCTNATTA CTATTAGAAT TATTAAATTT CAAAATGAAT 120  
 CAAA 125

SEQ ID NO:2789

10 SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03251

15 SEQUENCE DESCRIPTION:

GATCGATTCT NTGACACAAA CCCACCAAT TGTNAATGCA AGTTTTTATT TGGCTGTATA 60  
 TACAATTTAA GCTATTAAAA TTTGTACAAT ATTTACAAAT NAAA 104

SEQ ID NO:2790

20 SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03252

25 SEQUENCE DESCRIPTION:

GATCATTACA TCTNAGATGT ACGTNGGTTT AGTCGAAAG GTGGGACGAT TTGAAGGGGA 60  
 GGNACTTTCA GGTACATAGG GATTAAAAAN ATGTCCTGAT TAAA 104

SEQ ID NO:2791

30 SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03253

35 SEQUENCE DESCRIPTION:

GATCCAAGCT ATGANATANC CAACAGTATT CAAGANGCAA CCAGCACCAT CATGTGATAA 60  
 TGGTACTATG GCATATATGC AACATTAAAN TTTTAANTTA GAAA 104

SEQ ID NO:2792

40 SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03255

45 SEQUENCE DESCRIPTION:

GATCCAGTCT TAATTTGAGC ATGAGAGCAA AATTTAGTCA TCTACACAAG AAGCAAAAGC 60  
 AAGGAATAGT TGTGGGTTT TNGTTTTTTG GTTGTGTNT TTTTTGTN GTTAGGNANG 120  
 ANGTGTTCCC GN 132

50 SEQ ID NO:2793

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SEQUENCE LENGTH:102  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03257  
 SEQUENCE DESCRIPTION:  
 GATCCAGGTG GTGTTACATG TCCATTTTCAT GTTTTGGGGG CTTTGTAGCCC NACAAAACAC 60  
 CTTCAGTAGA GCCTTGATTA AAAGGAAACC TGNAGACTCA AA 102

SEQ ID NO:2794  
 SEQUENCE LENGTH:100  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03258  
 SEQUENCE DESCRIPTION:  
 GATCTTCCCC TAGGGGGGCC TCTTACTCCT NCCTCTCTCC TCCTCCTTCC CCATTGCTGT 60  
 AAATATTNA ACGAAATGGA AAAGAAAAAA AAAAGACAAA 100

SEQ ID NO:2795  
 SEQUENCE LENGTH:100  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03259  
 SEQUENCE DESCRIPTION:  
 GATCACACAT CAAGACTATC TACAAAANTT TATTATATAT TTACAGNAGA AAAGCATGCA 60  
 TATCATTAAA CAAATAAAAT ACTTTTTATC ACAACACAAA 100

SEQ ID NO:2796  
 SEQUENCE LENGTH:98  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03261  
 SEQUENCE DESCRIPTION:  
 GATCTAAATA CAAAGGATAT ACAGTCTTGA NTCTAAAATA ATTTGCTAAC TATTTTGATT 60  
 CTTCAGAGAG AACTACTAAT AAAAATCTAA AAGGTAAA 98

SEQ ID NO:2797  
 SEQUENCE LENGTH:97  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03263  
 SEQUENCE DESCRIPTION:  
 GATCGTNCCT ATAAATAGTA GGACCAATGT TGTGATTAAAC ATCATCAGGC TTGGAATGAA 60  
 TTCTCTCTAA AAATAAAATN ATGTATGATT NGTTAAA 97

SEQ ID NO:2798

EP 0 679 716 A1

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

5 CLONE:HUMGS03264

SEQUENCE DESCRIPTION:

GATCACTAAA GTATATCTTT AATTCTGGGA GAAATGAGAT AAAAGATGTA CTTNTGACCA 60

TTGTAACANT AGCACAANTA AAGCACTTGT GCCAAA 96

10 SEQ ID NO:2799

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS03267

SEQUENCE DESCRIPTION:

GATCTGCTGT CTCCGTCCCT CCTGGGTCCC AGCAGCTGTC CTGCAGCTGT CAGCAGGAGG 60

GCCTGGCTTT AATAAAGAGT GGACAACTG AAA 93

20 SEQ ID NO:2800

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS03268

SEQUENCE DESCRIPTION:

GATCAAGTTC GAGGAGGCAG TCATCGCTCG AAACCGGGCC CTGGAGGGCC GCTNACCCTG 60

CCGGANATAA AGNATACAGA GAGCCCTCC AAA 93

30 SEQ ID NO:2801

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS03271

SEQUENCE DESCRIPTION:

GATCCATTCT TGTATTGATA GATATTTGAA TGTTTCCAGT TTTTCCTATT ATGAATAAAA 60

CTGCTATGAA CATTCTTGTA TAAATCAAA 89

40 SEQ ID NO:2802

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS03274

SEQUENCE DESCRIPTION:

GATCGACAGC GTCCTGGCCT AGGGTGCCGG GGCCTGAAGG TCAGGGTCAC CCAAGCAACA 60

AAGTCCCGAG CAATGAAGTC ATCCACTCCT GCAA 95

50 SEQ ID NO:2803

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SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03279

SEQUENCE DESCRIPTION:

GATCTCTACA GAGAGAAGTG GAAAATGCTG TATCAAGGGT GGGCTTAGCT GTGCCTTTCC 60  
AATAAAGATG TGAGAAGCTT CAAA 84

SEQ ID NO:2804

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03281

SEQUENCE DESCRIPTION:

GATCTTTGCC CCTGGTATGC ATTTNTGGAC TCCACTGAAT CCTGNGAAAA AAAATTAAAC 60  
TTCCTTCTTA CTTGCCAAA 79

SEQ ID NO:2805

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03282

SEQUENCE DESCRIPTION:

GATCCTGTCA GTTCCATNAG CTATTCCTCT TTGGTTTGGC TTTTGTATAT NATTAAATA 60  
ATNTTTAATT CCTTTTAA 79

SEQ ID NO:2806

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03283

SEQUENCE DESCRIPTION:

GATCAATTTT TATAAAAATC GAGACAGTTC TGTGGTTAAA TCTACAAATT AAAGGGAAAT 60  
TAGAAGTTGG CGTGAAA 77

SEQ ID NO:2807

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03284

SEQUENCE DESCRIPTION:

GATCTATTTT ATGCATATTG TTTATAAAGA CACATTTACA ATTTACTTTT AATATTAAAA 60  
ATNACCATAT TATGAAA 77

SEQ ID NO:2808

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

5 CLONE:HUMGS03286

SEQUENCE DESCRIPTION:

GATCTTCAGT AAGTCTCTCA GGCTCTCTGA GCTTGTTTCT CCTTGTTTT GAAAAAATTA 60  
CTCAACCAAT CCAA 75

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SEQ ID NO:2809

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS03289

SEQUENCE DESCRIPTION:

GATCCCTTCA CAGCAGTAAA CCAGCTCTTT GGAACCGATT CCATCACCCC AATAAAGGAG 60  
CTCTTCACAG CAAA 74

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SEQ ID NO:2810

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS03294

SEQUENCE DESCRIPTION:

GATCTGTTTC TTTTAAATT TACACTTTN CTTCCGGTT TGCCGGAATA AACAGGACCT 60  
TTGACATTG AAA 73

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SEQ ID NO:2811

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS03296

SEQUENCE DESCRIPTION:

GATCCATTCT AAGACTTATT GGCTGTTTGG AAGTGATAGC AAATAAAANC CACCTTGAAC 60  
TGGAAA 66

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SEQ ID NO:2812

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS03297

SEQUENCE DESCRIPTION:

GATCCGAGGG GGAGGGGTGG GAAGGGGAGA AAATNAAATA AAAGATAATT ACTGAACACG 60  
CCGNAAA 67

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SEQ ID NO:2813

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SEQUENCE LENGTH:63  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
5 CLONE:HUMGS03299  
SEQUENCE DESCRIPTION:  
GATCATTGAA TTAAAGGCC ACCCAAGTC CAGANTGACC TCGCAAGACC CTTAACTCAC 60  
AAA 63

10 SEQ ID NO:2814  
SEQUENCE LENGTH:62  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
15 CLONE:HUMGS03300  
SEQUENCE DESCRIPTION:  
GATCTTTTGT ACTTNTNATA ACCTAATGTC AGACTAAGAA AAATAAAATA TCTGAGAGTA 60  
AA 62

20 SEQ ID NO:2815  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS03304  
SEQUENCE DESCRIPTION:  
GATCCCTTCG AGACTAANTC TGTTACCAGT CATGAAACAT TAAACCTAC AAGCCTTAAA 60

30 SEQ ID NO:2816  
SEQUENCE LENGTH:68  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03305  
35 SEQUENCE DESCRIPTION:  
GATCTTTGTC TTTTGTCTG ACAAAGCATT TATTTAATAA AGTTATGCAN TCAGTTAAAA 60  
AAANCAAA 68

40 SEQ ID NO:2817  
SEQUENCE LENGTH:58  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03306  
45 SEQUENCE DESCRIPTION:  
GATCAGATT TTTATGCCAT CCTCATTAGT TTTCCAATAC AATATAAGTT GAAACAAA 58

50 SEQ ID NO:2818  
SEQUENCE LENGTH:58  
SEQUENCE TYPE:nucleic acid

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5      TOPOLOGY:linear  
CLONE:HUMGS03307  
SEQUENCE DESCRIPTION:  
GATCTCAGAC TTCTGGCTTC CACAACTGTA ACAATAAATT TATGTCGTTT AAGCCAAA      58

10      SEQ ID NO:2819  
SEQUENCE LENGTH:57  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03308  
SEQUENCE DESCRIPTION:  
GATCCACTGG GTGAATCCTC CCGCTCAGAA CCAATAAAAT AGAATTGACC TTTTAAA      57

15      SEQ ID NO:2820  
SEQUENCE LENGTH:56  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20      CLONE:HUMGS03310  
SEQUENCE DESCRIPTION:  
GATCTGTGGT CATTGTCCCT CTGCAGAATA AAGATTGCTC AGGCCTGCCT GGCAAA      56

25      SEQ ID NO:2821  
SEQUENCE LENGTH:59  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
30      CLONE:HUMGS03311  
SEQUENCE DESCRIPTION:  
GATCTTTGGT TTGTTCCAG GTTTGGTTAT TATNAATAAA GTTGCTGTGA ATACTTAAA      59

35      SEQ ID NO:2822  
SEQUENCE LENGTH:56  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03312  
SEQUENCE DESCRIPTION:  
40      GATCTTCATT GGGGGATTGA GCAGCATTTA ATAAAGTCTA TGTTTGTATT TTGAAA      56

45      SEQ ID NO:2823  
SEQUENCE LENGTH:54  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03313  
SEQUENCE DESCRIPTION:  
50      GATCTAAGAA ATAAAGAGAA ATGTTTCANT TTGCATTGAA ATAGGAAAAC GAAA      54

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SEQ ID NO:2824  
SEQUENCE LENGTH:53  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03315  
SEQUENCE DESCRIPTION:  
GATCATNACT GGCTTTGCGC ATCGAGGGGC CATTAAAGAG TCTACTTTTC AAA 53

SEQ ID NO:2825  
SEQUENCE LENGTH:52  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03318  
SEQUENCE DESCRIPTION:  
GATCTTTTAA AAAGTCAAG TGTGAATAC TAGAGGTTGT TAGACCNTTA AA 52

SEQ ID NO:2826  
SEQUENCE LENGTH:51  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03319  
SEQUENCE DESCRIPTION:  
GATCTTGCCA CTGTAGTCCA GGCTGGGCTA CGGAGAGACC CTGCCTCCAA A 51

SEQ ID NO:2827  
SEQUENCE LENGTH:54  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03324  
SEQUENCE DESCRIPTION:  
GATCCTTGCT GATAAATATA ACCATCAATA AAGAAGCATT CTTTCCAAA GAAA 54

SEQ ID NO:2828  
SEQUENCE LENGTH:50  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03325  
SEQUENCE DESCRIPTION:  
GATCTCACCA CACTGCAACC TCTGGCGACA GAGCGAGACT TGGTTTCAAA 50

SEQ ID NO:2829  
SEQUENCE LENGTH:50  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03326

## SEQUENCE DESCRIPTION:

GATCCACCCA CTCTCTGAAA CTTCTTTGCT AATAAAACAT TCCTACTAAA

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SEQ ID NO:2830

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03331

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SEQUENCE DESCRIPTION:

GATCTTTTTT TTTCTTACA GACACCCATA ATAAAATATC ATATTAAAT TCAAA

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SEQ ID NO:2831

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03332

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SEQUENCE DESCRIPTION:

GATCCAGGGG GAAATGCTGG AAGTCAATAA AACTGAGTTT TGAGAGCTTG AAA

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SEQ ID NO:2832

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03356

SEQUENCE DESCRIPTION:

30

GATCCACATA AAAAGAAATG TGAAGTTTTC TTTTACTATC TTTTCATTTA TCAAGCAGAG 60

ACCTTTGTTG GGAGGCGGTT TGGGAGAACA CATTTCTAAT TTGAATGAAA TGAAATCTAT 120

TTTCAGTGAA A 131

35

SEQ ID NO:2833

SEQUENCE LENGTH:431

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03374

SEQUENCE DESCRIPTION:

40

GATCTGCTGA TTGCATTATT TTAATTTGCT TTTCTGGGAA AGCAGTTTTC CTAAAAGCTG 60

TACAGACTTT TNCITTTTGTA CCTAGCAGTA CTTTATATAG TATAGCTTTG GGCCATGTAG 120

CATTTTAAGA CTCAATTTTA AAAAATNATT AATCTGTTGC TGACTCTTAA TTCCTATTTTC 180

AATATGTGTT TCCTTGAAGA ATTCAGGATA CAACTTCTTG TGTATGACAG CTTTCCTTCA 240

45

CACACTATTT TNGTGGGTGT GTATATATCT GATTGGGAA GAATTTAAAA AACACATAGC 300

TTTTNAATTN GTTTGAAACA GACTTTCTGC CTGTGACATT TNNGCNTTTA NCCAATTAAA 360

GAAGCCAATG GCATTTTNGG TTTTATATNG TGTTTCCAC TAGTATATCC CTGTGGATTT 420

GTTTGTGCCC N 431

50

SEQ ID NO:2834

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# EP 0 679 716 A1

SEQUENCE LENGTH:429

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03375

SEQUENCE DESCRIPTION:

GATCCCATGG GTGGCACATT GGGACTTCTN TCCCTCCCC ATCTACACAG AAGACTGTCA 60  
CCATGCTGAC AGAAGCCTGT CCTTGTAAAG CCCAGCCTTC CAGGGGAACA CTCAGACATG 120  
TTCATTCTCT TCCTGCTTCT GCTCTGGGCC GGTGGGTGGC TCTCAGAAAA TACTTGCTGC 180  
TGGCAAAAGG CCTGTACTCA GGCATTGCT TTGACTTGAT GTTGCCAAGG GACTGAGGCC 240  
ATTGGCAGGC TTAGTACCAC CTGCTCCTCA TCTTAGGAGT CTCCTTTTCA AATAATTAGG 300  
CTCTGTTCCC ATTTTAAAC TCTGATATTG GGCTTCACCT GTGACTGGAC ACTTTACTAG 360  
AGGCCCATTT NCACTAAACA NTAAAATCTA AATAAATTGG AAGGAATAAC AACNACAAAG 420  
GGNTAGAAA 429

SEQ ID NO:2835

SEQUENCE LENGTH:427

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03376

SEQUENCE DESCRIPTION:

GATCTGGGCT TCCTNACTTC TGGAGAAGTG GCCATCCCAT GCCACCTTT NCCATGGAGG 60  
AGTGGGCCCT GCCAGCTGCC ACAGCTGCAT GACCTGCTTC CCCACCCAC GGTGTCGTTT 120  
TNTTTNAAA GGTCACTGT CCTCACTCAC CCAGCCAGCC CTTCAGGTGC NTTCTACTCC 180  
CAGTGCCAAA GCCAGACCAC TGGGGTTTCC TGCTGCAGGA ATTGGGGGCT GGAACAGCA 240  
GAGGGGATAG AAGTNTGGTG GAGGTGGAGT GGGCAGCAGT TAGCCTACGG AAAGGNCCAT 300  
TTTTTGGGNC CACTGAGCTG CACTGGGATT TTTCANTTCT GGNCCTGANT NCCTTTAGGG 360  
NAAATAACAC AGCAGGACCN CGGTGGGGAT TTAAAGNACT TTTTTTNNA GATTNAAANG 420  
GNTTCTN 427

SEQ ID NO:2836

SEQUENCE LENGTH:416

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03377

SEQUENCE DESCRIPTION:

GATCCTGATG CTGCCAGAGC CATTGTGGAT GCTTTACCAC CACCCTGTGA ATCTGCCTGC 60  
ACAGTACCAA CAGACGTGGA TAAGTGGTTC CATCACCAGA AAAACTAATG AGATTTCTCT 120  
GGAATACANG CTGATATTGC TACATCGTGT TCATCTGGAT GTATTAGAAG TAAAAGTAGT 180  
AGCTTTTCAA AGCTTTAAAT TTGTAGAAT CATCTAACTA AAGTAAATTC TGCTGTGACT 240  
AATCCAATAT ACTCAGAAAT TTATCCATCT AAAGCATTTT TCATATCTCA ACTAAGATAA 300  
CTTTTAGCAC ATGCTTAAAT ATCAAAGCAG TTGTCATTTG GAAGTCACTT GTGAATAGAT 360  
GTGCAAGGGG GNGCACATAT TGGNTGTATA TGTTTNCNT ATGTTAGGGG ATAAAN 416

SEQ ID NO:2837

SEQUENCE LENGTH:398

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03378

SEQUENCE DESCRIPTION:

GATCAAAGAT GAGGCCACAA GGACACCAGC AACTGAAGAG GCTGCCTACT TGGTATCAAG 60  
 ACTGAAGGAG AACTACGTTT TGCTGAGCAC TGATGGCCCT GGGAGGAACA TCCTGAAGTT 120  
 TAAGCCCCCA ATGTGCTTCA GCCTGGACAA TGCACGGCAG GTGGTGGCAA AGCTGGATGC 180  
 CATTCTGACT GACATGGAAG NGAAGGTGAG AAGTTGTGAA ACGCTGAGGC TCCAGCCCTA 240  
 AGCCAGCCCT GCTCTGCCCTA AGTGTACTCC AGAAGAACT CATCTCATCC AAATACACGC 300  
 TATTGAGAAG GCGAGCCTGA CCTCCCTCTT ACAGATAAAG TCAGCTTTCA GAGGCTCAGG 360  
 GTGGGGGGGC CTGCCCAGAG CCATAATGCT ACCCACCN 398

SEQ ID NO:2838

SEQUENCE LENGTH:408

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03379

SEQUENCE DESCRIPTION:

GATCGCACAC ATGCTTTGTT TGGAAATATGG AGTGAACACA ATTATGTACC AAATTTAACT 60  
 TGGCAAATTT NCTATTGCCT GTCCCATGTG CATCTNATTT AAAATTTCCC CCATGGAAAT 120  
 CACTCTCCTG TTGACTATTT CCAGAGCTCT AGGTGTTTAG GCAACGTGTG GTGTCCTGAG 180  
 ANGGCCATAG CGCCATCATG GGCTGATTTT AATTACCAGG TCCCCCAGAA GCAGGTGGGA 240  
 GGCTCTGCTT CCTGCTGGCC GTTCTGCAGC CTGGACCTGT GGACCCTGGT TGTAAAGNGT 300  
 AAATTTGTTT CTTANGGAAA CCAGTGTCAC CTTNTNTNAA CCTTTAAANT TAAAAAATAN 360  
 TTTGGGGGAA NAAATTNCNG NNACNCGAGG GTTAAAATTT ANCNANN 408

SEQ ID NO:2839

SEQUENCE LENGTH:388

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03380

SEQUENCE DESCRIPTION:

GATCCACCAG CTGAGCAGGG CGGGGCTGAG TAAATGCCGG CTTACCATCT CTACCATCAT 60  
 CCGGTTTAGT CATCCAACAA GAAGAAATAT GAAATTCCAG CAATANGAAN TGAACAAAAG 120  
 ATTGAGAGCTG AAGACCTAAA GTGCTTGCTT TTTGCCCGTT GACCAGATAA ATAGAACTAT 180  
 CTGCATTATC TATGCAGCAT GGGGTTTTTA TTATTTTAC CTAAAGACGT CTCTTTTTGG 240  
 TAATAACAAA CGTGTTTTTT AAAAAAGCCT GGNTTTTCTC AATACGCCTT TAAAGGTTTT 300  
 TAAATTGTTT CATATCTGGT CAAGTTGAGA TTTTTAAGA ACTTCATTTT TTAATTTNGT 360  
 AATAAAAGTT TTNCAACTTT GATTTTAN 388

SEQ ID NO:2840

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03381

## SEQUENCE DESCRIPTION:

GATCTTGCTG AAAGTGTTTC TAAAGATAGC ACCACTTTTT TTTNAAAGC TTTTATATAT 60  
 NAAAAACGT ATCATGCAAA 80

5

SEQ ID NO:2841

SEQUENCE LENGTH:384

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS03382

## SEQUENCE DESCRIPTION:

GATCTTGTC TAGCCTTTN ACTTTTGCAA TTTCAGTATC TTCATCTCTA AACTAGGGAA 60  
 ACACTNGGAT TCTTTCTTAG CTGTGGGGGA AGGTATTTGG TTAGATGACT TTGAATGAAT 120  
 AGACTGCTGT GCTGAAAGAG CTTATCACA CTGTCTCAAA GTATGTAAAG ATACATAGGT 180  
 GGATGCTCTT ACTGCAGCAG TCATGAATAC ATTTTtagcc ATTTACCTAA GGAAAAAGAC 240  
 AGTTTTTCTA GGTACCATGA AGGAAGATTG ACCCTGTTGG TATGCCTGTG GGGGTGGGAT 300  
 GTGAGTGGGA CTGATAAACT GATACTTTTG GTTCGTATGT ACATACTGGN AGAATCTTCA 360  
 TANTAAATGN GACTACACAA CAAA 384

20

SEQ ID NO:2842

SEQUENCE LENGTH:376

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25

CLONE:HUMGS03383

## SEQUENCE DESCRIPTION:

GATCCAGGGC AAGGCCATTG GGATATTCTG AAAGTGAAT ATTTTGTTTT GTGCAGAGAT 60  
 AAAGACCTTT TCCATGCACC CTCATACACA GAAACCAATT TTNTNTNTNA TACTCAATCA 120  
 TTTCTAGCGC ATGGCCTGGT TAGAGGCTGG TTTTCTCT TTTCTTTGG TCCTCAAAG 180  
 GCTTGTAAGT TTGGCTAGTC CTTGTTCTTT GGAAATACAC AGTGCTGACC AGNCAGCCTC 240  
 CCCCTGTCCC CTCTATGACC TCGCCCTCCA CAAATGGGAA AACCAGACTA CTTGGGAGCA 300  
 CCGCCTGTGA AATACCAACC TGAAGACACC GTTCATTGAG GCAACGNACA TAACAGNAAA 360  
 TGAAGGTGGA CANGCN 376

35

SEQ ID NO:2843

SEQUENCE LENGTH:370

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS03384

## SEQUENCE DESCRIPTION:

GATCCCAAAC CTAGCCCCCT AGTGGGACAA GGACCTGACC CTCCTGCCCG CATACACAAC 60  
 CCATTTCCTT TGGTGAGCCA CTTGGCAGCA TATGTAGGTA CCAGCTCAAC CCCACGCAAG 120  
 TTCCTGAGCT GAACATGGAG CAAGGGGAGG GTGACTTCTC TCCACATAGG GAGGGCTTAG 180  
 AGCTCACAGC CTTGGGAAGT GAGACTAGAA GAGGGGAGCA GAAAGGGACC TTGAGTAGAC 240  
 AAAGGCCACA CACATCATTG TCATTACTGT TTTAATTGTC TGGCTTCTCT CTGGACTGGG 300  
 AGCTCAGTGA GGATTCTGAC CAGTGACTTA CACAAAAGGC GCTCTATACA TATTATAATA 360  
 TATTCGCTTN 370

50

55

SEQ ID NO:2844  
SEQUENCE LENGTH:367  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS03385

SEQUENCE DESCRIPTION:

GATCTGTCAT CTGGTGTCTG CAGCTGTGCT CACTCTGGTT TTCTGCTCAG GGTCTGAAGC 60  
AGCTGCTGTC TNCCTCCTCT GCCCCCATCC CCTGGCTCTC CCCTGGGCAC AGTGCCACTC 120  
CCTTGAAGG GAGGGAACCA CCCGTNAGCC CCAGGGCTTG GNAAGCCTGA GCGGGTGNCT 180  
CTGCCTCTCC CTGCCCCCAG CACAATTGGC AGAGATGAGG CGGGTGGTGG ACGGCTGGGG 240  
GTGTCGTGGC AGGGTCTNGC ACAGGGNCAT GTCCTGGCTG TAACCCAGGC AGTGGGAGGT 300  
CTGCAAGCCT GGTTCATGGCC TTCACAGCAN GGTNCCTGTT GGACAGACAT ATCTGNATAT 360  
TTATNAA 367

SEQ ID NO:2845  
SEQUENCE LENGTH:366  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS03386

SEQUENCE DESCRIPTION:

GATCTCCAAC ACTATCCGAT AAAGTAGAAG CAACTGAGGT ACCGTGAAAG AGAAAGGAGC 60  
TGGAAGTGAAG AAAAAGCAGA GGATTCGGAC GGAGAGCGCG AGGACTCGGC GGCTGAGCGC 120  
GCCCCACAGC AGCTAGAGGC GCTGCTCAAC AAGACTATGC GCATTTCGCAT GACAGATGGA 180  
CGGACACTGG TCGGCTGCTT CCTCTGCACT GACCGTGACT GCAATGTCAT CCTGGGCTCG 240  
GCGCAGGAGT TCCTCAAGCC GTCGGATTCC TTCTCTGCCG GGGAGCCCCG TGTGCTGGGC 300  
CTGGCCATGG TACCCGGACA CCACATCGTT TCCATTGAGG TGCAGAGGGA GAGTCTGACC 360  
GGGCCN 366

SEQ ID NO:2846  
SEQUENCE LENGTH:365  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03387

SEQUENCE DESCRIPTION:

GATCCCCCA AGGNGAAGTG TGAGACAATG GTCTATCACC CCAACATTGA CCTCGAGGGC 60  
AACGTCTGCN TCAACATCCT CAGAGAGGAC TGGAAGCCAG TCCTTACGAT AAATCCATA 120  
ATTNATGGCC TGCAATATCT TTNCTTGGAG CCCAACCCCG AGGACCCACT NAACAAGGAG 180  
GCCGCAGAGG TCCTGCAGAA CAACCGGCGG CTGTTTGAGC AGAACGTGCA GCGCTCCATG 240  
CGGGGTGGCT ACATCGGCTN NACCTACTTT NAGCGCTGCC TGAAATAGGG TTGGCGCATA 300  
CCCACCCNNG GCCACGGCCA CAAGCCCTGG GCATCCCCTG CAAATANTTN TTGGGGGGCC 360  
ATGGN 365

SEQ ID NO:2847  
SEQUENCE LENGTH:364



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03388

SEQUENCE DESCRIPTION:

GATCTAGAGT ATGTTGAAGA AGATGGACAT GTGGTGGTAC GAAAAACAATT CCCCTGTGGC 60  
CTGCTGGACT GGGTGGAACC AGAACAGGCT AAGGCATACA GTTCTTGACT TTGGACAATC 120  
CAAGAGTGAA CCAGAATGCA GTTTCCTTG AGATACCTGT TTAAAAAGGT TTTTCAGACA 180  
ATTTTGCAGA AAGGTGCATT GATTCTNAAA TTCTCTCTGT TGAGAGCATT TCAGCCAGAG 240  
GACTTTGAA CTGTGAATAT ACTTCTGAA GGGGAGGGAG AAGGGAGGAA GCTCCCATGT 300  
TGTTTAAAGG CTGTAATTGG AGCAGCTTTT GGCTGCGTAA CTGTGAACTA TGGCCATATA 360  
TAAN 364

SEQ ID NO:2848

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03389

SEQUENCE DESCRIPTION:

GATCTGGGGA GGCAGGCATT CCTGAAGGGA ACTAGAGGTG TTACAGAGGA CCCTTACGTG 60  
AGAAATAGCT GAAAAGGGCA CTCGCAACCC TGGGCTGGGG AGGAGGAGAG AGTCCCAGAG 120  
CTCATCCCC CTGCTGCCCA GTGCAAACCA CTTNTCCATG CTGCAAAGGA GAAGCACAGC 180  
TCCTGCCAGG GTGAGCAGGG TCAAGCCTCT TATTCCAGGA GAAGGGGGCT CTGCCCAGGC 240  
CCTACTACCN ATTGTNCCCT TCCTCTTCTT GCCCTTGAA CCCCCTNCCT GTCCCAGGGC 300  
CCTTCNAGCC CATTGCTGCC AAGGTGGAGG GANGGATAAA GNCACCTCTG GGTTTTGAAG 360  
CCN 363

SEQ ID NO:2849

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03390

SEQUENCE DESCRIPTION:

GATCTGGGTG TGGCCAAAAA CAATTTTNTT TATTCTGTCT ATCAAATAGT ACTTCTACCA 60  
CTGTTTGGAG AAAATTGAAG AAAAGAATAA GATGATTAAA TGAATTCTCT AAAAGAACAT 120  
ATTTTAAGAG ACAGAACTTA GACATAACCA AGTAGTTGTA TACCTGATTG TAACAATCAT 180  
CTTTTATAAA AGCAAAATTA TGCATAAATG TAAACACCC CTAAACAAAG GGAACAAATG 240  
ANTTTTGGT TATATTGTTT TCTTGGCTCA AAGTATCAAT TTATTATTAT AATAGAAATT 300  
TATAAGTTGC TAGAAAGTCT ATATTTTAA CGCACGGAAT AAAANTATGT TTTCTATTAA 360  
A 361

SEQ ID NO:2850

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03391

## SEQUENCE DESCRIPTION:

GATCTGTCTC CAAGACCTTG GCCTCTCCTT GGAGGACCTT TAGGTCAAAN TCCCTAGTCT 60  
 CCACCTGANA CCCTGGGAGA NAAGTTTGAA GCACAACTCC CTTAAGGTCT CCAAACCAGA 120  
 CGGTGACGCC TGCGGGACCA TCTGGGGCAC CTGCTTCCAC CCGTCTCTCT GCCCACTCGG 180  
 GTCTGCAGAC CTGGGTTCCC ACTGAGGCC TTTGCAGGAT GGAACCTACGG GGCTNGNAGG 240  
 AGCTTTTGTG TGCCTGGTAG AAATATTTC TGTTCAGTC ACATTGGCCA TCACTCTTGT 300  
 ACTGNCTGCC ACCGNGGAGG ANNCTGGTGA CAGGNCAAAG GCAGTGGAAG GAAAN 355

SEQ ID NO:2851

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03392

## SEQUENCE DESCRIPTION:

GATCTAGTTC TACGTATTAC ACAGGTGTAA TATCTGTGAG TGTAATAAC TGGAACGTGA 60  
 CACTGATTAA CATGNCAGTT TCTCTTTTGT TGTCTTATC TGTACTGTAT TATAGTATGT 120  
 GGGTATAAAT ATCTACAAGT ATACACACAT ATGTNCTNGT ATTCCACTAT TGTAACCTGG 180  
 AAGAAAGACT ATGNATNCCC TTTNNAAAT CCGTACTGGT ATNNGTGTTA TTTAAAAAGC 240  
 AAAATNCGGC TCTATTTAGT TGTATAATAT TAGAGGGTAC TNNGCTTGN CACAATTCCA 300  
 AGTGGCCTTA GAGCATTGTT TAGCTNNCCG AAGTATATAT AANN 344

SEQ ID NO:2852

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03393

## SEQUENCE DESCRIPTION:

GATCTATGAG CCTGTNTNGG ACAGCCAGAT GGTCAATCATA GTCACGGTGG TGTCGGTNTT 60  
 GCTGTCCCTG TTCGTNACAT CTGTCTCTGT CTGCTTCATC TTCGGCCAGC ACTTGCGCCA 120  
 CNGCGGATGG GCACCTACGG GGTGCGAGCG GCTTGGAGGA GGCTGCCCA GGCTTCCGG 180  
 CCATAGCAAC CATGANTGGC ATGGCCACCA CCACGGTGGT CACTGGAAC NAGTGTGACT 240  
 CCTCAGGGTT GAGGTCCAGC CCTGGCTGAA GGAATTGTNA CAGGCAGCAG AGACTTGGGA 300  
 CATTGCCTTT NNTAGCCCGA NTACAAACAC CTGGACTTAA A 341

SEQ ID NO:2853

SEQUENCE LENGTH:567

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03394

## SEQUENCE DESCRIPTION:

GATCTCAAGA CCAAAGACAG ATGTCACTGG GCTGCTCTGG CCCTGGTGTG CACGGCTGTG 60  
 GCAGCTGTTG ATGCCAGTNT CCTCTAACTC ATGCTGTCCT TGTGATTAAA CACCTCTATC 120  
 TCCCTTGGGA ATAAGCACAT ACAGGCTTAA GCTCTAAGAT AGATAGGTGT TTGTCCTTTT 180  
 ACCATCGAGC TACTTCCCAT AATAACCACT TTGCATCCAA CACTCTTCAC CCACCTCCCA 240  
 TACGCAAGGG GATGTGGATA CTTGGCCCAA AGTAACTGGT GGTAGGAATC TTAGAAACAN 300

# EP 0 679 716 A1

5 GACCACTTAT ACTGTCTGTN TGAGGCAGAA GATAACAGCA GCATCTNGGN CCAGTCTCTG 360  
 CCTTAAANGG AAATCTTTAT TAATCACGNA TGGTTCACAG ATAAATTCTT TTTTAAAAA 420  
 AANCCCANNC TCCTNGGGAT GCACANCCTG TCAAGNGTCT TTTTACACAC AANTTTCAGG 480  
 TTTNNCATCA CGGGGCTTTG ANTTNAGGA AATNAAAGGN GGGACAAATT TNGTTNGTTT 540  
 ACNCTATGGT NCTTTNNTAA NAAACNN 567

10 SEQ ID NO:2854  
 SEQUENCE LENGTH:349  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03395

15 SEQUENCE DESCRIPTION:  
 GATCTTTACT TTTTACTTT TTATTCATCT TTGTGTTTTT ATTTATCTAA AATGGGTATT 60  
 GATTTTAAAG ACGGTTTTGA AAAAGAAAAG TGTTGGGAAT GAAGCAAGTG ATTGATTGGA 120  
 AAACATACTG AATGGAAGAA ATATTTAGAT TAAAAATGAG GTAGGTTGAA GTTCTNCTC 180  
 TGAAATNATA GATAAATGGT GAAGATAAGG CTTATTGTGA GGNTTCAGTG AGGTAATATA 240  
 TGCAAAGTAC TTACAATGTT CTGGCACATA GTAATTNATT NNGANAATCG AGCACCCCTTA 300  
 20 ATTACCTAGA ATGCAGGGTT GTTAGTTTTT NGGTTGACTT TTGTTTTNN 349

25 SEQ ID NO:2855  
 SEQUENCE LENGTH:334  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03396

30 SEQUENCE DESCRIPTION:  
 GATCCGCTGT ATTGTGGAGT ATCAGAACAA GGGCCGCGGG AACGAGNGCG TGCAGTACCA 60  
 GCATGTGTTA CATAGAAATC TCATTATTT GGCTACCATT GCAGATGCCA GTCCAACCAG 120  
 CACTTCAAAA GCAATGGAAT AATCTTTCAA AAGCAATAGA ATAATCTTCC ATTTGGCTGT 180  
 CGTGAGGAGT AATTGAATGT AATCCATCTC TTACAAAATG GAGACAGGGT CTTTACCAAC 240  
 TCAACTGGTT AAAACATGAN TGAAACCTCT GTGGCTCTTT CAAAACGTGG AAAATGTGAA 300  
 35 GAANGCTACT TAACTTNGGC TGTATTCTCA TGGN 334

40 SEQ ID NO:2856  
 SEQUENCE LENGTH:332  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03397

45 SEQUENCE DESCRIPTION:  
 GATCGGCCTG CTGCTCCGCA ACTTCGACCG CTACGGCGTG GAGTGCTGAN GGACTCTGCC 60  
 TCCAACGTCA CCACCATCCA CACCCCGGAC ACCCAGTGAT GGGGGAGGAT GGCACAGTGG 120  
 TCAAGAGNAC AGACTCTAGA GACTGTCAGA GCTGACCCCA GCTAAGGCAT GGCACCGCTT 180  
 CTNTCCTTTC TAGGACCTCG GGGTCCCTCT GGGCCAGTT TCCCTATCTG TAAATTGGGG 240  
 ACAGTAAATG TATGGGGTCG CAGGGTGTG AGTGACAGGA GGCTGCTTAG CCACATGGGA 300  
 50 GGTGCTCAGT AAAGGAGAGC AATTCTTACA AA 332

55

SEQ ID NO:2857

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03398

SEQUENCE DESCRIPTION:

GATCCTGGGT GTNTNTGTAA GGGTNTTGCC AAAGGAGGTT AACATTGGAC TCANTGGGCT 60  
GGGGAAAGGC AGACCCACCC TTAATCTGAG TGGACACCAT CTAATCAGCT GCCAGCGAAA 120  
ATAAAGCAGG CAGAAAANTG AAAAANNTAG ACTGGCCTAG CCTCCCAGCC TACATCTTTN 180  
TCCCATGCTG GATGCTTCCT GCCCTTGAAA ATTGGACTCC AGGTTCTTNA GTTTTGGGAC 240  
TTGGACTGGC TCTCCTTCCT CCTCAGCCTG CAGACATCCT ATTGTGGGAC CTTGTGTTTC 300  
TGTAAGTTCA TACTTAATAA ACTCTCCATA N 331

SEQ ID NO:2858

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03399

SEQUENCE DESCRIPTION:

GATCGAGTCT ATACGCTGAA GAAANNTGAC CCGATGGGAC AACAGACCTG CTCAGCCCAT 60  
CCTGCTCGGT TCTCCCCAGA TGACAAATAC TCTCGACACC GAATCACCAT CAAGAAACGC 120  
TTCAAGGTGC TCATGACCCA GCAACCGNGC CCTGTCCTNT GAGGGTCCCT TAAACTGATG 180  
TCTTTTCTGC CACCTGTTAC CCCTCGGAGA CTTGTAACC AAACNTTTCG GACTGTGAGC 240  
CCTNATGCCT TTTTGCCAGC CATACTTCTT TGAGCATCCA GNNTNTNGTG GCGATTTGAT 300  
TATGCTTGTT GTGAGGNAAT CATGGGTNGG CNTCNCCNT TAANGGGGTG N 351

SEQ ID NO:2859

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03400

SEQUENCE DESCRIPTION:

GATCCTGGGG GCCTGGGTTG GGGGCTAGGG AGACGCCATG TGATGGACAC TCCAGGGACA 60  
CACAGCCTAG CACAGCAGCT TATAATGGGC TCTCCGGGGC CATTTGCAAT AACAGCTGCA 120  
ATTCCCTGGA TAGACGAGTT GATTCCTCC CTCTGCCCCT CCCCAGCCA TGCCAGCTGG 180  
CCTTTGTAAG TGCAGGAAAC CGAGTAGAAA ATGTGACCCT CCAAATGGAG AAGCTGCAGG 240  
CTTTGCCATT GTGAACCATG GTGAAGTGCT TGGAACATAC TGTTCCTCA CTCTAAAGGN 300  
GCTGAGACTG TGCTGTTGTT CTCGTTTTN 330

SEQ ID NO:2860

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03401

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTGGAAA GGACATGACT TCTGAAATAG CCGCTGCTGG GTTTTAAAAG CTGAGGTCTC 60  
TCAAAGTGTG GAGGAGACGT TGCCGTCAGN GGGAGCCAAG TGCCGGAAG ATGTCTATTT 120  
TTTTCCTTGT GTATTGAAAA TCATGATGTT TGTTATGACT GCTGATGCGA TTGTNTTGT 180  
AAATNTNATT GTGGCATATA CAGTATTGTC ATACAGTTGA AGAGAAACAA TGTTTCCTAA 240  
TGTAAGTNCT CTGAAAATGT TGACACTGTA TATATATATA TNAGGATAGT TTGTNTTTCN 300  
NTGTTTGGGG TTTNNNTTN TTCNGNTGN 330

SEQ ID NO:2861  
SEQUENCE LENGTH:396  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03402

SEQUENCE DESCRIPTION:  
GATCTTAAAC CCAAAGTACG AGAAATGTTT CTGTTGAATG TAATGCTACA TGAATGCTTG 60  
ATTTATCAAG CGCCAAAAG GCATTGTATA GTAGGAAATG TAAGTGGGGT GGCTTATGGC 120  
TTCTTTATCC TCTGATTCTA GCACTTTCAA GTGAGCTGTT GCGTACTGTA TCATATTGTA 180  
GCTATTAGGG AAGAGAAGAA TGTTGCTTAA GAAAGAACAT CACCATTGAT TTAAATACA 240  
AGTAGCAGGG TATTGCCTTT GATTCAACTG TTTTAAGTCC TCATTTTCT CAAACTAAGT 300  
GCTTGCTGTT CCCAAATATG GCAAGGNATA GCTTTTACAC TTTTCCCTG CCAACANNTC 360  
NTNGATTGGC TTTGCAGANA TNNAGGTTTG ANTTGN 396

SEQ ID NO:2862  
SEQUENCE LENGTH:330  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03403

SEQUENCE DESCRIPTION:  
GATCCAAAGT GACCCACCA GGGGACAGCC AGAGGAAGGG GACCATGGGG TATCCNNAGT 60  
GTCCTGGTCT ATCACCCAG CTTCTTTGTC CCCAGTACC CCCAGCCCAG CCAGCCAATA 120  
AGAGGACACA AATGAGGACA CGTGGCTTTT ATACAAAAGTA TCTATATGAG ATTCTTCTAT 180  
ATTGTACAGA GTGGGGCAAA ACACGCCCCC ATCTGCTGCC TTTTCTATTG CCCTGCAACG 240  
TCCCATCTAT ACGAGGTGTT GGAGAAGGTG AAGAACCCTC CCATTCACGC CCGNCTACCA 300  
ACAACAAACG TGCTTTTTTC CTNTTTGAAA 330

SEQ ID NO:2863  
SEQUENCE LENGTH:329  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03404

SEQUENCE DESCRIPTION:  
GATCTTATTT TCTGAGAAAT TGATAGCAAA TATGCCAGAA AGTGGACCTA GTTATGAATT 60  
CCATCTAACC AGACAAGAAA TAGTATCATT ATTCAACGCA TTTGGAAGAA TTTCTACAAG 120  
TGTGAAAGAA TTAGAAAAC TCAAGAACTT GTTACAGAAT ATTCATTAAA GAAAACAAGC 180  
TGATATGTGC CTGTTTCTGG ACAATGGAGG CGAAAGAGTG GAATTTTCATT CAAAGGCATA 240  
ATAGCAATGN CAGTCTTAAG CCAAACATTT TATATAAAGT TGCTTTTGTA AAGGAGAATT 300

ATATTGTTTT AAGTAAACNC ATTTTAA

329

SEQ ID NO:2864

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03405

SEQUENCE DESCRIPTION:

GATCACTTCA GCTGCCTGCT GTGGACAAAG AACATCAAAT TACAGCATCA CGAGTGCTAT 60  
TNTTGCCTGT GGTGGTCTCC CTGTCCAAGC GGGNCCGCTT TGCAGAGACC AGAGGCATAT 120  
CGCGGCTTGA GCTGAAAATG CATTNTTTC AGCTTAGGTT GAATTATTTT NCGTTTGCTC 180  
TTTCTTCTAC ACGCGCCTGA TGGATAGTGA ACCTATTCAT CAAAAAAGTG CACTGCTCTN 240  
CTGTCTATTG TACCGACTTA ACCTCTTCCA CCCAAGTCCG CATCTGTGTG TATCATCAAT 300  
AAAGTTGGTN GTGCCTTGGN TTGGGCAA 329

SEQ ID NO:2865

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03406

SEQUENCE DESCRIPTION:

GATCGGCGTG ACCACCCCTT GCCGGAGGTG GCCCATGTNA AGCACCTNTT TGCCAGCCAG 60  
AAGGCACTGA AGGAGAAGGA GAAGGCCTCC TGGAGCAGCC TCTCCATGGA TGAGAAAGTC 120  
GAGTTGTATC GCATTAAGTT CAAGGAGAGC TTTGCTGAGA TGAACAGGGG CTCGAACGAT 180  
NTGGAAGACG GTTNTNGGGC GGTNCCATGT TCTTTAATCG GTTNAACGT GCTCGTTNCC 240  
CCTNTGGAAA AAGGNCTTNT GTTTACCGGC CCCCTTCCCG AAAAGTTTTN ACAAANGGT 300  
GGGGTTGCC AAGNAGGCC AANAGGNN 328

SEQ ID NO:2866

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03407

SEQUENCE DESCRIPTION:

GATCTACAGA GTTAGAAATT CGAAACTAT TCCAGGACTA ATTCTTAATC GGCATTATTT 60  
ATACAAGAGG TCAAGTAACA TTTACTAGCG CAATACTGCA CTTGTAAATG AATTATAAAC 120  
GCTCTTCTGG AATATATTTA AATAACCATT AAAGAACTGC TTATTCATNC TGGACACTGC 180  
ATGTNGATGT TGAATCAACT GATGCCAGCA GAAAGCTATT TTGATTTGTG AACATACTGC 240  
CTTATTTAAA GGGTCCTGAT TGCTTGTATT TTANGNCATT CATTAAAAAG AAACCAGGAA 300  
ACACTTTTGA ANTAACAGCA TANGGNN 327

SEQ ID NO:2867

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03408

SEQUENCE DESCRIPTION:

GATCACCTC CTCCCAAAAA GCAAGAGCTT GTTTATGGCT GAGGAATCGG CGGATTGTCT 60  
 GAATGACACA TATACAGAGC CCCCACGGAT TTCTNCACAC TCTGGGTCTG TGCTGGTGGA 120  
 ACATTGCCAA TNAGTTCTTA ATGAGGCACC TGTGTGTAAG TACATGCTTG GTCTTCTCTG 180  
 CAGAGAACTG AGGCTAAACT CTGTCCCTAC TTCTGGTTTT GCCCTGTNAT GTCGTAACGA 240  
 GGTGGGCCTT TTGAGGCCAT TTTAGTTTGA GTTCGAGCCA ACCACCTCTG GTTGGTTAGA 300  
 TGATTGAATA AAAAGGTTCT GAAGAAA 327

SEQ ID NO:2868

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03409

SEQUENCE DESCRIPTION:

GATCCAATCA CCTCCACCA GGCTCCACCT CGAATACTGG GGATTACCAT TCAGCATGAG 60  
 ATTTNGGCAG GAACACAGAC CCAAACATA CCACACACAT TATCATTGTN AAACCTTTGTA 120  
 AAGTATTTAA GGTACATGGA ACACACGGGN AGTCTGGTAG CTCAGCCCAT TTNTTTATTG 180  
 CATCTGTNAT TCACCATGTA ATTCAGGTAC CACGTATTCC AGGGAGCCTT TTTGGCCCT 240  
 CAGTTTGCAG TATACACACT TGCCANGTAC TCTTGGTAGC ATCCTGTTTG GTATCATNGC 300  
 ACTGGGTCAC ATTGCCTTAC CTAAAN 326

SEQ ID NO:2869

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03410

SEQUENCE DESCRIPTION:

GATCTATGGA ACAGAGGAGG AGCGATGCAG TTGGGAGAGG AAGCTAGAAG GGTTATGGTT 60  
 GGAGTTCTGT ACAGTGTGTA GTTCCGACA GGGAAAGAGG ATTCCTCAA TGCGCCTAGA 120  
 GAGAAAGCCT GAGCAGGAGA TGATGCAGCA GAGGGGAAGG GCCCTGTGGT GCCGCCGCC 180  
 TTCCTTCAGC CTCCGAAGGT GATGGAAATG GAGAGTGGAG GACCAGGCCT CCAGCTGTNT 240  
 GGCTTNGCCN TTCACGCCTT AACACTAAGC CCACCTCCCC TTNTCTCCTT CCCAGCATTG 300  
 AGCCCTTGGT TGCCTGGGCC CAGGN 325

SEQ ID NO:2870

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03411

SEQUENCE DESCRIPTION:

GATCTTCAGA AACCTTGCTA GGAGAAGTTA ATGAAAATAG AGTATCAATA GCATTGAAAA 60  
 AAACCTCTGA AATCCTTAC GATATTGACT GTCTTCTATC AAACCTCTAA AAGTGAAAAA 120  
 TGGAATTATT ACAACATATT ATTTAAAGTTT AAGGATGTTG TTTCAAGTGA CTGGTATAAA 180  
 ATTACTAGTA AGCCAAGATA TTGTACGTAT TACCCCGGCA CAATGATTGT GAAAGANCTG 240

ACATTTAACT TTGAAGGTAT TTTTAACTTG TACATTTTAA AAATATGTAT TTATATCTNA 300  
 NTANTAAATN TTTCGAAGTT TTAATA 325

5 SEQ ID NO:2871  
 SEQUENCE LENGTH:325  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03412

10 SEQUENCE DESCRIPTION:  
 GATCCAAGCG GAGATTGACG CTGCAGCGGA NACTCATCGA CTTCTTCCGG TTCAATGCCA 60  
 AGNATGCGGT GGAGCTGGAG GGGCAGCAGC CCATCAGCGT GCGCCCGAGC ACCAACAGCA 120  
 CGGTGTACCG GGGTCTGGAG GGCTTCGTGG CGGCCATCTC GCGCCNTAAC TTTACTGCAA 180  
 15 TCGGCGGCAA CCTGGCGGGG GCACCGGCCC TGATGCTTCG AGAGGGAGTT GTGACTCTGC 240  
 CTCCTTGCCA GATGACAAAA CTGAGACACA CAGCCGTGAC TTACTTGGCA AGACTGAGTG 300  
 ACTAGTAAAT AAATGATGGA GCAGN 325

20 SEQ ID NO:2872  
 SEQUENCE LENGTH:323  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03413

25 SEQUENCE DESCRIPTION:  
 GATCCTCCTT CTAGCTCATC TGTAAGTACT AGTAGTAGTC AACCAAAGCC TTTCAGACGA 60  
 GTAAGACTTC AGACAACATT GAGACAAGGT GTCCGTGGTC GTCAGTTTAA CAGACAGAGA 120  
 GGTGTGAGCC ATGCAATGGG AGGGAGAGGA GGAATAAACA GAGGAAATAT TAATTAANTG 180  
 GTCTGTAAAC AATAACAAC GTGAATAAGA TTATCAAATC TTTTGTAGTG TAATGATTGT 240  
 30 CAAGTTTAAA ANCATTTTNN TATATAACCT GGTATACTCA TGTCATATN CTTTATTAAT 300  
 AAAANGNTTT TCAGTGTCAT AAA 323

35 SEQ ID NO:2873  
 SEQUENCE LENGTH:322  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03414

40 SEQUENCE DESCRIPTION:  
 GATCTGCCCA TCTCAGCCTC CCAAAGTGCT GGGATTACAG GTATGAGCCA CAACGCCCAN 60  
 CCATCATTTA TCTTTTTCAC TCATTTTTC ATGAGTATGC AGAGGAGTTT TCAAGAGGCT 120  
 ATCTGGTGTG ATATTGTAAT AGGCTGAATG CAAAAGCAGA TACAAGATTC CAGCTTTCGT 180  
 CTGTCATCAG ACATTGAAGA GATTGGGAGA AATGTAAAGC AGCAGTACTC TTCTCACTAA 240  
 45 TTTTGTGTGT GGTTAGTTAG AAAAATGGTT ATTTTNAGTG GGTTTTAATA TGTGAAAAAA 300  
 ATAAAATTAG CTATTTGCCA AA 322

50 SEQ ID NO:2874  
 SEQUENCE LENGTH:319  
 SEQUENCE TYPE:nucleic acid



TOPOLOGY:linear

CLONE:HUMGS03415

SEQUENCE DESCRIPTION:

5 GATCACCTNT GGC GTGTTCC TNCCAAAACN GCATAGCCCC AATCTAATAT CATCCCGAGG 60  
 AAATACCAGA CACACGCAAG GGAAAGGACA TTCTACAAAG GAACGGACTC ATACTCTTCG 120  
 AAAAGTGTCA AGGTCTCTA CGACAAAAGA CTGAAAGGAC CCCAGTCGAA AAAAGNCAAG 180  
 ATGACAAANT GCAACGTTTC ATCCTAGACT GGATTCTGGA CCCAAAAAAT CCCCTTCTTT 240  
 10 TGT CAGAAAG GAAATTTGTG GAACAAC TGG CAAAATCTGG AGTTGGGTCT GCAGATTACA 300  
 CACTGGTATC GCAGCGAAA 319

SEQ ID NO:2875

SEQUENCE LENGTH:320

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03416

SEQUENCE DESCRIPTION:

20 GATCTCCCTT CGTGGAGACG ACACCGGGGT CCTCCTGCCC ACCCCAGGGG AGGCCAGGA 60  
 TGCTGATTTG AAGGATGTAA ATNTNATTC AGCCACCGCC TGACCATCCG CCATTCCGAC 120  
 TGCTAAAAGC GAATGTAGTC AGGCCCTTT NATGCTGTGA GACCTCCTGG AACACTGGCA 180  
 TCTNTGAGCC TCCAGAAGGG GTTCTGGGCC TAGTTGTCCT CCCTCTGGAG CCCNGTCCTG 240  
 TGGTCTGCCT NAGTTTNCCT CTNCTAATAC ATATGGCTGT TTTCCACCTG GNTAATATAA 300  
 25 CCANGAGTTT GGGCCGNAAA 320

SEQ ID NO:2876

SEQUENCE LENGTH:308

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03417

SEQUENCE DESCRIPTION:

35 GATCTCTGCT GTGNCTCCCA GAGTTACTGC TGCCAGACTG AACTGGAAGG GGAGGATGTA 60  
 GGAGCCTGCA CAGCTCACAC CTACTCCTGT GGCTCTGGAG TGGGCATCTN CCTGAGAGTA 120  
 CGGGAATGTN AGGTGCTATT TTAAGCTGGC AAAACCAAAG GCTGTTTTNA TTCTCCTCCT 180  
 TACCTTGATG ACTATGGGGA GACCGACCAG GGAATCANAC GGGGAAATCC TTTACATTTA 240  
 TGCAAAGAGC GATTCAAGAA GATTCAAGAG CTCTGGCACC AACACAGTGT CACAGNGGAA 300  
 40 NTTGGNCN 308

SEQ ID NO:2877

SEQUENCE LENGTH:308

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03418

SEQUENCE DESCRIPTION:

50 GATCTTGACC ATGACAGTTT TNCAC TTTTA ATGAAACGGG GAACCAAGAG GAACTTACTT 60  
 GTGTAAC TNA CAATTNCTGC AGAAATCCCC CTTCCTCTAA ATNCCCTTTA CTCCACTGAG 120  
 GAGCTAAATC AGAACTGCAC ACTCCNTCCC TGATGATAGA GGAAGTGGAA GTCCCTTTAG 180

55

# EP 0 679 716 A1

GATGGTGATA CTGGGGGACC GGGTAGTGCT GGGGAGAGAT ATTCCTTAT GTTTATNCGG 240  
AGAATTTGGA GAAGTGATTG ACCTTTTCAA GNCATTGGGA AACAAATAGA NCACANTATA 300  
NTTTNNCN 308

SEQ ID NO:2878  
SEQUENCE LENGTH:307  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03419  
SEQUENCE DESCRIPTION:

GATCTAGAAG ACGATTAAGG GAAGGTCGTT CTCAGTGAAA ATCCAAAAAC CAGAAAAAAA 60  
TGTTTATACA ACCCTAAGTC AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT 120  
TCAGGAACTG AAACATCAGC ACAAAGAAGC AATCATCAAA TAATTCTGAN CACAAATTTA 180  
ATATNNNNNT TNCTGAATGA GAAACATGAG GGNAATTGTG GAGTTAGCCT CCTGTGGTAA 240  
AGGAATTGAN GAAAATNTAA CACCTTACAC CCTTTTCCAT CTTGACATTA AAAGTNCTGG 300  
CTAACTN 307

SEQ ID NO:2879  
SEQUENCE LENGTH:307  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03420  
SEQUENCE DESCRIPTION:

GATCTTGAGG GCAGACAGCA GAATTCCTCT TATAAAGAAA ACTNTTTNGG AAAATACGTT 60  
GAGGGAGAGA NGACCTTGGG CCAAGATGCT AAATGGGAAT GCAAAGCTTG AGCTGCTCTN 120  
CAAGAGAAAA TAAGCAGGNC AGAGGATTN CTCTGGACAG AGATGGAAGA GCCGGGAACA 180  
GAGAAGTNTG GGGAAAGAGAT AGGAACCAGC AGGATGGCAG GGGNNNNGGG CTCAAGGGTN 240  
AGGAGGCCAG TGGGACCCCA CAGAGTTNGG GGAGATAAAG GAACATTGGG TTTGCTTTGG 300  
TGGCACN 307

SEQ ID NO:2880  
SEQUENCE LENGTH:305  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03421  
SEQUENCE DESCRIPTION:

GATCTGCCGT GTCCTTATAA AGTGGATGAA AAATGTTTTG TACCCATCTG GAAAACCAAC 60  
AACTTGAAAT CTCAGGTATT CCAGGTCAC TACATGAATT TGAAGATATA TCTATCTGTA 120  
TGGATATATA TCTATATGTA TATAGATATA TAANTACAGA GAGATATCTG GCTTGGTTTT 180  
AATTATGTNC TTAAATTTGT GTGCCAATAA TTGCATATAG ATTTTNTTNC TTAAATATTT 240  
GACTGTGGAA CATGCCATTT TAAATATGTN GTAAGGCCTG TNNTAATAAA ACGTTTAGTA 300  
TGAAA 305

SEQ ID NO:2881  
SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03422

SEQUENCE DESCRIPTION:

GATCCACTGA TGGCTCCAGA CCCCAACTTT AGCCATTGCA CGTGTGTAAC TCCAGGTTGA 60  
GCCTTTGCTG GAGCCGCCTG CAAGGNGCAT GTTTGACCAA TCCCAGTGG AGGGGAGGGT 120  
GGTGTTCCT TTCTGGGACT TCCACAAGTT GAGAACAGAC CATGCTGCCC TGGGCAGTTC 180  
TTGAAGGCTG TGAGAGTGGG CCTGACAAAG TTTATTCCTT TTTTTTTTC CATTNCCTTT 240  
TATNATNATA ATTGTTTGAA ATNGNCAANT AAAAATNATG TATATTTATG ANGNCANCA 300  
NGAAA 305

SEQ ID NO:2882

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03423

SEQUENCE DESCRIPTION:

GATCAGGAAA GTCATACTGT TCACTTTCAA GNTGGCTGTC CCCCCGCGG AGCCCCCCA 60  
CCCCCATATG TACAGATGAT ANTAGGGTGT GGAATGTCGT CAGTGGCAA CATTTCACAG 120  
ATTTTATTT TGTTCCTGTC TNNANCNTTT TTGNCACTGT GCTAATAGTT ATATTCAGTA 180  
CATGAAAAGN TACTACTGTG TTGAAAGCTT TTAGGAAAT TTTGNCACTA TTTTGTACA 240  
AAACATTTT TTGAAAAAAT ACTGGTTANT TTATNCTATT TTAATTNGCC AATGTCAATA 300  
AAN 303

SEQ ID NO:2883

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03424

SEQUENCE DESCRIPTION:

GATCACCAGA CACAATCCTG CAGAAGGACA CACGACTCTA TTTCCTACAG TGCGAAACTT 60  
GTCATTCTAG ATGTNCTGTT GCCAGTATCA AAACCGGCTT CCAGGCTGTC ACGGGCAAGC 120  
GAGCACAGCT CCGTGCCAAA GCTAACTAAT TTGCTAATCA CTGATTTTNC AAAGCTTGTT 180  
GTGGAGATGT GGCTGGACAG GTTTGCCATC AGAGTGGATA TACCGTTGTA TAAAAACAA 240  
GATAAAAAAG CTGCCAAGAT TTTTGGCGNG TGGTTGGTCT GAAGTCCTTG CAAGACGCTG 300  
NTGCTCAAGC TGTTGACATA CTCATTGGCC TACTTTTAAC ACCTGTCCAG AGGAAACGTG 360  
NTATGGGGGT AAGTN 375

SEQ ID NO:2884

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03426

SEQUENCE DESCRIPTION:

GATCAGATAG GAGCACAAGC AGGGGACGGA AAGAGAGAGN CACTCANGCG GCAGCATTCC 60

CTNCCAGCCA CTGAGCTGNC GTGCCAGCAC CATTCTGGT CACGCAAAAC AGAACCCATT 120  
 TAGCAGCAGG GAGACGAGAA CACCACACAA GACATTTTTC TACAGTATTT CAGGTGCCTA 180  
 CCACACAGGA AACCTTGAAG AAAATCAGTT NCTAGGNNNN GCTGTTACCT CTTGTTTACA 240  
 GTTTATATAT ATATGATAGA TATGNGNTAT ATATATAAAA GGTACTGTTA ACTACTGTAA 300  
 A 301

SEQ ID NO:2885

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03427

SEQUENCE DESCRIPTION:

GATCGGGGGA GGGTAAATAA TGCAAAAATT GCACAGTGGA AGAAGGGGTC TCACAAAAAG 60  
 CAATCCATCC TGTAATATAG GTANNNGNGT TGGGGGAAGC AGCTTCCATT CTGGATGTTT 120  
 GGAACCCCTT AGCTTTGTTT TGAATGGCC CACCATTCTC ACTGGAAAAC AGTGGTCTGC 180  
 TGTGAAAGGC CAGCTCTCGG CAGCCCCTGT GGTTCAGCG CTGCCGCTCT GTGTCATTCA 240  
 GGTGTGCAC ATTGTTTTTC TTCTGACTTC CAGAAATAAA AGTGTTTCCA TGGGAAA 297

SEQ ID NO:2886

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03428

SEQUENCE DESCRIPTION:

GATCTGGGTG CCTTGGGAGA NCCAGTCCTT CCTTTNACC CACCCCAGGA AGATGGAGTN 60  
 CTCTTTNCTA GGCCCATGTC CTGCCAGCAA CCGGGATGCG TGGGCAACTG GACTCTGCAC 120  
 GGGGGTCTAC AGGTTGAGGG AGGTTGGTCA CAATNAGAAC CTCGGGGTTT GAGGTGGCCA 180  
 TGGGCAGACA GCCNNAAGGG AGGGAGGGTG TGGGTGTNCG TGTGTGCATG TCCTGGTNTG 240  
 TAAGGGGGAA AGGGTCTTTC CTGGTTTTAT TAAATAAAG TAGTTTATGT AACAAA 296

SEQ ID NO:2887

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03429

SEQUENCE DESCRIPTION:

GATCTGTGCN GTGGTCTCTNA GGCAGTTGTN TCCACACAAG TACTACTTCC TCGTGGGCTA 60  
 CAGTNAACT TTGCTGTCCT ACTTTAACAA ATGTCCTGTG CGACTCCACC TCCAAACTGT 120  
 GCCCTCAAAG GTTGTGTATA AGTACCTCTA GAACAATCCC CTTTTTNCCA TCAAGCTGTA 180  
 GCCTGCAGAG AATGGAAACG TGGGAAAGGA ATGGTATGTG GGGGAAATGC ATCCCTCAG 240  
 AGGNTGAGG CATAGTCTCT CATCTGCTAT TGANTAAAGA CTTCTATCT TGTAAG 296

SEQ ID NO:2888

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS03430

SEQUENCE DESCRIPTION:

5 GATCTACTCT GTATGGGTAC CAAAATCACC TTCTCTCTTC AAGTCAAAGT TGAATTTAGA 60  
 ACTTTGAATA CAGGTCAAAA AATGTAGAAA ATATCATTTT ATATCCCTA ATCTATATAG 120  
 CTGAAAAAGG GTTGTATTTT CTTAGCTGAA TATGAATACC TCTTAAACAT AAATTAGTTC 180  
 CTCTCCAGTG AAGTATCTTA TTTTACCAAT CCATTTTCAGG AAAGAGGTTT TGCTGCCGTA 240  
 10 AAGGCAGAAA TTTTATTTT ATCCCTTTTA TTTGAATGAG AGATTGAAA ATCGAATTAT 300  
 GTAAATATTT CAATGCATCT GCTATTATTT TGTGGAGTTT ATTAAACTAC TTAAAA 356

SEQ ID NO:2889

SEQUENCE LENGTH:293

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03431

SEQUENCE DESCRIPTION:

20 GATCCCAAAC CAAATCTTAG AATCANTTCA TTTAAAATAC TGAGCGGTAT TGANTACTTC 60  
 GAAGCAGAAC AGGCAATGTG CAGCCCTCAT TTATGAGAAA ACCCTCAGGA AACTCCCAGG 120  
 GTGATGCTTG GNGAAGCTGT GAGTTGAGCT GAAGCTGGAG AACTTCCTCC AGAGCAAAGG 180  
 GCTTAAGAAA GAAAGANGAA CTCTAAGCTG GGTCTGCTAA CATCACTCCA GTTTAGATGG 240  
 NTCCTGTTTT TCCTTAACAN GTTGAGGCGT GGGTAGAGCA GGANTTGGTT TTN 293

25 SEQ ID NO:2890

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS03432

SEQUENCE DESCRIPTION:

35 GATCTGAAAT AACATTAATT TGATTGTAAC CCTATTGGGG TTAGTCCCA CCCTTTGTTC 60  
 CATCTTGAGC AGAGATGNCC TGCATTTCTT AACGTTTGGT CTCTATACAT TATACCATCT 120  
 GCTGAAGTTT AGCTTTGTGT GTGTGTATAT GTACCCATGT GTGCACTTTA AATATCAGTA 180  
 CAAACTGATA AACAATGTTT CTGGTTAATG TTGCAAAAAT GGAACACTGT ATTTNACATA 240  
 ATTGATTTTC TACTCCTGCC CTGTGAATTA AGGCAGAGTT TTACTGTAN 289

40 SEQ ID NO:2891

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03433

SEQUENCE DESCRIPTION:

45 GATCTTCCCA CACCAGCCTC CAAAATACT GGGATTACAG GCTTGAGCCT CCATGCCTGG 60  
 CCCAGGTAAC ATGTTTATTG AGCTGTACAT GCATATGAGA AATAAGAAAC TTTTTTTTCC 120  
 TACTATCATC TCTTAAATNT NGTNTTCTTT TTCTTTTGCT TCCTCTCTT CTNTNCTATT 180  
 TNTNATAAT ATCATGCACA ACTATAACCT ATGGGAATNA TGTAAGTACA CAGATTATTC 240  
 50 ATCTTGTTAG AGTTGTATTA AAAATAAACA AGCATTTCAA ATTAAA 286

55

SEQ ID NO:2892  
SEQUENCE LENGTH:286  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03434

## SEQUENCE DESCRIPTION:

GATCCAAGAC CAGGGTGGTT GGGGGCTGCC CCTGGCCGAG TCACTGAAGC GACTNATGTC 60  
CCTGTNTCCA GGACGANCTC CTCTCCTACT TTGGGACGCC CACGTGGCAG ACCGTGACCA 120  
TCTTTGTGGC GGNAGTGCTC ACCGCCTCAC TCACCATCTG GAAGAAGATG GGCTGAGGCC 180  
CCCAGCTGCC TTGGACTGTG TTTTTCCTCG GGTAAANNNGN GGCATTNTTC TGGGAGGGGT 240  
GGGGATTGGG GGACATGGGC ATTTTCTTA CTTTGTAA TATTGN 286

SEQ ID NO:2893  
SEQUENCE LENGTH:285  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03435

## SEQUENCE DESCRIPTION:

GATCTGCNGG GGCNTGTNCA GCTGCAGCAT TCCTGAAAGA TTTCGTAAC CATCCTAAGT 60  
GGGCACATTT AGACATAGCA GGCCTGATGA CCAACAAAGA TGAAGTCCC TATCTACGGA 120  
AAGGCATGAC TGGGAGGCCC ACAAGGNCTC TCATTGAGTT CTTACTTCGT TTCAGTCAAG 180  
ACAATGCTTA GTTCAGATAC TCAAAAATGT CTTCACTCTG TCTTAAATTG GACAGTTGAA 240  
CTTAAAAGGT TTTTGAATAA ATGGATGAAA ATCTTTTAAAC GGAAA 285

SEQ ID NO:2894  
SEQUENCE LENGTH:284  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03436

## SEQUENCE DESCRIPTION:

GATCAGCTCT TTCTATTTTT ACTCGTAAAA ATTATGGAAA TAAATAATTT TGCTAACAAC 60  
TTTGAAATTT CAACTTCTG GAAAANATGA AAATATTCAT TGTTCAATTAT GAATTTAAAT 120  
TGTAAGGTAT GAATGTNATT TGTCTGTACA TCTTGTATCT TTTCCAAAAA ATGATTCTGT 180  
ATCTTTTGGA AAAAAGCCGA GAGTTGAAGA TAGTATATTT CTGGTAGTAC TGAATATTTA 240  
CTTACAGTTT CTATCAAAAA TATATATTTG TTTCTAAAAA TAAA 284

SEQ ID NO:2895  
SEQUENCE LENGTH:283  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03437

## SEQUENCE DESCRIPTION:

GATCTCCTTG TTAGTGGTGG TAGGGAGCTA GACAAGGATG GCAACTATTT CTGTATCTTA 60  
CATACCTTN ATTTNGAGGC CCTGTCAATG TTTTATATAA TANNCATTTT TTGAAAAGGC 120

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AACTCTTAAA ACTAAAACAA ACTTAACAGT CTGTCAAGTT GGTGATATAA CCCACAGAA 180  
GACTTACTTC AAGTGACTTG AAAACTTAGT ATTTGTCTG TNCTTTGCTA ATGGGNATAN 240  
ATCCTACAGA CCAACANCC NCAGNTAANT CTTAANCTGC AAA 283

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SEQ ID NO:2896  
SEQUENCE LENGTH:279  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS03438

SEQUENCE DESCRIPTION:

15

GATCCCGGGA GACCTGGGGC TGCCGAAGAA GCTCTGCTCC AAATGGAGAG TGTAGCCTGA 60  
GGGCTGGTGT TGCCTGCCTC CCCTGTNCTT GTNCCTTGTC CCAAAATAAA TCCTTTCAGA 120  
ATGTAGCACT CACGNCCTAA TAAGGAGCGA ATCCTACATC CACCAAGGCG GGCCTCTGG 180  
CCCTCCCTTC CTTAAGCCCA GTCCTGTGTC CTCTGAAAGA GGTTCAGTC ACTCACACCN 240  
GCTTGCGCTC ACCATCAATA AAAGTAATTT CACNGAAA 279

20

SEQ ID NO:2897  
SEQUENCE LENGTH:278  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03439

25

SEQUENCE DESCRIPTION:

30

GATCCCTCC CCCAAGATAC TCTTTGTGGG GAAGAGGGGC TGGGGCATGG CAGNCTGGGT 60  
GACCGACTAC CCCAGTCCCA GGAAGGTGG GGCCCTNCCC CTAGGATGCT GCAGCAGAGT 120  
GAGCAAGGGG GCCGAATCG ACCATAAAGG GTGTAGGGGC CACNNNCTC CCCCTGTNCT 180  
GTTGGGGAGG GGTAGCCATG ATTTGTCCCA GCCTGGGGCT CCCTCTCTGG TTCCTATTT 240  
GCAGTTACTT GAATAAAAAA AATATCCTTT TCTGGAAA 278

35

SEQ ID NO:2898  
SEQUENCE LENGTH:276  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03440

40

SEQUENCE DESCRIPTION:

GATCTGCTTA CCAAGCATAT TAGGAAATAC CTCTTAGGAA GCATTAGCGG TCTCAGGCCA 60  
ATTACTGTGG AGCAGCTTTC ATTCCTACCC ACTTGCAAAC CTGGCGCTG TTGTCTGAGA 120  
TTGCTGCAGC CATTCTTGTT ACCATGGTAC TTCTCAAACCT TTGTGAAAAC CTGCACTTTT 180  
CCTTGCATGA CAGGTTCTTG TCTTGTCTGT CATGGGAGCC ATTCTGCCAA TTTAAATGCG 240  
ACTGTGGTAT AAACAGTAAA ATGATTTAAA AGTAAA 276

45

SEQ ID NO:2899  
SEQUENCE LENGTH:274  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03441

50

55

## SEQUENCE DESCRIPTION:

GATCAGTGTT ATATTTTACT GGAGAAGCTA TTGAAGATGA TGATGATGAT TATAATGAAG 60  
AAGGTGAAGA AGCGGATGAG GTAATGTTTA CCAAATAAGC AAATAATTCT NTGTGGTTAA 120  
CACATTGAGA AGCAAATTGA ATNACTTATG TATTCCTTTG CTATAATCAT TCTGTGATTT 180  
GGGATAAAAA CATTTTGGAA AACATGATTT TAGAATTCTA CAGCCAAACA ATGTATGTAT 240  
AAGGTTTCAA TAAATAANTT GCAAAACTCA GAAA 274

SEQ ID NO:2900

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03442

## SEQUENCE DESCRIPTION:

GATCCCCACC TGCCATCCTA TAGTGTGTC TTCCTGTGTG TTCCGGGGCT TCTGGGCAGC 60  
TGGGCCTGCC CGGGGAAGTC CTTGCAGGTG GGAGGCCATA CAGAGACCCA CTGTGTGCCA 120  
CTGAGCGTCC CACTGCTGCT GGGCAACTGG AGGACTGCAG GGGGCGCCAG GTGACTCTCT 180  
CCTTTTATAT CACAGCAGCT CCTGTGCTGA CCTTCAAGTT ACGTTTGGGA ACTGTAATAC 240  
TAAAGGAAGA AATAAACTAC TAATTTGTAT AAA 273

SEQ ID NO:2901

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03443

## SEQUENCE DESCRIPTION:

GATCTGGTTA AGTTGTGTAG TAAAGCATTG GGAGGGTCAT TCTTGTCACA AAAGTGCCAC 60  
TAAAACAGCC TNCGGAGAAT NNNTGACTTG CTTTCTAAA TCTNAGGTTT ATCTGGGCTC 120  
TATCATATAG ACAGGCTTCT NATAGTTTGC AACTGTAAGC AGAAACCTAC ATATAGTTAA 180  
AATCCTGGTC TTTCTTGGTA AACAGNTTTT AAATGTCTGA TATAAAACAT GCCACAGGCG 240  
AATTCGGGGA TTTNAGTTTC TCTGAATAGC ATATATNTGA TGCATCGGAT AGGTCATTAT 300  
GATTTTNNNC CATTTGCGCT TCATAATGNA AACCAGTTCA TTTTACCTAT CAGGTTATN 359

SEQ ID NO:2902

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03444

## SEQUENCE DESCRIPTION:

GATCAGAGCA CAGTTGAAAT TCATGGAAC GGCATTATTT AAGCAACCAG AATTCCACAC 60  
TGTAGGAAGG TTTTGAAAAT TGTTTCGTGA TAGATTTTAT CTTATCTTTT GGTGTTGTCT 120  
TGGTTTTTCT CATAGACTTT ATAAGTTTGA ACTGGACTTA TTTGATTATA ACCACAAATT 180  
GTGTGTGTGT GTGTGTGTGT ATATATAGAA GTCATTATGG CAGATGCACA AATTGTGCAG 240  
TGATGTAAAT ATACATACTT CACAGAAA 268

SEQ ID NO:2903



SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03445

SEQUENCE DESCRIPTION:

GATCGGTAGT GTTGTGTGTA GGCCATTCTT CTGGAGAGCC ACAAGCAGGA AGAGCAGCGC 60  
 TGTGTTGCAG AATGGAGTTC CATGGATTTC TACCAGACCA CTGAAGGAGT TCCTNGAAGC 120  
 CCTGCGGTAG CTAGCACTGA AGACTATTTT NCTATTGGTA TAACCNGCCC ACCTGAAGGG 180  
 GAAAGGGGAA ATCAANTTAA TTTCTCGTT AGACATANGG AAATTTAAGG AAAAACAGNT 240  
 TTAGGANCAG TTACTCAGCG TAGN 264

SEQ ID NO:2904

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03446

SEQUENCE DESCRIPTION:

GATCCATAGT GAAATTGCCA GAGTTTTGCC TGCTGCTTTC CTCGTGGCCT CTTCTTGGGT 60  
 AGTGAAATNA AGTGACATTT GGATTTTAAT TTGGGTGGGA GGGCTGGGAC AGTTTTNTT 120  
 CTAGAAATGT CTGTTGAGAT TTCCCCCTTT AGTTTCCAAC CTTCTCCCA ACCCTTGGAG 180  
 CTAAATGCGT TGTAATATAT TGCCAAATG AAAAGTGTTT TGTAATACTG CAATAAAGGC 240  
 TGCTTGTTTT TGTGGAAA 258

SEQ ID NO:2905

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03447

SEQUENCE DESCRIPTION:

GATCGGACAT GAAAGNACCC TGNGAGTCGA TTGTCCTANC TCCAGCGGCC CTGTCATCCA 60  
 GCTCACTCAT CAATGGGGCC AGTCAGGCC AGGCACTGGG CTCCGGAGGA CTCACCACTG 120  
 CCCCCTGCTG CCATGTGGAC TGGTGCAAGT TGAGGACTTC TTGCTGGTCT AGTCACGCAT 180  
 GCAGTGTGG GGGATGCCTT GGTTTTTACT GCTCTGAGAA TTGGTTGAGA TACTTTTACT 240  
 AATNAACTG TGTAGGTTGG GAAA 264

SEQ ID NO:2906

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03448

SEQUENCE DESCRIPTION:

GATCTGCTTT CAACACTTTT AGCTCTTCTA GAATTCAGA AAAATGGTAT CGGATGTACA 60  
 GCATGGACCC TTCTNTGGTG GGCTTCTTTA CTGTAATGCT TTTAANATTC ATCTGTGCTG 120  
 TTNAGTGTCT CTGCAGTCCA TTCCTTCTGT TGAGTGTATC AGTAGTCCAT TCCTTTTCAT 180  
 GGCTGAGTAG TATTCATTG TATAATTATA CCACTATTG TNCATTTACT AGATAATANN 240

CAGTTGGCTT GTTTAAA

257

SEQ ID NO:2907

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03449

SEQUENCE DESCRIPTION:

5  
 10  
 15  
 GATCCATCCG CCTTGGCCTC CCAAAGTGCT GAGATGACAG GCATGAGCCA CTGCACCCGG 60  
 CCATATAATC AAATTTTAT TGATTTTAGA GCAAAGGACT TTTCAATGT AACTGCTTAG 120  
 AAATCGAGCA ATTTTCTATT GTATAGAGTG AAAGTCAAAC TTGTTTATTG TACAAGTCTT 180  
 TAAAGGGATA GTTAGGAGTA AGTTGTATTT GCTGAATATA TAGACCTCAT TTGTAGCCAT 240  
 TAGTGATTCT GTATTN 256

SEQ ID NO:2908

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03450

SEQUENCE DESCRIPTION:

20  
 25  
 30  
 GATCTAATTA AAAAAAAGGC AATATTTTTA TATTAAAGTA CTATACTAGG AGAGAATGTT 60  
 TCANAATCC CTGATGAATT TCTAAGTGAG CAACTTGATA TAAAATTGTA ATCTTCATTT 120  
 TTGTCAGTGT ATCCAGTTAC AGAATGCTAC ACACTTACCT TTTTATTGGC TGAGAAATCT 180  
 GGTATTTTCA TCTTAATCTC AAGATTGTTT TCAAGTGTTT TATAATTAAA TCATAATAGC 240  
 ATATTTTAAA ATCAAA 256

SEQ ID NO:2909

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03451

SEQUENCE DESCRIPTION:

35  
 40  
 GATCAAACCA GCTCTTNTNA CCCAAACCAN TGCCGCTGCA TTAAAGGGAG GCCCAGCTAC 60  
 TCCTTCCCAG CTGAGATGTG GGTACAGGTC AGATTNTCA GGGAGATGGC ACTAACACGA 120  
 CACAAGCTCA CTCCCAGAAC CGCAGCTGAT GTTTATAATA ATCGTATGTA CTGTGCAATT 180  
 TAGGAGGGGA AAAAAAGGCT GTACAAGCTT TAACTCTAAA NNAATNTCT ATTTTTTNCC 240  
 TCTTGCAAAAN TAAA 255

SEQ ID NO:2910

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03452

SEQUENCE DESCRIPTION:

45  
 50  
 GATCTGCCCT GTACAGCCAT GTAGGCTGTG CGCTGCATAA CTCCAGGGAC ATGAGTCACA 60

CAGACACAAT GTGAGTGTGC TCCCCGTCA TGCAACATCT GGACACAAC AACAGAGCAT 120  
GGTGAATACA TGCTGAATTG CATTAGTAT GGCTGTGAAC TAGGCCTGGG GACAAGANTG 180  
ANTTTTACAT GGAAAGAATT TCCTGTAGCA GGAACAGAGG GGATAACAAC AGCAGTAAAT 240  
AATAATAAGN CAAA 254

SEQ ID NO:2911

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03453

SEQUENCE DESCRIPTION:

GATCCCCAC TAGTNCCCTC CCTCTNCCCC TGTAATCCTG GTCTAATAAC CCCCCACACA 60  
TACACCTCTG GTGACCTATT TGCACAGACC GTNGTCTTCC CTCCAGTNTT CTNAGGGATA 120  
GGGGACATTC CATCCCAAGC TTCTNCCTTA CCCACACCTA TCCTTTTNAG GGGCTTTGGG 180  
GTGGGGCTGG GGCAAGCAGA GGGACTGGGT CTTCACTTCT NGGGCTAATA AAATTGTTTC 240  
TTTGTGGACT AAA 253

SEQ ID NO:2912

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03454

SEQUENCE DESCRIPTION:

GATCAAACCG GTTCTNTCCT TTCTTGTGTT GCCATGTTAC TATGCCTCAA GCCCAGTTTN 60  
CTTTTNCCGC AGCGATGGGG CCAGTCTCAT TCCTCCCCAG GAGTGAACT NGCTTCANCT 120  
GAAAAGGTTG GGTGCATTGT CAGTAAAAAG GGCTTATTTG TTTCATTNA CTTTCCTGCA 180  
AAATTTTCTT CAAAGCAACA AGTCCTAGGN GCACACAAAG CAACCCAAAG GCTTTTCCT 240  
GGAAAAGCTC TTN 253

SEQ ID NO:2913

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03455

SEQUENCE DESCRIPTION:

GATCCGGGGC ATGCAGAAGC TGAGCACACC CCAGAAGAAG TNAGGGTCCC CGACCCAGGA 60  
GAACGGTGGC TCCCACAGGA CAATCGCTGC CCCCCAACCT CGTAGCAACA GCAATACCGG 120  
GGGACCCTGG CGGCCAGGCC TGGTGCCATG AGCAGGGCTC CTCGTGCCCC TGGCCCAGGG 180  
GTCTCTTCCC CTGCCCCNTC AGTTTTNCAC TTTTGGGGTT TTTTATTGNT ATTAACTGA 240  
TGGGNCTTTN TAAA 254

SEQ ID NO:2914

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03456

SEQUENCE DESCRIPTION:

5 GATCCTTGTT TTGTGTGTCAT GGAAACTTCG GGGCTGGTGG GACTTAGGCC AAAAGCTCAG 60  
AGGCACAGCC AAAATTTAGA AGCTTGCTAC TCCTACGACT CGGCCTATAA GGAAGAGAGA 120  
AGCTGTCTGT ACTTTGGGGA CTACATTGCT GAAGGAAAAA AATCACTCCC TGGCTAATTA 180  
AGATTGCTTC CAAATTGGGG GAATGTGTGT CATTTCTTTT ACCAAGGCCA GTCATCCCTG 240  
CTTCCACCN 249

10 SEQ ID NO:2915

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS03457

SEQUENCE DESCRIPTION:

20 GATCCAGGCC GGGCCTATAC AGAGGTGCTG GCTGCTTGTT TACATTCTCC TCTGGGGCTC 60  
TACCTCTCCA CACTTCCCCA GAAGGGAAAA GGGCACCCTG GATTACTNNN TTGGAAATNA 120  
CTCCTTGGTG GGCAGCATCC TGAGGGTTCC CCAGAACCAG GCCTCTGCTC TGGCCCTCTT 180  
GCATCTGGAA CGCCAGGTGG GTTTTNTTGG CATAGGAGCC CACTTGCAAT TTCATAGTTT 240  
TATTTGATN 249

25 SEQ ID NO:2916

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03458

SEQUENCE DESCRIPTION:

30 GATCACAGCC TCCAGGGCCC CCCAAATCCC AGGGAAGGAC TTGGAGAGAA TCATGCTGTT 60  
GCATTTAGAA CTNCTNCTT TGCACAGGAA AGAGTCACAC AATTAATCAA CATGTATATN 120  
TCCNCTATAC ATAGAGCTCT ATTNCNTNC GGTTTATAA AAGCCTTGGG TTCCAACCAG 180  
GCAGTAGATG TNCTTCTGAN CCGCAAGGNG CAAACACTGA AATAAAATAG TTTATTTTNC 240  
ACACTCAA 249

40 SEQ ID NO:2917

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03459

SEQUENCE DESCRIPTION:

45 GATCTCCTTT TGTGAAAACC AGTTTGATGT GCTAAAAGTA AAAAGTCTAN TTTCCAGTGT 60  
GGTCTTGTTT AGAAGCAGCC AGATTTCCAA TGTGTTTTT CCCCTCCACT CAGAAACCCC 120  
TGCCCTTTCC CTTCAGAAAA CGATGGCAGG CATTCCTCTG AGTTTACAAG CAGAGACTCA 180  
CTCCAACCCA AACTAGCTGG GAGTTCAGAA CCCATGGTTG GAATAAAGAA ATTGTGCGTC 240  
TTGGTCAAA 249

50 SEQ ID NO:2918

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03460

SEQUENCE DESCRIPTION:

GATCTATCCC TCGGNGCTCC ACACCTGAAC TTGCCTAACT AACTGGCAGG GGAGACAGGA 60  
 GCCTAGCGGA NCCAGCCTGG GAGCCCAGAG GGTGGCAAGA ACAGTGGGCG TTGGGAGCCT 120  
 AGCTCCTGCC ACATGGAGNC CCTCTGCCG GTCGGGCAGC CAGCAGAGGG GGAGTAGCCA 180  
 AGCTNCTTAA TCCTNAGCCT NCCCCTGTGT ATTCACCACC AATAAATCAG ACCATGAAAA 240  
 CCAAA 245

SEQ ID NO:2919

SEQUENCE LENGTH:384

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03461

SEQUENCE DESCRIPTION:

GATCAGGAAA CCAGAAATAC CACATTTATG GACCATGAAN GGTGGTTCT TGACTCTGAA 60  
 GGGACTTTTG AGTTAATCAG CGTAAGGGGA TTTCTAAAGC AGGCAATCCC TGTAGCCGCA 120  
 GAGAATAAAC GCCTTCCCAA AATGGNAACT NCCCACAGCC ACATTTGAGA CCTGCTGAGA 180  
 CTGCTGAGTG AGGAATGGCA GTGAGGTTT TCAATNAGT CTCAGTTCTC TTAATTTTCA 240  
 GGAAGAAAGG GTAATTGCAG CCCCTCAGCC CCCAGGATTG ACCTCTNGGG AGNCATGGTA 300  
 GCGTTGTGTG CCAGGCCGTN GGTTCAGGTG TTNGCAGAAG CTTTCAGATT CGTCCGAAGG 360  
 GAAATAAAGT GTGTTGGCGT TAAA 384

SEQ ID NO:2920

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03462

SEQUENCE DESCRIPTION:

GATCCCAGCA GCCCTCCCTT CACCGTGACC CCTGACCTTT GTTAGGAAGG TGCAGTTTTT 60  
 NTTCTCAATC TAAATNCCTT TNAGGTGGGC CGCTTCCTTG GCTACCTGGT TCCAGGGGGC 120  
 TGTTTTGTAA TNAGATGCTG CTGGCAGGCC ACTCAGAGGC TCCCAGCTGG GTTGGTGGGA 180  
 CAGCCAGGCC AGATGACCTG ATTCCAGCAA AAATAAACT CAGATTGGG CAAAATGAAA 240

SEQ ID NO:2921

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03463

SEQUENCE DESCRIPTION:

GATCCCTAGC AGCTCATCCT GCCCTTTGAA TACCCTCACT TTCCAGGCCT GGCTCAGAAT 60  
 CTAACCTATT TATTGACTGT CCTGAGGGCC TTGAAAACAG GCCGAACCTG GAGGGCCTGG 120  
 ATTTNTTTTT GGGCTGGAAT GCTGCCCTGA GGGTGGGGCT GGCTCTTACT CAGGAACTG 180

CTGTGCCCCA CCCATGGACA GGCCAGCTG GGGCCACAT GCTGACACAG ACTCACTN 238

SEQ ID NO:2922

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03464

SEQUENCE DESCRIPTION:

GATCACCGGT TTCCGACTGA GTCTGGGGAT TTTGGCCTTG TTGACCCTCC TAGGTGCCCT 60  
GGGAATTGCA AACAGCTTTC TGGATGAATA TCTGGACCTC AATATTGCCA AGAAACTGAG 120  
GCGGCAATTC TAACTTTTTC TCTTCCCTTT AATGCTTGCA GAAGCTGTTT CCACCATGAA 180  
GGTAATATGG TATCATTTGT TAAATAAAAA TAAAGTCTTT ATTCTGTTTT TCTTGAAA 238

SEQ ID NO:2923

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03465

SEQUENCE DESCRIPTION:

GATCTACTGT GTGGTGTCTG GGCAGATGAA AGTACACTGC TTAGNGTGAT GCTTAGCATG 60  
GGGCAGATGC TTGGTAAATT GTAATCACTT TTGTTGTCAG TTAAATGGAT ATTTCACTGT 120  
TGCCTCTNAA ACGCTTACGG TAATATATAC TAATTATACA TGTATTATC AGTTTATATT 180  
TATTGAACAT TTCGGGGAAG TAATTATAAA ATAATCTTGT CTACTGTCTT ACCCCAAA 238

SEQ ID NO:2924

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03466

SEQUENCE DESCRIPTION:

GATCTATGGT GCAGACTGCC TTCGTCGGGT GCAGACTGAG CGACCGNAGC CCCAGACACT 60  
ACAGCTGGAT TNCTTGATGA AAATCTTGCC AAATTACCAC CACCTAAAGA AGACTATGNA 120  
AGGAAGCTCA ACTCCAGTAA AGAACTAAGA ACAGTGTATA ACATGAAGAT AACATTTTGT 180  
CTTTGACCAC TGTCTTTTGA ATGGGCCAC AGTGTATTATG TACTCTTAAC AACTCACAGA 240  
ATAATACATG TTTCACTTTAT TTTGTAAAAT TGGGTTGAGA GGAACTAAT GGAGTTTCAT 300  
TGTAAGTGTC CTTTNTAATT TATATAAATG TATTATTNTC CTATAAA 347

SEQ ID NO:2925

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03467

SEQUENCE DESCRIPTION:

GATCCTGTGA TATGGTTTTN GGCCAGCAA ATCTAGGAGA AGATGCAATT AAAAACTTCA 60  
GAGCAAAACA TCACTGTAAT TTTGCTGTA GAAAGCTTAA ACTTCAGGT AAAAAATTTT 120

TTAATCAGTA TAGTATATAA TTNGTTACGA AACTNGGTTA CTACAATACC TCATAAGGCC 180  
AGAGGTACAA NTGTTTAATG TAATGGTCTC TAATTGTGCC AGCTTCAGCA GCTCTN 236

5

SEQ ID NO:2926  
SEQUENCE LENGTH:271  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03468

10

SEQUENCE DESCRIPTION:  
GATCCCGCAT GCCTGAATTC ACTAAAGCCA AGGGTCTNTA AGCCACGCTN NNTCTTCTGA 60  
GACTTCCATT CCTTTCTGAT TGGCACACGT GCAGCTCATG ACAATCTGTA GGATAACAAT 120  
CAGTGTGGAT TTCCACTCTT TTCAGTCCTT CATGTTAAAG ATTTAGACAC CACATACAAC 180  
TGGTAAAGGA CGTTTTCTTG AGAGTTTAA CTATATGTAA ACATTGTATA ATGATATGGA 240  
ATAAAATGCA CATTGTAGGA CATTTTCTAA A 271

15

SEQ ID NO:2927  
SEQUENCE LENGTH:235  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03469

20

SEQUENCE DESCRIPTION:  
GATCTAAAAT GTTATTTCCT TCTGTAGTGT ATTAATCTCT GTGTGTTTTT TTTGGTTTTG 60  
GAGGAGGGGT ATGAAGTATC TTTGACATGG TGCCTTAGGA ATGACTTGGG TTTAACAAGC 120  
TGTCTACTGG ACAATCTTAT GTTTCCAAGA GAACTAAAGC TGGAGAGACC TGACCCTTCT 180  
CTCACTTCTA AATTAATGGT AAAATAAAAT GCCTCAGCTA TGTAGCAAAG GGAAA 235

30

SEQ ID NO:2928  
SEQUENCE LENGTH:234  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03470

35

SEQUENCE DESCRIPTION:  
GATCCATCTN CCCTCATAAA AGTGTTTCAGG TACAGCAGCT GAGGCTGCCC TGAGGAATCA 60  
NGGGGCCATT ACCAAGGGGC AGGTAAAGGG TATNTAAGAG GTGGCCTTCA TGGTAGAGCT 120  
TGACCCAAGA NCTACTCCAC ATTCGGNTNG CCCAGACTGA CTCCATCCCC TGANTTTCCC 180  
TTNGACTTCA CCCTGTTTGT AAATAAAACA NTAAATGGA AGGTGCTNTG GAAA 234

40

SEQ ID NO:2929  
SEQUENCE LENGTH:233  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03471

45

SEQUENCE DESCRIPTION:  
GATCTCAAAT CCTGGAACCC CGATTTCAAT CTACGTTCTA GTCAGTGGCC TCAAAGGACC 60  
CCACAGCACC TGGGCCAGAC CAACAGCTCG AGGGAGAACC TGAAGGCCCA GGGGGTCCAG 120

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GGCGGACCTG GGGCCCCGAC CACCAAGGAC AGCTCAGCAG TGCCCTTNA CTGCATGTCC 180  
 CCAAACCTNAG CATGACTCCT GTCCTCTTCA ATAAAGACGT TTCTATGGCC AAA 233

5 SEQ ID NO:2930  
 SEQUENCE LENGTH:231  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03472

10 SEQUENCE DESCRIPTION:  
 GATCAGCAGA AAGCACAAAC ACAACTGCTT CTGTATTCAAG GAGGTTGTGA GTGGGCTGCG 60  
 GCANCCGTTG GTGCCCTGCA TAGTGGGGAT GGCTCGCAAC GTCTCTTCAT TCTGGAAAAA 120  
 GAAGTTATG TGAAGATACT TACCCCTGAA GGAGAAATTT TCAAGGAGCC TTATTGGAC 180  
 15 ATTCACAAAC TTGTTCAAAG TGAATAAAG GTTGGCTTTT TAAATTTTAA A 231

SEQ ID NO:2931  
 SEQUENCE LENGTH:231  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03473

20 SEQUENCE DESCRIPTION:  
 GATCAGCAAA AATAAAGGGG CTACAGAAAC ACTCATTTTT ATGCTGTTCC CTCTTGGGCT 60  
 25 TCATGCAAAG ACAATTCTNT GTAAATNTAC AGTTGACTCT GATTTGGAAG TATGAAAATC 120  
 AGTCCATCCT TGTATATAAA AATTTTTTTA CAATTGTAAT TATATTGATG TTCATATTGT 180  
 GTAAATAAAC TCATTTAATA AAATAGTACT TTGATTTACG ACATCAATAA A 231

30 SEQ ID NO:2932  
 SEQUENCE LENGTH:230  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03474

35 SEQUENCE DESCRIPTION:  
 GATCCCACCC CCAGCCATTT GCATTGCTGG CCCAGCGCCT GGCCTGGGGG GCGGGGAGAG 60  
 GCAGCAGAAG GGGCTGGGCA GGGGCGGTGG AGGACTCAGG AACTNCCCGG GGAGAGTGGG 120  
 TATGGCGGCT GAGCCAGGGN CCCTCCTGTN TTNACTTCC CGGGATGGGT CCTTGCTTNN 180  
 40 AAGCTGTNTC CGACCCACCC ATNTAATAAA ACCCAAAGGA ACAGCCCAAA 230

SEQ ID NO:2933  
 SEQUENCE LENGTH:328  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03476

45 SEQUENCE DESCRIPTION:  
 GATCAGCCGG AAACCCCTGG CAGCCAAGAA CAGATAAGGA AGGGATTGGC ATCGGCTGGC 60  
 CTTCCAGCAC CTTCTCTCTC CAACACTTCA TTCTCTCTTG CCCTGTNTCT CAAATAAAACC 120  
 50 CAATGCTGCG TGTGAGGCCT TTTTATTTT TCTTTTCACT CTCTTTCTAA TGCTTCCAC 180



CTTACCTTTT AGATTCTTTT GCTAGGTGGG AGATTGTTAT AAGGTCTTTA AACCATTTC 240  
 ATTTGTTTCT TTAACATTAC CAAAAGCAGG GNACAAAGCT CTTATTCAAC TGCGNATTCC 300  
 ATAGNGGGCT CTGGNTTNTT CTGAATN 328

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SEQ ID NO:2934  
 SEQUENCE LENGTH:220  
 SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear  
 CLONE:HUMGS03477

SEQUENCE DESCRIPTION:

15

GATCTTGCCC GGTGTCCTGG TCCTCTTGCT TCCGTCGCGG CCGCATGTGC GTGTGTCCAA 60  
 GCAGGTCCTG GCGCCTCAA CTGCTGCCCC TGGTTGAATG TTCTCTTGAT AGTGCTGGAC 120  
 CCTTTGTCTA TTTNAAAGCG AATTTTGTGT GATTTCCTGC CCTTTGCGTT ATATTGTATA 180  
 ATACCAACGT AAGGAAATAA ACCTTTGGAA TTGTTGAAA 220

SEQ ID NO:2935

20

SEQUENCE LENGTH:219  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS03478

SEQUENCE DESCRIPTION:

25

GATCCGAGGG CGATGGGACA GTGCACCGCA GATAGAAGAG GAGGACGTGC AGCATGGTGG 60  
 GAAACGGGGA CACCACCTCC CAGGACGACT GTTTCAGCAA AGAGCGCANT GCTCCAGGTG 120  
 ACCCAGCAAG GCTGTTGTNT GTATGGAAGG ACACGCTCGC GGCAAGGGCA GGGCCTGGGN 180  
 AGGGTGGCCT GTCCAGTCCT NNAGACAAGG GGAGGCCTN 219

30

SEQ ID NO:2936  
 SEQUENCE LENGTH:218  
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35

CLONE:HUMGS03479

SEQUENCE DESCRIPTION:

40

GATCACCTGA GGTCAGGAGT TCGAGACCAG TCTGGCCAAC ATGGTGAGAC CCCATCTCTA 60  
 CTAAGACTAC AAAATTAACC AGGTGTGGTG ATGCATGCCT TTNACTCGGG AGGCTGAAGC 120  
 AGAAGAATCG CTAAACTCG GGAGGCGGAG GTTGCAGTGA GTCCAGATTG TGCCATTGCA 180  
 TTCCAGCCTG GACAAGAGGA GCAACACTCT GTCTCAA 218

SEQ ID NO:2937

45

SEQUENCE LENGTH:218  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS03480

SEQUENCE DESCRIPTION:

50

GATCATGCCT GCGTGACAAA GCCTCCAGAA AAATCCTTGA AAGACAGGAC ATGGAGAGCT 60  
 GCTGGGTTGG CGAACACATC CATGTGCCGG GAGGATGGTG CACCCCAACT CCACAAGGAC 120

55

CCTTCCAGAC CTCACCCTGT GATNTCTTC ATCNNNTGT TCATTTGTAT CCTTTAAAT 180  
ATCCCCGTGA ATAAATCAGC AATAGTAAGT AAATAAA 218

5 SEQ ID NO:2938  
SEQUENCE LENGTH:218  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS03481  
SEQUENCE DESCRIPTION:  
GATCTAAACA GTGAATAGTA CATGCAAAGG CATAGTCTAG AGGATAAAAG TGAAAATAAT 60  
TAGTAGCAAA ATNAATGCCT TGTGGATGAG GTTTAGGGGC CAATAACTAT CTTGAGGTAA 120  
GGCCAGGTTG TGGCTGCCTT TGTGTTGTAC TAAGGGGTTT GGACCTTCCT AGGAGATTAG 180  
15 AGCTTNATTA AAGTCACAAC ATCCATAAGN GAAATAAA 218

20 SEQ ID NO:2939  
SEQUENCE LENGTH:218  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS03482  
SEQUENCE DESCRIPTION:  
GATCCCTTTG CTGTGAGGGT AGAAAACCTC ACCAACTGCA CCAGTGAGGA AGAAGACTGC 60  
25 GTGGATTCAT GGGGAGCCTC ACAGCAGCCA CGCAGCAGGC TCTGGGTGGG GCTGCCGTTA 120  
AGGACGTTCT TTCCTTACTG GTGCTGATAA CAACAGGGAA CCGTGCAGTG TGCATTTTAA 180  
GACCTGGCCT GGAATAAATA CGTTTTGTCT TTCCCAA 218

30 SEQ ID NO:2940  
SEQUENCE LENGTH:216  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

35 CLONE:HUMGS03483  
SEQUENCE DESCRIPTION:  
GATCTTAGAT TTGATGAAGC ACAGTATGCA GGTAGGCCTA ATGGGGGAAG ATGGTAATAT 60  
AAAAGCAAGA AGTATTTTTT TTTTGNAATG NCTGAAAGCT GTTCTGTGGA TGACCTACCG 120  
NTTCCTTTAA ACACGATTCT CTCATTCCA ACTCCAAACT TGCTCAACTA ATCCTTAAAA 180  
40 ATAAACTTGA GCTGGAATTT GAGGCTTGCC TGGAAA 216

45 SEQ ID NO:2941  
SEQUENCE LENGTH:213  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS03484  
SEQUENCE DESCRIPTION:  
GATCTCGGGG GTGTGGGGCC CTGTGCCTTC CTGAAGTGCT GGCAGCCCAG TGGCACCTCC 60  
50 TTCAGGCCCT TGGGGTATTC CCCTAGTGTG CCCAAGTNAG CCTCATATTC TGGGCGGACA 120  
GCTTGTCTGG ACTTCGGAGT TGGGGGTGGT CAGACACCAC AGGAGCTGTC ACCTCCTGCG 180

55

GATGGGCAAA TAAATTNGTG GAGGACNCCG AAA

213

SEQ ID NO:2942

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03485

SEQUENCE DESCRIPTION:

GATCCTCTCC CCTAGTATNT TCAGCACATG CTCACTGTTC TCCCCATCCT TGCCTTCCC 60  
 ATGTTTCATTA ATTCATATTG CCCC GCGCCT AGTCCCATTT TCACTTCCTT TGACGCTCCT 120  
 AGTAGTTTTG TTAAGTCTTA CCCTGTAATT TTNGCTTTTA ATTTGATAC CTCCTTATGA 180  
 CTTAACAATA AAAAGGATGT ATGGTTTNA AA 212

SEQ ID NO:2943

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03486

SEQUENCE DESCRIPTION:

GATCTTTTCA GAGTGGTGTT TCTAAAAGAG CATGTACAAA AGTGGCCTGT GGACATTTAG 60  
 GCCTAAAGTG ATGCATTTNC TCTTCCTNTT TGTGCCAATG TATCAATGTA GAGTTGCTCT 120  
 GTTTTCTNCA ACTGTATNNA TTGCTGCATT TCTCAGCATA AACTTATCCC ATTGTATTTT 180  
 TNATAAATAA ATATTTTTTT TGAACCTTCA AA 212

SEQ ID NO:2944

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03487

SEQUENCE DESCRIPTION:

GATCAAGGAT GAGGATTAGC ATCTGCAAAT TGAACCTCTAT CTAATTTNCA TTTTTATTTT 60  
 TTAGAATTGT AATTAAATTT GTGTAATAAA TGTNTCCAT TTCATTTGTA CACTTAAAC 120  
 TTGGGTGACT GAAATGCAGT TAAGTGAATT NCCTTTTNTT AAAAGCAAAT GTAGATTATN 180  
 CAATAAAGCA GCAAACCAAT ATTAANCATA AA 212

SEQ ID NO:2945

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03488

SEQUENCE DESCRIPTION:

GATCTATGTA AAAGAATACA ATTCTTTTTT ACATAATTAG TGAAATTTTA TTTTTTATTA 60  
 GGAAACACTA AATAGTGTA TATTTCTTTT GCTTTTAAAA AAATCCTGG TAGCAAATCA 120  
 AGATAAATAA TTGNTTCATT TTCTTGAGCA ATACTGAAGC AGGATGAAGT AAGAGGAATG 180  
 CATTCAATTA AACATGCTTT GCTTGNTGAA A 211

SEQ ID NO:2946

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03489

SEQUENCE DESCRIPTION:

GATCAAAGAA CTTTCTTAT AACCTGCAAT CAGCTACTCA GCCAAAAAAC AAAACAAAAC 60  
CTTGACTGCC TATGGAGGAA GACTGTGTTC GGGGGAGCTG GCATAGCTAG TGCAGAGTTC 120  
AGATTTTCTG CTGATAATCT TTTACACCTT GGGAAAACTT TAATATCCGT ACCTGAAGGN 180  
TGATTCACCT AAAAATGTGT TAACTGAAA 209

SEQ ID NO:2947

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03490

SEQUENCE DESCRIPTION:

GATCTTCTCT GTGAATCCAC CCCTGGCTAC CCCACCCCTG GCTACCCCAA CGGCATCCCA 60  
AGGCCAGGTG GGCCCTCAGC TGAGGGAAGG TACGAGCTCC CTGCTGGAGC CTGGGACCCA 120  
TGGCACAGGC CAGGCAGCCC GGAGGCTGGG TGGGGCCTCA GTGGGGGCTG CTGCCTGACC 180  
CCCAGCACAA TAAAAATGAA ACGTGAAA 208

SEQ ID NO:2948

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03491

SEQUENCE DESCRIPTION:

GATCACACTT NGGCCTTCAC TGCAGCGTGG TGTGGCCACC GTCCGTTTCC TCTCGGCCTT 60  
CCTCCGAGTC CAGGTGGACT CTGTGGATGT TTGGATGTGG CCCGAGCAGG CTCAGGCGGC 120  
CCCACTNACC NACAGCATCC GCCGCCACCC CTTGGGTGT NAGCNCTCAA TAAAAACAAC 180  
ACACTATAAA GTGTTTTTAA ATCCAAA 207

SEQ ID NO:2949

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03492

SEQUENCE DESCRIPTION:

GATCTGAAAA TTCTTGGAAA TTGTTCCATG TGATTAACAT GGAAGTGCCT CTACTTAATC 60  
ATTCTGAATN ATTAAATCGT TTCATTTTCT AAATGCNTTA TAATGTGTTT AGCCCTTTCT 120  
TGTTGCTGTA TGTTTAGATG CTTTCCAATC TTTTGTTACT ACTAATAATG CTATAAATA 180  
AATATCCTTG TACTTCTTTG AAA 203

SEQ ID NO:2950

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03493

SEQUENCE DESCRIPTION:

GATCTTNTCT GTNTGGGTGG GGAGCCGGCC GGCCGTGACC CAACGGCATC CCAAGGCCAG 60  
GTGGGCCCTC AGCTGAGGGA AGGTACGAGC TCCCTGCTGG AGCCTGGGAC CCATGGCACA 120  
GGCCAGGCAG CCCGGAGGCT GGGTGGGGCC TCANTGGGGG CTGCTGCCTG ACCCCCAGCA 180  
CAATAAAANT GAAACGTGAA A 201

SEQ ID NO:2951

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03494

SEQUENCE DESCRIPTION:

GATCGTATAT GTGGGTCCCT TCCCTAGAAG AATGGTTGCT GATATGGCTA CTGCTTCTAC 60  
ATCTNGAGTT TTTNAATTTA CTTTTTTNAC ACTGTAGCAT TGAGACTGCT TGATTCAAGT 120  
CTGGTGCTTT GCCAGATGTA TTAATTNCCA TAAATGCTTT GTGAGTTTGG TTAATGAA 180  
GATTCACTTG GGAAANCAAA 200

SEQ ID NO:2952

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03495

SEQUENCE DESCRIPTION:

GATCACAGCC GGAATGCAGC TGAAAGATTC CCTGGGGCCT GGTCCAACC GCCCACTGTG 60  
GACTCTAAGG CCTCTGCATT TGTGGGTGGT CTGNCTGTAA TATTTTGGTC ATNGGCTGGT 120  
CTGGTCGGTT TCCCATTGTG NTGGCCAGTC TCTATGTGTC TTAATCCCTT GTCCTTCATT 180  
AAAAGCAAAA CTAAAGAAA 199

SEQ ID NO:2953

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03496

SEQUENCE DESCRIPTION:

GATCTCTAGT TTTTNTGGTT TAATTTTNAG TAGCAGGTCA AAAACCTGCC CTCCTGTNAC 60  
TTATCCCTG AGACTTTTCA GGAGAGCCAG CCCACAGATG ATGAAGAAAT GATGGAAGTT 120  
CATTTGGAGA GTCAAATGGG AAAAAAACAA AAAAAAACT GCCTTTAATA CAGGCAATTC 180  
AGTGGACTAT AATAATAGTG GAGGGTTGAG ATGTAGAGTT TTAAAAAGT GAACAGTTGC 240  
TGTTCTTACA TCTNTAANGA AAGCCATAAT GTCTTTAAAT CACTCTTCTG TAAATAGATG 300  
NCCNTTTTGT CAGTGTAAG 319

SEQ ID NO:2954

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03497

SEQUENCE DESCRIPTION:

GATCCTTAAT GCAGAGCTAG AGGACTTCTG GCAGGGAAGT GGGGAAGTGT TCCAGATAGC 60  
AGGGCATGAA AACTTAGAGA GGTACAAGTG GCTGAAAATC GAGTTTTTCC TCTGTCTTTA 120  
AATTTTATAT GGGCTTTGTT ATCTTCCACT GGAAAAGTGT AATAGCATAC ATCAATGGTG 180  
TGTTAAAGCT AAA 193

SEQ ID NO:2955

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03498

SEQUENCE DESCRIPTION:

GATCTGTTTC ATTTATAAAA GGTCCAGTTT TTAGGACTAG TACATTCCTG TTATTTTCTG 60  
GGTTTTATCA TTTTGCCTAA AATAGGATAT AAAAGGGACA AAAAATAAGT AGACTGTTTT 120  
TATGTGTGAA TTATATTCT ACTAAATGTT TTTGTATGAC TGTGTTATAC TTGATAATAT 180  
ATATATATAT ATN 193

SEQ ID NO:2956

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03499

SEQUENCE DESCRIPTION:

GATCCAAGAA TGTGCCAAGA GTCCCGCCAG CCTCAGCCAG GTGGGCCTGT ATATAGGGTC 60  
CATGTGCAAT AGGGAGGGAC GTCTTCTATT TTTNCTGCC CCCTCCCCGC CCACTGTCTG 120  
GGGCAGGGGG AGAAGGTATT TTCGAGATAA AGCACAGGCA CCACAAATAA AAGTCGTGAA 180  
GTTGCCACTC AAA 193

SEQ ID NO:2957

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03500

SEQUENCE DESCRIPTION:

GATCTGGGAG CAAGCTACCA ACAGGGGAGA CTCTTTCCTG TATGGACAGC TGCTGTGGAA 60  
ATACTGCCTG CTTCTCCCAC CTNCTCANAG CCACAGGAAA GAGGAGGTGA CAGAGAGAGA 120  
GCAAGGAAAG TAATGAGGTG GATTGATACT TTCTACTTTC CATTAAAATT ATTTTCTAGC 180  
CTGCAGTCTA AA 192

SEQ ID NO:2958

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03501

SEQUENCE DESCRIPTION:

GATCAGCCTG GGCATCATGG TGGCCTGCAC CTGTAGTCCC AGCTACTCAG GAGGCTGAGG 60  
 TGGGAGGATA GTTTGACCCC AGAAAGTTGA GGCTGCAGTG AGCCATGAAT GCACCACTAC 120  
 ACGCCAGCCT GGATGACAGA GCGAAACCCCT GTCTCAAAGT AATTAATAAT AATTATATTA 180  
 ATTCAGCAAA 190

SEQ ID NO:2959

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03502

SEQUENCE DESCRIPTION:

GATCTGCTTC CCACTGTGAC TGGGCTATGG GATTCTGACT ACCTTGCTTA CAGATTCATG 60  
 GTTTGATAAA TTTGTTGTAT TCAAAAACCT GAAATGCAGG ACGCCATTAA GTGTCTGTTT 120  
 ATATTTNTGG AATATTTGTA TTAATTACAA TTAATTAATA AAAGTGGGTT TAAAAAACCT 180  
 TTCCAGGAAA 190

SEQ ID NO:2960

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03503

SEQUENCE DESCRIPTION:

GATCTTGCCC CCTTTGACCT TCCCCAAAGG ATGGTCACAC ACCAGCACTT TATACACTTC 60  
 TGGCTCACAG GAAAGTGTCT GCAGTAGGGN ACCCAGAGTC CCAGGCCCTT GGAGTTGTTT 120  
 TCGGCAGGGG CCNTNTCTCT CACTGCATTT GGTCAGGGGG GCATGAATAA AGGCTACAGG 180  
 CTCCAACNTG AAA 193

SEQ ID NO:2961

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03504

SEQUENCE DESCRIPTION:

GATCAATCTG AACTATCTT AGCCCAGTCA GGGAGCTCTG CTTCTAGAA AGGCATCTTT 60  
 CGCCAGTGGA TTCGCCTCAA GGTGAGGCC GCCATTGGAA GATGAAAAAT TGCACTCCCT 120  
 TGGTGTAGAC AAATANNAGT TCCATTGGT GTTGTGCTT ATAATAACA CTTTTCTTT 180  
 TTAAA 185

SEQ ID NO:2962

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03505

SEQUENCE DESCRIPTION:

GATCCAACGA GGAATATTTT GCCACACGGC AAATATATAC CGTATAATTT TCTGTACCAC 60  
TTGATAGAAA GGTAAAGAAT GAATATTGTT TTTTAAATAA CTTTTTCTT ATATAAGTAA 120  
TATGTGCTTA TCGTGTAAC ACCTAAAAAC ATTGAAAAAT AAAAGGAAAA TAAAATTCAT 180  
ACATAACCAA A 191

SEQ ID NO:2963

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03506

SEQUENCE DESCRIPTION:

GATCAGAAAT GGAGCATGGC CTTGTCCTTT AATGGGGATG CAAATAAAGT TTGTGGGGTT 60  
AAAAGTTATA AGACAGNAGT GATACCCAC TCTCTCCATT ATTGTCCAGC GGGGTGACAT 120  
AATGACAGGT TAAATATTTG TGATTCATTG ATTAAATATT ATTTAAAGAA ATGTAAA 177

SEQ ID NO:2964

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03507

SEQUENCE DESCRIPTION:

GATCACAGNG NTGGTGTCAA ATNCTATTNN AGGTTTGAAC TCTTGAGCTG GAACCTCAGC 60  
AAACTAGAGT ATATATTGTT CAGTATTTCT TTGGAAACAT TTCATTAATG TACTTGTCTT 120  
ACAGAAATTT CTGAACTTTA GTAAAAAAA ATAAAGTTAA ACTTTTAAAA CTCAA 176

SEQ ID NO:2965

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03508

SEQUENCE DESCRIPTION:

GATCTGAACG ATGCCGTGTC CAGTTTGC GAAGTCTATTC CCCTCCTCCT GTCGTGTGCC 60  
TTTGTTT CAGG TGGGGATGTA TTTTATGTAG AAGGTGGAAG AAGGCTGCTA TNACTCTTTG 120  
GATGGGAGTC TGGCAAGAGG AAATTGGAAG ATAAATATAA TAATAAGTGA AA 172

SEQ ID NO:2966

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03509



## SEQUENCE DESCRIPTION:

GATCTGCTCT GCTGCCCTGA ACTCTTACGG CAATTTAGGT TTCTCATTTT NNTTTTCTTT 60  
TTACATATGT ACAAATTGTT TTAAGCTTTG GCCTCTATCC AGGTTATNCT GACAATGAAG 120  
AAATGGGAGT TGTGAGAGCA TTAAGATGCA ATCTTCACTA AAANCAGTGA AA 172

SEQ ID NO:2967

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03510

## SEQUENCE DESCRIPTION:

GATCTCTAAT ACAGTATCTA ACACAAAAGA AGCTTTAAAA AGACAGTTTC TTTCTTATT 60  
TGATTAGCTA GAAGTTTATC TAGGTAAAAG CAAAAAAAAA ANTTNCAAN GCATANCATA 120  
NCATTGGGGT TCTTTTATA CTCAAGATGT TTANCTGTTC AAANTGNCAN 170

SEQ ID NO:2968

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03511

## SEQUENCE DESCRIPTION:

GATCCAGGCG GGAGCAGAAG CTAAAGCCAA AGCCCAAGAG AGTGGCAGTG CCAGCACTGG 60  
TGCCAGTACC AGTACCAATA ACAGTGCCAG TGCCAGTGCC AGCACCAGTG GTGGCTTCAG 120  
TGCTGGTGCC AGCCTGACCG TCACTNTCAC ATTTGGGCTC TTCGCTGGCC TTGGTGGAGC 180  
TGGTGCCAGC ACCANTGGCA GCTCTGGTGC CTGTGGTTTC TCCTACAAGT GAGATTTTAG 240  
ATATTGTAA TCCTGCCAGT TTTTNTTTT TCAAGNCAGG GGTGTCATNC TNAGAAAACC 300  
CTACTCNACA CAGCACTTCT TANGGTAGGC CNCTTATTCA ANTTCAATTT NNAGN 355

SEQ ID NO:2969

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03512

## SEQUENCE DESCRIPTION:

GATCTCGGAT GCCATCCCCG AGCTGAAGGC CTCCATCAAG AAGGGGGAAG ATTTCTGTAA 60  
GACCCTGAAG TGAGCCGCTG TGACGGGTGG CCAGTTTCCT TAATTATGA AGGCATCATG 120  
TCACTGNAAG GCCGTTGCAG NTAACTTTG TATTTNAATT TGCTTTGGTG ATGATTACTG 180  
TNTTGACATC NTCATGCCTT CCAAATTGTG GGTGGCTCTG TGGGCGCATN ANTANAGCC 240  
GTCCTTGATT TTGGGAAA 258

SEQ ID NO:2970

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03513

## SEQUENCE DESCRIPTION:

GATCACAAGA GGCCCATTTG TAGTGGCTGG TTGACAACGG CTGGNGCAAA TTAAATAAAT 60  
AAAATAGCTC TNTCTTTCAA A 81

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SEQ ID NO:2971

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS03514

SEQUENCE DESCRIPTION:

GATCTNAGAC ATCCCATCT TTGTAAGCAG AACAGTACGG CACTTCACCA CATCTNCTTC 60  
CCACCATGCT TCTAAGCAGC TGTNTTCCCC CTGCTAATGT TACAACCAAA GCAGCCACCC 120  
CACCTCCTNT NGTGTGAGC CTCACGACCT NTGACCCAGC TGGAAAGCN 169

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SEQ ID NO:2972

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS03515

SEQUENCE DESCRIPTION:

GATCTCATT CTGCTTTTCT TTTATGTCCT TTTGTCTCCA TGGGAGGTTG AGCTTCTTTT 60  
CCTACAAGTT TACTTACTGT TTGCATTTAC TTTTCTTTG CATTGTCTGT TCCAGTCCTC 120  
TGGCTATTTG ACTATTGTGT AATAAAAGGA CAAAAACAA ATGTGGTN 168

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SEQ ID NO:2973

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS03516

SEQUENCE DESCRIPTION:

GATCTTGCTG CAGCCACAGT GCAGNTCCAC ATTAACCTCTA CAGACCAAAC CATTTGTATC 60  
TGGCATCACT TACTAACACA CGNCATGCGG CTTTCTGCA TCAACTGCTA TGACGGTTAA 120  
GANTGTCAGT ATACAAGNAG GGATAGAAAA CTGGTACTGT TTAAATAAT CTGTAATNTC 180  
AATGTTTTTT TTTTNTTTC GGAAANNCNT NGTTTGCCC GNTTN 225

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SEQ ID NO:2974

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS03517

SEQUENCE DESCRIPTION:

GATCTTCTGT GGTGCTTAAG GNAACTTACT AGAGCTCCAC TAACAGTCTC ATAAGGAGGC 60  
AGCCATCATA ACCATTGAAT AGCATGCAAG GGTAAGAATG AGTTTTTANC TGCTTTGTAN 120  
GCAAATGGNA AAGGTCAATA AAGNTATATT TCTTAGNAA ATGGGCAAA 169

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SEQ ID NO:2975  
SEQUENCE LENGTH:167  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03518  
SEQUENCE DESCRIPTION:  
GATCCCAACT CCCATGACCT CTGGCTTCAG TGGTGGGTGG GGCAGGGCAG ATGAAAGGGC 60  
TTCAGTGGGA ACCTCTGAGA GCATTTTCCT GTTCCCCCTA TCAACCGCCC CCAGTGATAA 120  
CATCTGTGAA GCCAGCCATT ACTCAATAAA CTGCAAACCT GTCTAAA 167

SEQ ID NO:2976  
SEQUENCE LENGTH:167  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03519  
SEQUENCE DESCRIPTION:  
GATCAGNAGC CCACTGATAA GGGGCCCTAG GGTACAGGGT GCTGCCCAGC AGGTCGCCAC 60  
CGAGTGTCTT CTCATTTTAT TTCAGCTCCA TTTTGCCCAT AGATGGGCAG AGGGGTGAGA 120  
TTGGCTCATC CCCCTTCCAG ATTCTGCAAT AAAGCGGTGT GAGGAAA 167

SEQ ID NO:2977  
SEQUENCE LENGTH:167  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03520  
SEQUENCE DESCRIPTION:  
GATCATTCCC TCTTTTNGGA TGTATAAGAN CCTTCCGGAC AACAGAACCT ATTTNTGGAA 60  
TTGCAGAAGA TAACATATTT CCCTATTATT NATTTAATCA CCATAAACCA TACCTATTTA 120  
ATGAGTGTAT TCTGTGCAAT TTTTCCTCA GATTGTNTTT AACTNNN 167

SEQ ID NO:2978  
SEQUENCE LENGTH:166  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03521  
SEQUENCE DESCRIPTION:  
GATCGACTGC CAAGCAGCAG CCGCTGCCGA GGGGCTGCGT CTGACATCCT GACCTCCTGG 60  
ACTGTAGGAC TATATAAAGT ACTACTGTAG AACTGCAATT NCCATTCTTT TAAATGGGTG 120  
AAAAATGGTA ATATAACANT ATATGATATA TAANCCTTAA ATGAAA 166

SEQ ID NO:2979  
SEQUENCE LENGTH:165  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03522

## SEQUENCE DESCRIPTION:

5 GATCTGGGCG GGGTGGTGGC CTCCTCAGGG CGGATGCCAC CGGGTTCCCC AGGGAATAC 60  
ATGTCCCCAG CTCTGGGAGG GGTTCCTAC TGGCCTCCTA CTTTCCTCCC TAGGTGGACA 120  
GTGCTCCTCT AGAGAGCTGC GACTTTAATT AAAACAACA GGAAA 165

SEQ ID NO:2980

SEQUENCE LENGTH:165

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03523

## SEQUENCE DESCRIPTION:

15 GATCAGTGTC AGATATTGTT GAGGGAAGTA ATTTATAAA GTTACACAAA GGTAGTTATA 60  
AAAAAGCCC AGTTTGTTC TCAGAAGGTG ACTTTCATGT GCTTGAAAAG TTTAATATTT 120  
GANTATTGTG TTTAACCACA TGGTATTAAA ATTTGCAAT ATAAA 165

SEQ ID NO:2981

SEQUENCE LENGTH:163

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03524

## SEQUENCE DESCRIPTION:

25 GATCATGAAA TAATGTGCTT TGTAAGGAGA TTTCAAGTTA TTAGGAAGCA TACTCTGTTT 60  
TTNAATCATG TATAATATTC CATGATACTT TTATAGAACA ATTCTGGCTT CAGGAAAGTC 120  
TAGAAGCAAT ATTTCTTCAA ATAAAGGTG TTAAACTTT AAA 163

SEQ ID NO:2982

SEQUENCE LENGTH:162

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03525

## SEQUENCE DESCRIPTION:

35 GATCCGCCTG CTTGGCCTC CCAAAGTCT GGGATTATAG GTGTGAGCCA CCCTGCTCAA 60  
CCAGGTTTNA TTATTTAANT TAGTTAACT TTGGATAGAT TGTATAATAT ATAGTTTAAT 120  
GTAATCATGC TCATATTTT NAAATAAATA AAACACTATA AA 162

SEQ ID NO:2983

SEQUENCE LENGTH:161

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03526

## SEQUENCE DESCRIPTION:

45 GATCACTTGT TGTTTACTA AAGAAAGATT ACTTAGAGGA AATAAGAAAA ATCATGTTTG 60  
CTCTCCCGGT TCTCCAGTG GTTTGAGACA CTGGTTTACA CTTTATGCCG GATGTGCTTT 120  
TCTCAATAT CAGTGCTCGA GACACAGTGA AGCAAATTA A 161

SEQ ID NO:2984

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03527

SEQUENCE DESCRIPTION:

GATCTGAGGT CTAACATTGT TATCCTATAT CATTTTCATC CCAAGTAGTG ATATCTGTGA 60  
AATCACAGGT TTGATGTGTG CTAATNATGT ATTCTTCTAA TACATATTAA AAGACATAAC 120  
TATCAAAACA AAATAAATT GTCTGTTTTT AACCAAAGAA A 161

SEQ ID NO:2985

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03528

SEQUENCE DESCRIPTION:

GATCTCCATT TGATATTTTC ATTTGTATAA CTCATTGCA GTCTGAAAAT TTTTTTAGT 60  
GCCAGTCCCT GAACATATCA TTGAAAGTTA ATTTTCTTTG CATTTTAAAA TATCTGGATT 120  
ATGAAGAAAA AGTGATGAAA ATAAATTAAA ACTGAATTAA A 161

SEQ ID NO:2986

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03529

SEQUENCE DESCRIPTION:

GATCTGTGCT AGCTGTGAGG CAGCTCTGGA ACGTGAAGAG CTGTTTGGTT TGAACCGTGA 60  
ACAAACTGT GTTTTGAGTT TAGCTGACAT TATGGAAAAA AGTTCATCAC GTGACTGTTA 120  
ATGTAAACCT GGTTATTAAA ATAACNATGA AATTACCAAA 160

SEQ ID NO:2987

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03530

SEQUENCE DESCRIPTION:

GATCTCTCTG TNACTGACTT TGTGACTGTC CTGTGGTTTC TCCTGCCATT GCTTTGTGTT 60  
TGGAAGGACA TGATGGGGGT GATGGACTGG AAAGAAGGTG CCAAAAGTTC CCTCTGTGTT 120  
ACTCCCATTT AGAAAATAAA CACTTTTAAA TNATAAA 157

SEQ ID NO:2988

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03531

## SEQUENCE DESCRIPTION:

GATCAAANCA CCTNGGAGTG GTCACCAGGG GGACAGGGAG CCCCCACCA ATGTATCANT 60  
 GGGTGATTTA TNATGCCTTC TGCCCTTTGG CGAGTGAATG GNTTCCCAT AGGGGAAGTT 120  
 5 GGCCTCCCTC CGTGAGCTTT GGAAATNTTT TCTAATN 157

SEQ ID NO:2989

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

10 TOPOLOGY:linear

CLONE:HUMGS03532

## SEQUENCE DESCRIPTION:

GATCCGAATG GNCTGGGTGA GCACGAATTA CCGAGGCCTT CCCTTTGNTA CAGTCCAGGA 60  
 15 TTTGTAAGGN ATGAAGACCC CTGGNCCCCA TTCTNTTGGG GTCCATACAT ACTCTCCGAA 120  
 GATAGCAACT TGCTTCAGGT CAAAGTNAAC CCNAGAN 157

SEQ ID NO:2990

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS03533

## SEQUENCE DESCRIPTION:

25 GATCTCCTTA CGTAGCAGCC AAAATAAATG AAGCAAAAGA CTTGCTAGAA ACAACCACCA 60  
 AACATTGATG CTTAAGGACC ACACTGAAGG AAAAAAAAAG AGGGGACTTC GAAA 114

SEQ ID NO:2991

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS03534

## SEQUENCE DESCRIPTION:

35 GATCTGATTT ACAAGAAAAA GTCAGAGCTA AACACTAGTG ATGGCATAGC ATTACTGAAA 60  
 TCATTGTTTC TTAATTTTCAT TTTACTACAT TGTGAAGTTG TGATTCAGAT TCCATTTTCT 120  
 CAGAGAATTA AAAACAAAAA AAGTACTCTT GTAAA 155

SEQ ID NO:2992

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS03535

## SEQUENCE DESCRIPTION:

45 GATCTATTTT TNAGTATGTG GTTCATGCTG TTGTGAAAAA TGTTTACCT TTNACCTTTG 60  
 TCAGTTTGTA ATNAGAGGAT TTCCTTTNAC CCTTTGTAGC TCAGAGAGCA CCTGATGTAT 120  
 CATCTCAAAC ACAATAAACA TGCTNCTGAA GGCAAA 156

50 SEQ ID NO:2993

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03536

SEQUENCE DESCRIPTION:

GATCAAATTA GTAATTNNGT TTATGCTGCT CCTGATATAA CACTTTCCAG CCTATAGCAG 60  
AAGCACATTT TCAGACTGCA ATATAGAGAC TGTGTTTCATG TGTAAGACT GAGCAGAACT 120  
GAAAAATTAC TTATNGGATA TNCATTCTNN NCTN 154

SEQ ID NO:2994

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03537

SEQUENCE DESCRIPTION:

GATCTCATTT ATAATTAAAT TATGTCTATT GGATTGTTTT NATTGACTT NATGTTTTNT 60  
NAAGAAATTG TGATTAAATA TAACTTAACG ACTTTCTATT TTNCAGTTAT TTTAATTAGT 120  
TACTTCATTT AANCTTTTGG CATTNCATGA TTTN 154

SEQ ID NO:2995

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03538

SEQUENCE DESCRIPTION:

GATCATATAT GTNTTAGTGG ACAGGGGTCT GAAGTACACT GGAATTTACT GAGAACTTG 60  
TTTGTAAGAA CTATAGTTAA TAATTATTGC ATTTTCTTAC AAAAATATAT TTTGGAAAT 120  
TGTATACTGT CAATTAAAGT GTTTTGTGT AAA 153

SEQ ID NO:2996

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03539

SEQUENCE DESCRIPTION:

GATCAAATA CACATGNGTT TTCATTCCAA AAGTGGGTTC TAAANGCCTG GCTGCATCTG 60  
TATGNAATCA AGGCACACTC CAGGAAGACT GCCGCGTCGC GCCAACACGT CATACTCAAT 120  
GCCTCAGACT TTCATATTTC TGNNGTGCTG NNN 153

SEQ ID NO:2997

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03540

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCCCAGCA TCTTCTCCAC TTCAGCGCTG AGTTCAGTAT ACACAAGTGT CTGCTACAGT 60  
CGCCAAATCA CCAGTATTTG CTTATATAGC AATGAGTTTT ATTTTGTSTA TTTGTTTTGC 120  
AATAAAGGAT ATGAAGGTGG CTGGCTAGGA AA 152

SEQ ID NO:2998

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03541

SEQUENCE DESCRIPTION:

GATCATTGG ATATAGCAAT CTA CTCTGAG AAATGGAACA CAAGGAGTTA CCTATCACTT 60  
TCACTTATAA TTCCAAAAGA TGA CTACAAC CATGTCCATG CTCAGATTCA AACAGTTTTT 120  
CATATCACTT TTGGGTGGTA ATTACAGTTT TN 152

SEQ ID NO:2999

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03542

SEQUENCE DESCRIPTION:

GATCCCTGTN TGCNCGNCCC CTCTGCAATG TATGCCCCCTT GCCCCTTCCC CACACTAATA 60  
ATTTATATAT ATAAATATCT ATATGANGCT CTAAAAAAA CATCCCAACC AAAACCAACC 120  
AAACAAAAAC ATCCTCACAA CTCCCCAGGA AA 152

SEQ ID NO:3000

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03543

SEQUENCE DESCRIPTION:

GATCCAGAAG CAAACACAAG CAATGCAAGA CCTCCACAGA GTGAGCTTGG AGAGAGAGAA 60  
AGCCAAGATA AGAGAGGAGT ATGANGAGAA ANTCAGAAAG CTGGAAGATA AAGTGGAGCA 120  
GGNAAAGAGA AAGANGCAAA TGGNGANGAN N 151

SEQ ID NO:3001

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03544

SEQUENCE DESCRIPTION:

GATCTGGAGA TAANTTTATG CCTTTGGCCA TAGACAGGAC TGAATCCCA GTTCTGCCAC 60  
TTACTGGCTG TTTGACCTTA GGCAAGCCAC TCCTCCTTTN TNAGCCTCAG TTTCTTTNCC 120  
TGTAAGATAA AAAGAATGAN TCATTACTAA A 151

SEQ ID NO:3002



# EP 0 679 716 A1

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03545

SEQUENCE DESCRIPTION:

GATCAGGGCT GGGGCGGGGA AACAGGGAA GGACCTTGGA AGGGGCTGNN CCCAGGCCTG 60  
GGGGGCAGTC GTGGGAGCCC CTCTCANCTG TGGGGCTGGC ACAGAGCCCC AGGCAAGCTT 120  
TTAATAAACT GTTGGTTATT CTAACAGAAA 150

SEQ ID NO:3003

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03546

SEQUENCE DESCRIPTION:

GATCTCAAAA ATAGGTAATT TTTCTTTGCC GACCTGTAAA AGTGTGCCAA TACTACTAAAT 60  
TTGTGATTTT AAATTAATTC CTCCAGCTGT TGAAATGAAG TCTGCCAAAT CTTGCTCTAA 120  
CAAATAAAAT GTTATCTAAA TGAAGTAAA 149

SEQ ID NO:3004

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03547

SEQUENCE DESCRIPTION:

GATCCTAAAA GGGAAAATTG CCTTGTAAC TTTNAGATTC CTGTGGAATT GTGAATNCAT 60  
ACTAAGCTTT CTGTGCAGTC TCACCATTG CATCACTGAG GATGAAACTN ACTTNGTNT 120  
TTNGGAGAAA AAAAAGTGTN CTGCTTGTN 149

SEQ ID NO:3005

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03548

SEQUENCE DESCRIPTION:

GATCCTAGGA TCGTCCCAG ACGCTCAGTC AGAAGTGCTG GAGGTGGGGC CTGGGAAGCT 60  
GTATTTGTAA TNAAGTCTGG NGTTTTTGT CCATTAAAGT GTATCTTTGT CCATCCTATA 120  
AGNTTANNGG AAAGAAAAAG CATCTCAAAT NAGTGTAAGT TGTCTTGAG AAAAAATGT 180  
ATCAGACTTT TATGATTGTA ATGAAATGTA TTATAGNAAA ANATAAACAC NTTTAAANTA 240  
AA 242

SEQ ID NO:3006

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03549

SEQUENCE DESCRIPTION:

5 GATCCAGTTG TACTTAAGTG TGTAACAGGA ATATTTTGCA GAATATAGGT TTAAGTGAAT 60  
 GAAGCCATAT TAATAACTGC ATTTTCCTAA CTTTGAAAAA TTTTGCAAAT GTCTTAGGTG 120  
 ATTTAAATAA ATNAGTATTG GGCCTAAA 148

SEQ ID NO:3007

SEQUENCE LENGTH:148

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03550

SEQUENCE DESCRIPTION:

15 GATCATCGTG CTCTCAGACT CTGATTAGCT GCCTCCCCTT CTCCCTGCCT CCAGAATGTT 60  
 CTGGGATAAC ATTTGGAGGA AGGTGGGAAG CAGATGACTG AGGAAGGGAT GGACTAAGCT 120  
 AATCCCCTTT TGGTGGTGT TCTTTAAA 148

SEQ ID NO:3008

SEQUENCE LENGTH:148

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03551

SEQUENCE DESCRIPTION:

25 GATCAGTCCA CCCAGAGTTA GACATTGTTT TTGTAGAAAA CAGGTATTTA TTATGTCTAG 60  
 GGTTTTGTGT TTTTTTTTTT TCCTNANAGG NTAAAAGCCT TTATACAGAA ANAATTGGA 120  
 ACCTTTNATA TAAAACCTTT TCTTTAAA 148

SEQ ID NO:3009

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03552

SEQUENCE DESCRIPTION:

35 GATCGCTGTG GTTCTTATTA TCAAAATTAA GTTACTTGT ATACGGAACA ACCACAAGAA 60  
 ATTTGATTCT GTAAAGAATC CTCTTTAGCT GTGGCCTGGC AGTATATAAA TGGTGCTTTA 120  
 TTTAACAGAA TACCTGTGGA GGAAATAAAG CACACTTGAT GTAAAANTAA A 171

SEQ ID NO:3010

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03553

SEQUENCE DESCRIPTION:

50 GATCTTTTTA TTTTGCAATC CTGGGCCAGC TAGAAGCCAG GAGCTGATTG ACCTTTTAAC 60  
 TTTTTCAGT GGCCACATTT TGGTTATCGA TGTACCTAGA AGTATGTAAA TNAGATTAAA 120  
 TTTCTCTTCT GGAAACACCC TGAAG 145

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144

SEQ ID NO:3011  
SEQUENCE LENGTH:144  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03554  
SEQUENCE DESCRIPTION:  
GATCATAGAG AATGGTGCTT TTTACTACAG TTAGCACATG CATTTTTAGA AACTACTACA 60  
TGTTTTAGAG AATCTTTGCT GTGTATATGT AAAGTGTATT GTTCAACTGT TAACAAATAA 120  
TAAATTATTT CATTATTAAA GAAA 144

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144

SEQ ID NO:3012  
SEQUENCE LENGTH:144  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03555  
SEQUENCE DESCRIPTION:  
GATCTGCCCT NCTCCTTCTA AAGGGTAAGT CATAATCTGT GTAATACTAC AATTNATGGG 60  
NTGCTCACTA TGCCCTGTTT CTNTNCTAAA CAATTTACAT GTAATGTCTC ATTCCTCACA 120  
ATAACCCTTG TAAAGTGGGC ANNN 144

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142

SEQ ID NO:3013  
SEQUENCE LENGTH:142  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03556  
SEQUENCE DESCRIPTION:  
GATCCCCAGC TGCCTCACTT CTCTCTTGAG AACTTGGCTC AGGGCTCCTG AGGACCTTTC 60  
CCAGCATTAC CTTCCCTTCC CTTGAAAGGC AATTGTTGGC TGTTTTATA AGCAGGAAAA 120  
NTAAACAGAA GTATAAGGA AA 142

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142

SEQ ID NO:3014  
SEQUENCE LENGTH:142  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03557  
SEQUENCE DESCRIPTION:  
GATCAAATGT GCCTTAATAA ATTNNTTTTC ATTTAGATTT CAAACAGTGA TAGACTTGCC 60  
ATTTTAATAC ACGTCATTGG AGGGCTGCGT ATTTGTAAAT AGCCTGATGC TCATTTGGAA 120  
AAATAAACCA GTGAACAATA AA 142

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SEQ ID NO:3015  
SEQUENCE LENGTH:147  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS03558

SEQUENCE DESCRIPTION:

GATCTAAAGA AACAGTTGGC TGTAGCTGAG GGGAAACCCC CTGAAGCCCC TAAAGGCAAG 60  
 AAGAAAAAGT AAAAGACCTT GGCTCATAGA AAGTCACTTT AATAGATAGG GACAGTAATA 120  
 AATAAATGTA CAATCTCTAT ATACAAA 147

SEQ ID NO:3016

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03559

SEQUENCE DESCRIPTION:

GATCCCAGCA ATGAACTGTT CTAGGGAAAG TGGCTTCCTG CCCAACTGG ATGGGACACG 60  
 TGGGGAGTGG GGTGGGGGGA GCTATTTCCA AGGCCCTCC CTGTTTCCCC AGCAATTAAA 120  
 ACGGACTCAT CTCTGGCAAA 140

SEQ ID NO:3017

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03560

SEQUENCE DESCRIPTION:

GATCTCAGCT TTGAGAAGCC TTCAGCTCCA GGAATCCAA GCCTCCACAG CGAGGGCAGC 60  
 TGCTATTTAT TTTCTAAAG AGAGTATTTT TATACAAACC TACCAAAATG GAATAAAAGG 120  
 CTTGANGCTG TGGCCTGAGT GCCTCACTGG AAA 153

SEQ ID NO:3018

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03561

SEQUENCE DESCRIPTION:

GATCACGAAG GTGGTTTTCC CAGGGCGAGG CTTATCCATT GCACTCCGGA TGTGCTGACC 60  
 CCTGCGATTT CCCCAAATGT GGGAACTCG ACTGCATAAT TTGTGGTAGT GGGGGACTGC 120  
 GTTCGCGCTT TAAA 134

SEQ ID NO:3019

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03562

SEQUENCE DESCRIPTION:

GATCTATCTT NCAGAAAGTA TGTTTTTCCT CATAAAAGTG CCTCTTAATT GGCCATTGTA 60  
 CCAGCCACTT GTCCTAGCCA AATGTCCAAA ACACGCCCTT GGGCCCCGCC ACGTTACAAT 120  
 CCACANNNNN N 131

# EP 0 679 716 A1

SEQ ID NO:3020

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03563

SEQUENCE DESCRIPTION:

GATCACTGTN ATGTGTGGTC CATCTCTGAC CAAAACGTTA TGCAGTACGT GACTGTATCC 60  
 TNATCCTCAA TAATCCTTGG TTATTATTCT AGAATTTCAA ATAAATGGAA TCATATCATT 120  
 TACTATGTAA A 131

SEQ ID NO:3021

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03564

SEQUENCE DESCRIPTION:

GATCCAGTGA ATGATTCAAG AGAGCTACAT TTGAAGCCTG TACAAAAGCT TATCCCTGTA 60  
 ACACATGTGC CATAATATAC AAACCTTCTAC TTTCGTCAGT CCTTAACATC TACCTCTCTG 120  
 AATTTTCATG AATTTCTATT TCACAAGGGT AATTGTTTAA TATACACTGG CAGCAGCATA 180  
 CAATAAANCT TAGTATGAAA CTTTAAA 207

SEQ ID NO:3022

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03565

SEQUENCE DESCRIPTION:

GATCCTGAGA ATTACTTTTA ATAAAATCAT TTTTGTGCTG TTATTAAAAC TAGNCNNGAA 60  
 TTGCCTAAAN CCAAGAACTC TGCTTGATAA AATAAGCATA GTNTTAGGAA CAGCCATGCA 120  
 GATATAANTN 130

SEQ ID NO:3023

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03566

SEQUENCE DESCRIPTION:

GATCATCGAC CCCAAGGGA CCCGCAGACC CTTAAAAAAA TCACCCACAA CCCTCTGGAA 60  
 GTGGCCTTGC CCGGTCCCT TCCCAGGGGC GAGGTCGGCA AAGCAACATG GCAGAGCAGT 120  
 CATAGGAAA 129

SEQ ID NO:3024

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS03567

SEQUENCE DESCRIPTION:

5 GATCACCTTT TTTTATGC GTTGTGAATA GCAGTCTGCA TCCTAAGTTT AAAATATTTG 60  
AGAATCCTCT ATGGGACTCT CTGTAAATNT TTAAATACT GTTGTTCATA ATAAATATTT 120  
TATACTAAA 129

SEQ ID NO:3025

10 SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03568

15 SEQUENCE DESCRIPTION:

GATCAGCTGT CCTCTCTGAA AAAAATTGCA CCNNTTTTTC TTTTAAAAA TTTGTGTGCA 60  
TCTTCGTAGT AATGTAATTG TATTTTATGC CTGCTTTTTT ATAAAAAAAT AAAATAAAAT 120  
AAATGGAAA 129

20 SEQ ID NO:3026

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS03569

SEQUENCE DESCRIPTION:

GATCTAAATN TGACTGTGGT TGCACATATC TGTGNATATA CTAAAAACCA NTGATTTGTA 60  
CACTTTACAT GGGTGAGTTG TATGGTGTGT GAATTATATT TCAATAAAGC TGGGTTGTTT 120  
TTTGTCAN 129

30 SEQ ID NO:3027

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS03570

SEQUENCE DESCRIPTION:

GATCCCAGGA TTCAGTATTC CTGGCCCAGA GGNCNTTGCT GGCTACTGGG TGTTAGTTTG 60  
CAGTCCTGTG TGCTTCCCTC TCTTATGACT GTGTCCTGG TTGTCAATAA AATATTCCT 120  
GGCCTCCTGG AATCTNTAAA 140

45 SEQ ID NO:3028

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03571

SEQUENCE DESCRIPTION:

50 GATCCTACGA CAGGACCCAG ATGCCAGTGA AAGTGACCAC AGCCCTGCTC TAGTACCCCC 60  
GGAAGCTGAC CAGTCTACGC ACGGCCGAAG CTTCGTCAAG GAAGTAAATG TAGTTAGAAA 120

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TCTTAAA

127

SEQ ID NO:3029

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03572

SEQUENCE DESCRIPTION:

GATCTAGAGT ATAAGCTGCG CAAGGGCAGA AGTTTTTATC TGGTTTGTTT ATGGATGTAT 60  
 TCTAAGAGCT GAGAACAGGG CCTGGACACA ATAAGCATTG AATAAATATT TACTGAATGA 120  
 ATGAACTCCT ACCTATATTC CTATTTATAA TTTGGCTCCA CTTTATCCTA CTTTAGCTCC 180  
 CATTCAATTC AATAAAAAAA ACATTTTTTN GNACACATAT AAA 223

SEQ ID NO:3030

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03573

SEQUENCE DESCRIPTION:

GATCCATCTC AGTCACTTTT TCCCCTGCAA TGCCTCTTGT GAAATTGTGT AGAGTGTTTG 60  
 TGAGCTTTTT GTTCCCTCAT TCTGCATTAA TAATAGCTAA TAATAAATGC ATAGAGNAAT 120  
 TAAACTGTGA AA 132

SEQ ID NO:3031

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03574

SEQUENCE DESCRIPTION:

GATCCAGTTT TNCTACAAAG AACAAAGTGG TTGACAACAG TGACAGTAAT TNCTGGAGCA 60  
 AAACCAAAAG ACATAGGTAA AGANCATATA ATTGTTAATA AAGCACACTG CTTTCAACAC 120  
 AAA 123

SEQ ID NO:3032

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03575

SEQUENCE DESCRIPTION:

GATCCAAGTG TTTTAAACAAT TGGGGCTGTT AAGTCTGACC ATACATCACT GTGATAGAAT 60  
 GTGGGCTTTT TCANGGGTGA AGATACAAGT CTTAACCACA GTGTAACCTA CAGTTTCCTT 120  
 TAAA 124

SEQ ID NO:3033

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03576

SEQUENCE DESCRIPTION:

5 GATCAGAGCA AGCCTTGCCT CTTATCTTCG GGAAACCAGA ATATGTTTGG GGTGGTAGGA 60  
GCCACACAGA CTCTTCTGAG CCCCTCACT CACTTCCTTC CCCCTGTGCC TTCCTTTGA 120  
GAGTGAAGGT GGGTNGAGTT GACCAGAGAA AGGGGAGAGA ATTCGGGAAA GACCCAAAGT 180  
10 NTTTGTAATT CTCTTTGTC CTTTACCTA CAGAAATGGT CACATGGTTC TATTAAATA 240  
GCCTAATAAA CACATCTGGA GCCTGTCAA 270

SEQ ID NO:3034

SEQUENCE LENGTH:127

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03577

SEQUENCE DESCRIPTION:

20 GATCTCAAAG ATACACAGTA CCTACTTAAT TCCAGCTGAT GGGAGACCAA AGAATTTGCA 60  
AGTGGATGGT TTGGTATCAC TGTAATAAA AAGAGGGCCT GGGAATCTT GCGATTCCAT 120  
CTCTAAA 127

SEQ ID NO:3035

25 SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03578

SEQUENCE DESCRIPTION:

30 GATCCCTACC TGCTCCCGC TCCGGTTGCC AGCAGCACTC ACTGCACTCC TTTGTCATAT 60  
ACTCTGCATC ACTGTCATAC TCACANCTTC GTGAATAAAG TTGTGTGCTT TATTCGTAAA 120

SEQ ID NO:3036

35 SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03579

SEQUENCE DESCRIPTION:

40 GATCAGGGAC CTCACGCATC TTTTTCTCAT ATACATGGNC TCTCTGTTGG CCTGCAAACA 60  
CATTTNCTTC TCCGCTTATN AGACTATTTA NCTTTAATAA AGCACTGGAT ATAAATCAAA 120

SEQ ID NO:3037

45 SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03580

SEQUENCE DESCRIPTION:

50 GATCTAAAGC TNAACAATGA AAATCTTCAG CAGAAATAGA AATNGCCGTG GATTGTAATA 60

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CACACTGAAA TTCTNACTTT CTGAATTTAA ATGTAGAATA AATTTNACCA ACTTGGAGTA 120  
CTGTATGAGT ATTCNAGTA GGGGGAATAA ACTCAAANTT ATATTNTNT TGCAA 176

5 SEQ ID NO:3038  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03581

10 SEQUENCE DESCRIPTION:  
GATCTGAAAT GTCTGAGAGT AATAGTTTCT GTTGAATTTT TTTTGTTC TTTTCTGCA 60  
CAGTCCATTC TGTTTNTATT ACTATCTAGG CTTGAAATAT ATAGTTTGAA ATNATGAAA 119

15 SEQ ID NO:3039  
SEQUENCE LENGTH:234  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03582

20 SEQUENCE DESCRIPTION:  
GATCAGAATA TGACATTGCA GTAAAGNGCT TAAATAGTTT CATCTNTGGT TTTTTTTTCT 60  
AGACACTTTT CTTTATCCC AGNCATCTCT GAATTACAT TTTATATTAA AGAAATTGAG 120  
CTATCCATAC AACCTGTATT TACTTTAATT TCACTATGCT TTCAGCTTAC TTTATTGTAT 180  
25 GNTATGTAGG TCTAAAATAT AGTTTGAGTC AAATAAAATT AGGGGGGCTT TAAA 234

SEQ ID NO:3040  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS03583

SEQUENCE DESCRIPTION:  
GATCATGACA CTNAAGCGTG ATGAGACGCT CCAGGATGGC TGTNATACTC ACTTCTGCAA 60  
35 GGTCAATGAG AGAGGAGAGT ACTTCTGGGN GAAGAGGGTC ACAGGCTNCC CACCCTTTNA 120  
TGAACACANG TN 132

SEQ ID NO:3041  
SEQUENCE LENGTH:118  
40 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03584

SEQUENCE DESCRIPTION:  
GATCCCTAAA AATGTTGAGG GACTTCTGTT CATTTCATCCC GAGAACATTG GCTTCCACAT 60  
45 CACAGTATCT ACCCTTACAT GGTTTAGGAT TAAAGCCAGG CAATCTTTTA CTATGAAA 118

SEQ ID NO:3042  
SEQUENCE LENGTH:117  
50 SEQUENCE TYPE:nucleic acid

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# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS03585

SEQUENCE DESCRIPTION:

5 GATCGGACCG TTCATGCTGC CTATAGGCAT TATGTCCCTC AAAAAAAAAAC TCCTTTNCCT 60  
GCATCCTGTG TACAACATGA CATTTTAAAC CAATCCAATC TAAAAATGTN CCAGAAA 117

SEQ ID NO:3043

SEQUENCE LENGTH:117

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03586

SEQUENCE DESCRIPTION:

15 GATCAGAAGT GGCAGTCTAT AACTNAAAAT GTGGTAAAGT ACTTGANGCA AACATCCCGC 60  
ATCGCTGTG GACCTCTNAN ACTTTCTACT TTAACAGTTT CACAGTCTTT NCCAGTN 117

SEQ ID NO:3044

SEQUENCE LENGTH:116

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03587

SEQUENCE DESCRIPTION:

25 GATCTCCTCC ACCCTGTACC AGGCAGCAGC TCCAGTCCTC ACACCAGCCA AGGTCACAGG 60  
CAAGAGCAAG AAGAGAACT GACCCTGAAT GTTCAATAAA GTTGATTCTT TGTAAG 116

SEQ ID NO:3045

SEQUENCE LENGTH:116

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03588

SEQUENCE DESCRIPTION:

35 GATCTGAAAT CNNGGTCTTC CAAGGNAGAA AATCGANCTG GGAATAAAAG AGAAGACCTG 60  
TGATGGGGCA GCAGTGACGC NCTGTGGGGG GACAGGTGGA CGTGGAGAGC TCCTTN 116

SEQ ID NO:3046

SEQUENCE LENGTH:116

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03589

SEQUENCE DESCRIPTION:

45 GATCCTGAAG AAATCATATG TTAACATAC TTNACACCT ACTGTGTTAT AAAATATATC 60  
ATCAGATGTG CCTTGAGAAT AGTATATGTA ACATTAAAAA AAAGTTGCTG GCTAAA 116

SEQ ID NO:3047

SEQUENCE LENGTH:115

50 SEQUENCE TYPE:nucleic acid

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# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS03590

SEQUENCE DESCRIPTION:

5 GATCCTTGGA CTTTGTGTTT TTGATTNTAT GTTGATATTC TAAAAACATC TATTTTAATG 60  
TTATTTCTGT TCTAAAAATA AGATAATAAA TATTAACAAA CTTTGCTTTT TTA 115

SEQ ID NO:3048

SEQUENCE LENGTH:179

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03591

SEQUENCE DESCRIPTION:

15 GATCTCAACA AGAAGCTGTA TTTAAGTAT TAAGACAGTT CTTTGTTAGC TGGTTTCTAG 60  
TTGGTTATCT AGTTACCAAT GCTGCAGTCC TGCAGTCACC TATACATTAT TAAATNTAT 120  
TTAACTGTTA AATGCGCTAC CCACCAATAA TGAAATAGAC CTTTATGAAA ACTGTGAAA 179

SEQ ID NO:3049

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03592

SEQUENCE DESCRIPTION:

25 GATCTGAGG AAAGACTTGG AAGAGACCAG CATGTCTTCA GTAGCCAAAC TACTTCTTGA 60  
GCATAGATAG GTATAGTGGG TTTNCTTGAG GTGGTAAGGC TTGCTGGAC CCTGTTGCAG 120  
GCAAAAGGAG TAATTGATTT AAAGTACTGT TAATGATGTT AATGATTTNT TTTTAACTC 180  
ATATTATTGG GATTTTCACC CAAAATAATG CTTTTTGAAA AAAGGAAAAA AAAACCGGN 239

SEQ ID NO:3050

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03593

SEQUENCE DESCRIPTION:

35 GATCTGGCT TTCTNTTTC TCTTCTCCTN CAGGGTGTCT GTNACTGCNN GGTACTTCCA 60  
GCCAACCTCG TGAGCCAGGC GCCCCAGATA GGCAAACCTT CTTGTAGGCT TCAN 114

SEQ ID NO:3051

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03594

SEQUENCE DESCRIPTION:

45 GATCTGTATA TGCTATCCTA ACTGTTAATT GTATTATTGA TTATNTTGAT TATCTTGCTT 60  
GAAGGTTTCACTTTTCAAT TTGATAGAAA TAAAGTTTTT NCCTGCTTAT AAA 113

EP 0 679 716 A1

SEQ ID NO:3052

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03595

SEQUENCE DESCRIPTION:

GATCCTCTCT TCATTTTACT CAGCCAGGTT TTGTACTGAT GTACAGGTGT TAAATNACTT 60  
CAAGTATTTT TGTAAGAGGT GTATATAATT CAATAAAAAA GGTA AACAT AAA 113

SEQ ID NO:3053

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03596

SEQUENCE DESCRIPTION:

GATCGACAAG GAGTACTTGC TAAAAATGGC AACAGAGGAG TGAGGAGTGC TGCTGTAGAT 60  
GACAACCTCC ATTCTATTTT AGAATAAATT CCCAACTTCT CTTGCTTTCT ATGCTGTTG 120  
TAGTGAAATA ATAGAATGAG CACCCATTCC AAAGCTTTAA A 161

SEQ ID NO:3054

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03597

SEQUENCE DESCRIPTION:

GATCCGNACC CCAAGCCCAT GCAACCCACG CTCGGTCCCG TTCCGGCCCC TGCNCCCCGC 60  
TGCNCTTCGC TCCCCGNCCT TGCNCCGTTA GTAAACATCG CTCAAACGAA A 111

SEQ ID NO:3055

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03598

SEQUENCE DESCRIPTION:

GATCTAACAA GTTACATTGT ATAGTTTCTG GGACTGTTTG AATATTCTAT TCCAATGGGC 60  
ATTTATTTT TATCCTGTCA TAAAAA AAGACTGTTA CCCTGCTAAA 110

SEQ ID NO:3056

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03599

SEQUENCE DESCRIPTION:

GATCTCCTCC ATCCTGCTGC CCACCCCTCT TGAGTGTCTT AAGGGACAGA NCTTTCCACC 60  
CCTGGAAGAT GGAAATAAAC CTGCGTGTGG GTGGAGTGT AGGACCAA 109

# EP 0 679 716 A1

SEQ ID NO:3057

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03600

SEQUENCE DESCRIPTION:

GATCAGAGTG TTNTAAATCA TCACGCCCTT AGCTTATCCC TNGTCGAGCC AGGACACGGG 60  
GTGCTTCAGT GGGTCTGTNA CCCTCTCTCC TTGAAGCATG TTGCTGNNN 109

SEQ ID NO:3058

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03602

SEQUENCE DESCRIPTION:

GATCCCTGAA TGTGAACCTG AAGTTCAAAG GACTTGGAAG GCTCTGGAAT GTGTTGGTTT 60  
TTCCCCCCA AAATGGGTCC TAAGGAGGGT AAAGTGACTT GTTCAAA 108

SEQ ID NO:3059

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03603

SEQUENCE DESCRIPTION:

GATCAGTTTC TTTNGCTTCA AGATTGAAA CCAGAAAGGA AAGTCCNACT TGCAGATGAT 60  
TGTCCTTAAA ACCTAATGGA AAANTAAAAG ANAGACATAC CATGGAAA 108

SEQ ID NO:3060

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03604

SEQUENCE DESCRIPTION:

GATCCATCAT TGTTACAAAA CTTCACTGTC AAGAACCTTT TCGTTGCATA ATGTGCAAAT 60  
AGTTAAAACC ACTGTACTAT AACTTAAAA ATGATTAAGA TAGTAAA 107

SEQ ID NO:3061

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03605

SEQUENCE DESCRIPTION:

GATCTGGCAG CTGAGGCCCG AGGCAGGGTT GGNGTGATGC CAGGGCAAAG TGGTGAGGAG 60  
AAACAGGAA NCGGGCTTTC NCCNCATTGG TAAATGGGAA AGAGGTGAGC AACTTAAGAT 120

EP 0 679 716 A1

TGTCACAATT AATCACAAGT GTACAGGATT AGACTGGGTT TATATTTAAC TCTTGCTNCA 180  
TAGGTGTACC ATTTAAAGAG TGTTATTTAA TGCTAAGTTT AACTGCTTTA ATAAAGTTTA 240  
TTTTTAAATA AA 252

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SEQ ID NO:3062  
SEQUENCE LENGTH:103  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03606  
SEQUENCE DESCRIPTION:  
GATCAACAAA ATAAGTTGTA TCTCCTGCTT AANTCCTTTA TACTACCTGG NGAAAAGTAT 60  
TTCCCATATT TCCAATAAAT GTCAGACACT ATTGAGAAAAG AAA 103

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SEQ ID NO:3063  
SEQUENCE LENGTH:103  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03607  
SEQUENCE DESCRIPTION:  
GATCCTGNAT NANGCCCGGG CCAGCGAGTG CAGGGACGTG GAGGGNTTCA AAACCGAGAT 60  
GGCCATGCTG GTGACCCAGG CCAGGAAGAA CACCATCACC CNN 103

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SEQ ID NO:3064  
SEQUENCE LENGTH:159  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03608  
SEQUENCE DESCRIPTION:  
GATCCTCACA GTCAAGTGAC GAGGCTGGGG CTGAAAGCAG AAGCATGCAC AGGGAGGAGA 60  
CCACTTTTAT TGCTTGTCTN GGTGGATGGG TCAGGAGGGT CTGAGGGCCT GTCCAGACA 120  
ATAAAGGTNC CCTCAGCGGA TGTGGGCCAT GTCACCAAA 159

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SEQ ID NO:3065  
SEQUENCE LENGTH:102  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03609  
SEQUENCE DESCRIPTION:  
GATCCTATCG CCTTTNAGTA GAATATGAAA TATTCTTTNA GAAATCCAAT ATAAATAGGT 60  
TATAATAGCC ATATNCTTNA TNACTTTATT GAGATATAAT TN 102

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SEQ ID NO:3066  
SEQUENCE LENGTH:186  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS03610

SEQUENCE DESCRIPTION:

5 GATCTNAGCT CCCACCTCCC TTCCCACCTA CTGCACTTTC CCCCTTCCCG CCTTCCAAAA 60  
CCTGCTTCCT TCAGTTTGTA AAGTCGGTGA TTATATTNT GGGGGCTTTC CTTTNATTN 120  
TAAAATGNAA AATTTATNTA TANTCCGTAT TTAAAGTTGT AAAAAAATA NCCACAGAAC 180  
AGNGAN 186

SEQ ID NO:3067

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SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03611

15

SEQUENCE DESCRIPTION:

GATCTCAGAC AGTGTGCGGC GGCACATGAG CGGCTTCCG CAGTGTCTG TTTGAGCCA 60  
CTGCAGTCTG GGCCCATCA TTAAACGGGC TGC GTTAAA 100

SEQ ID NO:3068

20

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03612

25

SEQUENCE DESCRIPTION:

GATCTCCAGT NAGACTCCAG GGTTC TAGAC AGAGGCCAGT NTTGGCCACT CACCCACAC 60  
CCCGCGGACC CCAATAAAGG CTTGCATAGC TCCAGAAA 98

SEQ ID NO:3069

30

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03613

35

SEQUENCE DESCRIPTION:

GATCCTGAAG CTTNACCGG CTCCAAAGG CAAATGGAGC TGCCCTCNTC TGTATCAGGT 60  
TTATTGGTTG TACATATAAA TNATACTNC CTTTCAA 98

SEQ ID NO:3070

40

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03614

45

SEQUENCE DESCRIPTION:

GATCCTGTTT AACAAAGATA CTTGAGACAT CCATTTGTTT TAATGAAATC TGTATGGATA 60  
TGGAAATNCT TGCCCTAATA AAAGCCTACA TATACCTTCT GGTAAA 107

SEQ ID NO:3071

50

SEQUENCE LENGTH:97

55

# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03615

5 SEQUENCE DESCRIPTION:

GATCTNTCCG TTCTCAGGCC AGACCCCTGG TGCTGCCGTT AATTTTTTTT TCTCTGTCTT 60  
TGCTGCAATN TTNAATAAA ATGCCAAAGA ACACAAA 97

10 SEQ ID NO:3072

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03616

15 SEQUENCE DESCRIPTION:

GATCCTAAAC AAATCATCTT TGTCAGTTAA GTATAGTTGC GCAAAAATTG TTAAATCCTT 60  
TGCTTTTATT AAAGAAAAAT TTGAGTAACA TTAAT 95

20 SEQ ID NO:3073

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03617

25 SEQUENCE DESCRIPTION:

GATCTAAGTG ATGAGTCTAG GTGTGTTATT GTNCAGTTTT TNCAACTTTC CTGAAAAACG 60  
AACTTTTCAA AATAAAAAAT TGGAAAAATA GAAA 94

30 SEQ ID NO:3074

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03618

35 SEQUENCE DESCRIPTION:

GATCACTTTG AGAAACAAAC TTTTATTAAA TGTAAGGCAC TTTTCTATGA ATTTTAAATA 60  
TAAAAATAAA TATTGTTCTG ATTATNACTG AAAAGATGTC AGCCATTTC AATGCTTGGG 120  
AAACAATTTT TTGTTTTTGT TCTGTTTTCT TTTTGCTTCA ATAAACAAT AGCTGGCTCT 180  
AAA 183

40

SEQ ID NO:3075

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS03619

SEQUENCE DESCRIPTION:

GATCTGCCAT ATTTGNTNTT GGTTTTAATT TTCATATCCA GCCTAAAGGT GGTTGTTTAT 60  
NATATAGTAA TAAATCATTG CTGTACAATA AA 92

50

55



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SEQ ID NO:3076

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03620

SEQUENCE DESCRIPTION:

GATCAGGCTG CCTCCTGGNT TGGNTGTCGG GGGAGCTGTC CGGCAGCCTG GCAGGGAGAT 60  
GCAAGGCCTA AAGTAAATTT TTNTCAAGTA AA 92

SEQ ID NO:3077

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03621

SEQUENCE DESCRIPTION:

GATCTAGCCC CTTCTTCAGG CCGAGAGAAT TTCGAGCGTT ANCCGTCTCT TGGCCACCAG 60  
CTAAATAAAC GGATTCTTCA TGTGTCTCAA A 91

SEQ ID NO:3078

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03622

SEQUENCE DESCRIPTION:

GATCTGCTAT TGTTATTCTT CCTCTTTATT GGAAAAAGGC CTCAGTTTTA ATTATTTTCT 60  
TCCCAAAATA AATNACACAT TTGGTTACAA A 91

SEQ ID NO:3079

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03623

SEQUENCE DESCRIPTION:

GATCCTGCAT CAGCATTGTA TATATGGNCT TAAGTGCCTG GCCTCCTTAT CCTTCAGAAT 60  
ATTTATTTNA CTTACAATCC TCAAGTTTTA ATTGATTTTA AATATTTTCC AATACAACAG 120  
TTTAGGTTTA AGATGACCAA TGACAATGAC CACCTTTGCA GAAAGTAAAC TGATTGANTA 180  
ANTAANTCTC CGTTTNNTTC ANTTNATTTC AGTGAATGA NAANGTTGCT TAGTATTTN 239

SEQ ID NO:3080

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03624

SEQUENCE DESCRIPTION:

GATCCCTGCC CTGCACCAGC ACCCTGANAT GGAGCTGAGA CTTTATTTAT TGGGGGTAGG 60

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GGGATGGAGG AGGTCCCTCC AACATGTTTG GACCCAGCTC CTTTGGGTTT CACTGACACC 120  
CCTGCCCCCTG CCCCTGCCCC GAACCAAGTG CCATTTCTCA CTCTGGAGCC TTAATAAACT 180  
GCAATTTGTA TCCAAA 196

5

SEQ ID NO:3081  
SEQUENCE LENGTH:90  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS03625  
SEQUENCE DESCRIPTION:  
GATCTGTGTA CTGTTTACTT CCCACTTCCC AGAATCCCTT GTATCTCCTT TCTCGGGAAT 60  
TGTATTTTCT AATAAATGAC ATTTGAGAAA 90

15

SEQ ID NO:3082  
SEQUENCE LENGTH:90  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS03626  
SEQUENCE DESCRIPTION:  
GATCTCTGGA AGTGTAATTN TGAAAGAAAC TTNCTTGCAG CTTTAACAAA ATGAGAAACT 60  
TNCCAAATAA AACTTGTTTT GAAGTTTAAA 90

25

SEQ ID NO:3083  
SEQUENCE LENGTH:89  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS03627  
SEQUENCE DESCRIPTION:  
GATCCTCGGG AAGAACAAAG CTAAAGCTGC CTTTTGTCTG TTATTTTATT TTTTGAAGT 60  
TTAAATAAAG TTTACTAATT TTGACCAAA 89

35

SEQ ID NO:3084  
SEQUENCE LENGTH:88  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40

CLONE:HUMGS03628  
SEQUENCE DESCRIPTION:  
GATCAATCTT TGATGGTGAG GGTTTTAGAA AGGAAAAATA TAGTAAATG TGTAATTTGT 60  
CTTAATAAAA TCTATCTNTA CATCTAAA 88

45

SEQ ID NO:3085  
SEQUENCE LENGTH:94  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

50

CLONE:HUMGS03629

55

## SEQUENCE DESCRIPTION:

GATCTAGATT GGGTGAGGGG GACGGGGATG TNAGGGAGGC AAGTGTGTTN TGTTACTGTG 60  
TCAATAANCT GGTTTAAAGT TGTAAGTGN GAAA 94

SEQ ID NO:3086

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03631

SEQUENCE DESCRIPTION:

GATCTGAATT TCACAAAAAG TTCATGGAGA AATATATTAA ATAGTACAGT TTTATGTGCT 60  
TAATTAAAGA CTGTAAACG TAAAGGAAA 89

SEQ ID NO:3087

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03632

SEQUENCE DESCRIPTION:

GATCATACCA CGGCACTCCA GACTGGGGAC CAAAGTGAGA CCTTGTTTCT AAAANTTAAA 60  
ATATTTAGAA TGTTTCCTAG CAAA 84

SEQ ID NO:3088

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03633

SEQUENCE DESCRIPTION:

GATCCCAAGG ATGGAGAACA ACTTACCCAG TAGCTAGAAT GTTAATGGCA GAAGAGNAAA 60  
CAATAAATCA TATTGACTCA AA 82

SEQ ID NO:3089

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03634

SEQUENCE DESCRIPTION:

GATCTCCAGA TGTGCATTTT CCTCTCTTAT TTAAAGTTAT GTTAAGATTA CTAAAACAAT 60  
AAAAGCTCCT AAAAAATCAA A 81

SEQ ID NO:3090

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03635

## SEQUENCE DESCRIPTION:

GATCCAACCG TGCCTGAAGC TAGAATATCC CCTGGACTTT TCAGTTATGT GAACCAATAA 60  
ATACCCTTTT TTGCTTAAA 79

5

SEQ ID NO:3091

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS03636

SEQUENCE DESCRIPTION:

GATCTGNGAN ATATTATGGT AATTGTGTCG GGGCGCCATG AACCGCACCC ATATAACACG 60  
GTAAACTTAA TCAGCAAA 78

15

SEQ ID NO:3092

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS03637

SEQUENCE DESCRIPTION:

GATCATGCTG AAAACCACTC AAACGATTAT ATTTTITACA TTATAAGAAG TAAAATATAT 60  
TATTCTGAAT AATGAAA 77

25

SEQ ID NO:3093

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS03638

SEQUENCE DESCRIPTION:

GATCTGTGCA TTGCTCCTTC TGATTGTGTC TAAGTTGTTA AATAAGAGGG ACCCTGAGAA 60  
AGGCCTTACT CTAAA 75

35

SEQ ID NO:3094

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS03639

SEQUENCE DESCRIPTION:

GATCACACAG CTAACGAGGC TGCCTCCAGC ATTCCTGAT TTCCTCTGTG GTAATAAAAG 60  
CTTCTGTGC TTAAA 75

45

SEQ ID NO:3095

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50

CLONE:HUMGS03640

55

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SEQUENCE DESCRIPTION:

GATCAGAACT TACAAACCAA ACTTTTATTC TGAGAAACTG GCTGTACAAT ATNTGAAAAG 60  
AAAGTGACAT GNAGGAAA 78

5

SEQ ID NO:3096

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS03641

SEQUENCE DESCRIPTION:

GATCTTTTNN AAGTNTTCTG AAAGGAAGTA GACAGTATTA CACCCTGAAT AAATAAGGTG 60  
TTGTTTTCCA CAAA 74

15

SEQ ID NO:3097

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS03642

SEQUENCE DESCRIPTION:

GATCTACTTC CCATGCAGAA GAGAAGTCAC ATCTTCCAGG GAATCGCAAT GTTGTGGCGT 60  
CTGACTTGTA TGTACATTT GTGTAAAATG GTATATNCTT TAAAATAGTG TTGATAACTG 120  
GAATATTGTA TGTATGCTTG GAGATGCTTT GTGTGAACCT AAGACTGTCA CTCAACAGAT 180  
GTTGGATTGG GGNAAATCCA AAGCACAAC TCAAANTAAN NTACATTTT AGGTTTCGAT 240  
GCTGCAAANC ANANANANN ACANNAN 267

25

SEQ ID NO:3098

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03643

30

SEQUENCE DESCRIPTION:

GATCATGGTG ATGTACGGGG TGAATTCTCT TGCCGTGTTG CAAATGTGTA AAATAAAGAT 60  
TATCTGGCAG AAA 73

35

SEQ ID NO:3099

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03644

40

SEQUENCE DESCRIPTION:

GATCCNAGNT CTANCGTCAT ATAATCATTT AATATAATTA AAGTTTAATT GCTGAAATAC 60  
TTATAATGAA A 71

45

SEQ ID NO:3100

SEQUENCE LENGTH:69

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03645

SEQUENCE DESCRIPTION:

GATCATGCAA TTCCTTCAAT TATGATGGAA AGACTTGAAC TTTCTGAAAT AAAACAAAAA 60

TACAGCAAA 69

SEQ ID NO:3101

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03646

SEQUENCE DESCRIPTION:

GATCCATTTA TTGCAATTCA TGCTGAATCT AAATTATAAA ATTTAAAATT AAATGCATAT 60

CCTCAAA 67

SEQ ID NO:3102

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03647

SEQUENCE DESCRIPTION:

GATCCGAAAC CTGTAAACA ATAAGATGTG TTCTCGGAAA ATNAAACAAG AGGTATCACA 60

AGAAA 65

SEQ ID NO:3103

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03648

SEQUENCE DESCRIPTION:

GATCATCTCT TCTCCATAAG ATAGTGTGAT AACACAGTC ATGAATAAAG TTATTTTCCA 60

CAAA 64

SEQ ID NO:3104

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03649

SEQUENCE DESCRIPTION:

GATCGCTCCA ATAAACATAT ATTGTGAAAA TGCATCCACA ATAAATGGAA TTCCTTCCTG 60

CAAA 64

SEQ ID NO:3105

SEQUENCE LENGTH:63

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03650

SEQUENCE DESCRIPTION:

GATCTACCTG TCTTGTTGCC ACATGTTTCT AAACCTTCCA ATAAATCACC TTCTACTGAC 60  
AAA 63

SEQ ID NO:3106

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03651

SEQUENCE DESCRIPTION:

GATCAGCATC AGGCTGTTAT CAAGTCTGTT GGTGCTAAAA AGTAAANAT GAAATGTTCA 60  
AAGAGAAA 68

SEQ ID NO:3107

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03652

SEQUENCE DESCRIPTION:

GATCTGTCTG GCTCCNTGT TTCTATTAA ATAAATTTCT GTCTTCTATT GTTTCAAA 58

SEQ ID NO:3108

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03653

SEQUENCE DESCRIPTION:

GATCAGCCTT NNTATAATGT TTTTAAATC ATTTCTAAAT AAAACAGAAA TACAGAAA 58

SEQ ID NO:3109

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03654

SEQUENCE DESCRIPTION:

GATCTAGACT TATATGAATA AATNAAATTA CATGCCAAGG GCCCTAAAAA GCAAA 55

SEQ ID NO:3110

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03655

## SEQUENCE DESCRIPTION:

GATCAGGGCC GAGCAGAACC GCACTCTTCC CAAATAAAGC TTCCTCCTTG AAA 53

5

SEQ ID NO:3111

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03659

10

SEQUENCE DESCRIPTION:

GATCATATTT TTTNATACAG GTATTTCAAT TAAATGTTT TTGTACATAG TGAAA 55

15

SEQ ID NO:3112

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03661

20

SEQUENCE DESCRIPTION:

GATCCAATCA NTTAAATAAA CCTGTATGTA TATGCATATG TNTACATGCA TATCCCCTCC 60  
TGCTAAAACT CATAAA 76

25

SEQ ID NO:3113

SEQUENCE LENGTH:451

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03679

30

SEQUENCE DESCRIPTION:

GATCCCTCAG TTTCTTCTTG ATTTCAGCAT GTNTCGGGTT CCTAATTTAT GGTATGAGTT 60  
AGCAAATTTA ACCATTGTGT TTGTGCCCTA CCCAGGGGAC TCCCCAGTTT CTGACTTGAA 120  
GTAGACTGAG AAGAATCCAC GAGGTGCTAT CTGGCCAGAT TTAAGTAGAT TCTATTTCCT 180  
TGGTTCTCCC TCTCCCTGAG GACCTCTTAT TTNATTGTCC CCTCTTCTAG GTTAATTCTC 240  
CTTTGATTG ACTTTGTTGA GAAGGAGGTT GGACAGTAGA TTAGCAAAGT TCCAAGTGCA 300  
AAATTACAGT GTGTTAGAGT GTGGGGGGAA AATTAGTCTT ATTTTCCCT ACATGGGATA 360  
CAACACTGTG AATTCAATCT TCAACCTGAA GGGCCCTGCA GTTCCTCCTA AAACATNGTT 420  
GTTTGNTTTT CTTTAACCAA GGTTTAAGCT N 451

40

SEQ ID NO:3114

SEQUENCE LENGTH:445

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45

CLONE:HUMGS03680

SEQUENCE DESCRIPTION:

GATCTAAGGA TGACTTGGAC ACACTCCNTG GCACTGAAGA GTCTGAACAN TGGCCTGTNA 60  
TTGGTCCATT CCAGGACCTT CATTTGCATA AGGTATCAAA CCACANCAGC CTCTGATTGG 120  
CCATGGGCAG ACCTGCACTN TGGCCAATNA TTGGTTCATT CCAGGACATT CATTTGCATA 180  
AGGAGTCAAA CCACANCAGT CTTGGATTGG CTGTGAGCCA ATTCACCTCA GTCTCTAATT 240

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5 GGCNNNGAGT CAGTCTTTCA TTTACATAGG GTGTAACCAT CAAGAAACCT CTACAGGGTA 300  
CTTAAGCCCC AGAAGATTTT NCTACCAGGG CTCTTGAGCN ACTTGCTCTA GCCCACTCCC 360  
ACCCTGTGGA ATGTNCTTTC ANCTTTTGNT TGGTTTCAAG TNCCTTGGTG CTTCCAATAA 420  
NTNCCACTTC CTTCAACCACC CNAAA 445

10 SEQ ID NO:3115  
SEQUENCE LENGTH:439  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03681  
SEQUENCE DESCRIPTION:  
15 GATCGGCGCC ACTGCTGTCC TGCTGGCTTC NNCTGCGCAG CANGGGGTAC CAAGTGTTTN 60  
CCCAGGGAGG CCCCGCGCTG GGACGCCCCT TTAAGGGACC CAGCCTTGAN ACAGCTGCTG 120  
TAAGGGACAG TACTGAAGAC TCTGCAGCCC TCGGNACCCC ACTCGGAGGG TGCCCTCTGC 180  
TCAGGCCTCC CTAGCACCTC CCCCTAACCA AATTNTCCCT GGACCCCAT CTNAGCTCCC 240  
CATCACCATG GGAGGTGGGG CCTCAATCTA AGGCCTTCCC TGTAAGAAGG GGGTGTGGC 300  
20 AAAAGCCACA TTACAAGCTG CCATCCCCTC CCCGTTTNA TGGACCCTGT GGCCAGGTGC 360  
TTTTCCCTAT CCACAGGGGT GTTTGTGTG TGTGCGCGTG GTGCGGTTN AATAAANGTT 420  
TGTACAACTT NTGTTTAAA 439

25 SEQ ID NO:3116  
SEQUENCE LENGTH:431  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03682  
SEQUENCE DESCRIPTION:  
30 GATCTTGAAG TGCTTTTAT ACAGCTCTCT AATAATTACA AATATCCGAA AGTCATTTCT 60  
TGGAACACAA GTGGAGTATG NNAAATTNNN TATGAATTTT TCAGATTATC TAAGCTTGCA 120  
GGTTTATAA TTAGAAGATA ATGTGAGANT TAATGGGGTT TATATTTACA TTATCTCTCA 180  
ACTATGTAGC NCATATTACT CACCCTATGA GTGAATCTGG AATGCTTTT CATGTGAAAT 240  
35 CATTGTGGTC TATGAGTTA CAATACTGCA AACTGTGTTA TTTATCTAA TCCATTGCTT 300  
AATGAGTGTG TTTTCCATG ATTGAATATA CCGTGGTTCA TATGTTAGCA TGGCAGCATT 360  
TTCAGNTAGC TTTTGGTTT GTTGGGAAGT TGGGGTTTG GGGGGAGGGG GGAGTNTNG 420  
TACGTTGCCT N 431

40 SEQ ID NO:3117  
SEQUENCE LENGTH:427  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
45 CLONE:HUMGS03683  
SEQUENCE DESCRIPTION:  
GATCAAAGTA TTATATGCTG TGTGCTTTTA AGGTGTTTGT AAGTACTGAA AAAGGCAAAA 60  
ATNCTTTCTA CATTGACATT CATTCCTATT TNACTGGGCA CCTATGAATG TATGCTGTGT 120  
GCTAGAAATA GACTAAAACA TATCCTATA GCATGTNAGT GTGTTTGCAT GTTTGCTGAA 180  
50 AATCCTTTGT GTATAANCCA GTTTGTAAGG TTCTCTGGGT TAGGTAGGGA CTCTGCAGTT 240

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TCTNCCTGTC NAAATCTCTC CTACCAAGAT GGTGTTCCAC TGTCCAGCCC AGCATGAGTA 300  
GCAGGTAGNG CACAGCTTTA CTGGCTGGTT TGTATGCTTT GGTTTTAGGT GCAATTGTTG 360  
TGGGTNGATT TACTTTNTCC AGAAAACCAT NGTATTGNNN ATGTCCTNGG ACCGGTGGAA 420  
AATAGGN 427

SEQ ID NO:3118  
SEQUENCE LENGTH:423  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03684

SEQUENCE DESCRIPTION:  
GATCAAAAAT ATTAGAAAAA ATAAAANTAA TACAAATAAA AATACAGTAT AACAGTTATT 60  
TAAATAGCAT TTACATTGCA TTAGGTATTA GTCTAGGGAT AAAGTATACA GGC GGATGTN 120  
CGTTGGTTAT ATACAAATAT GTCATTTTAT GNAANNGACT TGAGTATACT TGGNTTTTNG 180  
GTATCTNTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC AAGGGACAAC 240  
TGTA CTATT TNCNTTATT GTCATTGCAA GCTTCTTATG GAAACTTTAT AGGGAATGAN 300  
AATATACATG TTAAGGANGA TTAACATTA GATAGTAGAT GGTTTGTTC ATGCTAGAAC 360  
TGTTAGTATT GTTGATTCAA TTACTTTGGT TTCATGAAAA ANTAAACGGT AANTATCTTT 420  
AAA 423

SEQ ID NO:3119  
SEQUENCE LENGTH:421  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03685

SEQUENCE DESCRIPTION:  
GATCGAGACC ATCCTGGCCA ACATGGTGAA AACTCATCTT TACTAAAATA CAAAAAATTA 60  
GCCACGCNTG GTGGCGCACG TTGTGGTCCC AGCTACTCGG GAGGCTGAGG CAGTGGAGTC 120  
ACTTGAACCC GGGAGGCAGA GGTGTCAGTG AGCCGAGATT GCACCACTGT ACTCCAGCCT 180  
GGCGACAGAG CAAGATTCTN TNTGCCCCC CACCAAAAAA AAAGANTGAA ACACTGATAT 240  
TTGCTACAAC ATGGNTATAC CTCCAAAGCA TCCTGTTAAG TGAAAACAGG GAGACACAGT 300  
CACGTACTAT ATGATTGCNC TTACGTGAAA TATCCACANN GACGNNTCCA TGGNGACCAG 360  
GCAGATTGCC GNTTGCCAGA GGCCAAGGGT TAGGGAAAAA TTGGTGAGGG ACCCTGCGTG 420  
N 421

SEQ ID NO:3120  
SEQUENCE LENGTH:410  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03686

SEQUENCE DESCRIPTION:  
GATCTATGAC TTCTCAAAGC CGGGTCATGA ATGTCCATAA AATGCTAGGC ATTCTATTT 60  
CCAATATTTT NATGGTTGGA AATAATGCTT CANATTGGA ACTGGACCCC ATGAAGGATA 120  
TTCTCATCCT CTCTGCACTG AGGCAGATGC TGCGGGCTGC AGATGATTTT TTAGAAGATT 180  
TGCCCTCTNGA GGAAACTGGT GCAATTGAGA GAGCGTTACA GCCCTGCATT TGAGATAAGT 240

# EP 0 679 716 A1

TGCCTTGATT CTGACATTG GNCCAGCCTG TACTGGTGTG CCGCAATGAG AGTCAATCTC 300  
TATTGACAGC CTGNTTCAGA TTTNNCTTTN GTNCGTTTTN CNTTCTGTCC TTGGACCAGT 360  
CATATCTCAN GTTCCAAAGG CCANAACCCT GAGGAGCGGT NNGGCTAAGN 410

SEQ ID NO:3121  
SEQUENCE LENGTH:402  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03688

SEQUENCE DESCRIPTION:  
GATCTGAGGA CCCTGTACTG GTTACTCCTG TACACGTTC AATTTTCNT GTAAATNTAT 60  
TAATATACTG AGCAGTCCAG GAGCAGCCAT TAGGCAAACA CCACTCCTTG CTCCTTCAT 120  
GTGACCTATC ACTGAGCTCA CCAGCTGAGG TCAATNACAT TCTTCCCAAC CTGGAGAACA 180  
GAATTTGGGT CTGCTCAGAG GCATGATGTG AAACATGTCT GGGATAAAAG CTTTGTCTTA 240  
TTGACAGCAA ACCTTTTTGT GTTAAGGGGT AGGGGAAGAG CANGTGAAGG ATGCAGATTA 300  
ATTTCTATTT AGGANTATAC TTTTNTATAT NGTTTGAAAT TTTGGNCTTG TAAAAATATT 360  
CATCCATNTT TTNACCAANA NAATTTCCCT GTGGACNGGT TN 402

SEQ ID NO:3122  
SEQUENCE LENGTH:409  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03689

SEQUENCE DESCRIPTION:  
GATCAGTTTG ATTCTGTAAT GAGCACAGCA CCTAATATTT TGAGGAGCTC TGTTTTGAGG 60  
ACCAATGCTT AAGGTGGACT TTGTTCTGTA ACAATATCCC AATAGATTTG TTGACTTGAG 120  
GTCTGGTTTG GTTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT 180  
ATTCTAATGT TGA AAAACTG CACAAATTTT TATGGGACAA AGCCTAGAAA AGAGAAATGT 240  
AGTTTGAATC ATAATCTAAA TCATCGTATG ATAGANGAGG GAAAGTTTGT GTGCCATAAT 300  
TTCTCCTTTC ACTGGTGTG GGNCTTAAAT CAAGTTGAAA TGTATTCTG TACCACAATT 360  
TTANGGCTTT CAATAAAAAG TTTTAAATNG TCTAGGTGAC CATTCCAAA 409

SEQ ID NO:3123  
SEQUENCE LENGTH:400  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03690

SEQUENCE DESCRIPTION:  
GATCAACATC CACAGCGAGA CCTCCGTGCC CGACCATGTC GTCTGGTCCC TGTTCAACAC 60  
CCTCTTCTTG AACTGGTGCT GTCTGGGCTT CATAGCATTC GCCTACTCCG TGAAGTCTAG 120  
GGACAGGAAG ATGGTTGGCG ACGTGACCGG GGCCAGGCC TATGCCTCCA CCGCCAAGTG 180  
CCTGAACATC TGGGCCCTGA TTCTGGGCAT CCTCATGACC ATTGGATTCA TCCTGTACT 240  
GGTATTCGGC TCTGTGACAG TCTACCATAT TATGTTACAG ATAATACAGG AAAAACGGGG 300  
TTACTAGTAG CNGNCCATAG CCTGCAACCT TTTGNACTC ACTGTGCAA TGCTTGGCCC 360  
TGNACGNTGG GGCTGTTGCC CTTGCCCCNT TTGGTCCTGN 400

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SEQ ID NO:3124

SEQUENCE LENGTH:400

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03691

SEQUENCE DESCRIPTION:

GATCCTTCCT ACTTTGCTTC TNTCCACCCA TGACCTTTT NACTGTGGCC ATCAGGACTT 60  
TCCCTGACAG CTGTGTA CTGTTAGGCTAAG AGATGTGACT ACAGCCTGCC CCTGACTGTG 120  
TTGTCCCAGG GCTGATGNTG TACAGGTACA GGCTGGAGAT TTNACATAG GTTAGATTCT 180  
CATTCACGGG GNNGGTTAGC TTTAAGCACC CTAGAGGACT AGGGTAATCT GACTTCTCAC 240  
TTCCTAAGTT CCCTTCTATA TCCTCAAGGT AGAAATGTCT ATGTTTTCTA CTCCAATTCA 300  
TAAATCTATT CATAAGCTT TTGGTACAAG TTTACCATGN TAAAAAGGAA ATGTGATTTT 360  
GGTCTTCCCC NTCTTTTGCA CTTTTTGGA ATANAGGGTN 400

SEQ ID NO:3125

SEQUENCE LENGTH:397

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03693

SEQUENCE DESCRIPTION:

GATCCTNAAT TTNAATAATTT NACACCATCA TAAATNAACA AAGGTAGGAA GGAGTTTGGC 60  
TTCAATAGCT TACAGTAAAA GGAGTAAAGG AGTTCAGCCT CAAAACGATA TTGTTGACCT 120  
GTNATGTTAT GAAAAATAAT CCAGTGTTTA TACTTAACGG ATGCCATCCC TTATNATTTA 180  
CTATTTTCTT AGTCTAACTA AACAATCTTT ATTAATAATA GCAATGATAT TTGACATGGG 240  
CCTAAGAAAT ATATAGTTAG CTAACAATAT TGTCAGTTAG AGGGATTTCT TTTCTAAATT 300  
AAGTACAGAT TTCTTCACCA AACTCCAGGN TAACAGAAAN GGGGCCATAA AATTTGGNCC 360  
ATAGTTTCTG GGTTAAATAA NTGGTAATTT TAAANTN 397

SEQ ID NO:3126

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03694

SEQUENCE DESCRIPTION:

GATCAAGTAA CATGTTGCAT GTGGCTTACT CTGGATATAT CTAAGCCCNT CTGCACATCT 60  
AAACTTAGAT GGAGTTGGTC AAATNAGGGA ACATCTGGNT TATGCCTTTT TNAAAGTAGT 120  
TTTNTTAGG AACTGTCAGC ATGNGTNGT TGAAGTGTGG AGTTGTAAT NTGCGTGGAC 180  
TATGGACAGT CAACAATATG TACTTAAAG TTGCACTATT GCAAAACGGG TGTATTATCC 240  
AGGTACTCGT AACTATTTT TTNGTACTGC TGGTCTGTA CCAGAAACAT TTNCTTTNAT 300  
NGTNACTNGC TTTTNAACT TTGTTTAGCC ACTTAAATC TGCTTATGGC ACAATNGCC 360  
TCAAAANTCCC ATTCCCANGT NGGTAATATT GN 392

SEQ ID NO:3127

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03695

SEQUENCE DESCRIPTION:

GATCTAAGGA TGACTTGGAC ACACTCCCTG GCACTGAAGA GTCTGAACAC TGGCCTGTNA 60  
 TTGGTCCATT CCAGGACCTT CATTTGCATA AGGTATCAAA CCACATCAGC CTCTGATTGG 120  
 CCATGGGCCA GACCTGCACT CTGGCCAATN ATTGGTTCAT TCCAGGACAT TCATTGTCAT 180  
 AAGGNGTCAA ACCACAGCAG TCTTGGATTG GCTGTGAGCC AATTCACCTC AGTNTCTAAT 240  
 TGGCTGTGAG TCAGTCTTTC ATTTACATAG GGTGTAACCA TCAGGAANCC TCTACAGGGT 300  
 ACTTAAGCCC CAGGATGATT TTGGCTTACC CGGGNGTTTC TTGNGGCCNC TTTGGTNTTG 360  
 GCCNAGTTNC NCACCTTTGT GGAATTGGT N 391

SEQ ID NO:3128

SEQUENCE LENGTH:389

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03696

SEQUENCE DESCRIPTION:

GATCTCGGCT CACTGCAACC TCCACCTCCC GGGTTCAAGC GATTCTCCTN CCTCAGCCTC 60  
 CTGAGTATCT GGGATTACAG GCGTGACCA CCATGCCTGG CTAAGTTTTG TGTNTTTTTT 120  
 AGTAGAGATG GGTTCACACC ATATTGGTCA GGCTGGTCTC GAACTCCTGA CCTGTGATA 180  
 CACCTGGCCT CAGCCTCCCA AAGGGNNGGT GCCACGCGC CTGGCCCATT TTTCTTTTTT 240  
 TTGACCCATA CTTAATGTTG CAGAACTAT TCTTGTGATA ACATTATCTC TCATGTACAG 300  
 TAATTATATG TAAATTAATT GAAGCAAATN TGGGAAACTT TACAATAGAA ATAAAGNTAG 360  
 GCAGCCAGCG TNTGTTTCCA NTTNTNAAA 389

SEQ ID NO:3129

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03697

SEQUENCE DESCRIPTION:

GATCTCGGCT CACTGCAACC TCCACCTCCC GGGTTCAAGC ATTTCTCCTG TCTCGGCCTC 60  
 CCGAGTAGCT GGGATTACAG GCGTGAGCAC CATGCCAGC CAGAAGTACT ATNATTTCTT 120  
 ATAACATACAT ATGAATCTAA AATTATCACA AAAGGAAACT TCTTTTAAGA AAAAGAAAAG 180  
 AATCAGAACA TAAATATACA GCATGGCAAA ACTACATCTA AAACAAGTAT TATAGGTCTC 240  
 ATGGTGGAAG ANTTGGACCC ACAAGAAAAG TTGTTAATTA TCTCTGATAT TCTGAACCAT 300  
 TGNTATCTGC AAAATGATTA CTAGGTATGT GCAATGANGG CTATTGATGT TACCCTGTAT 360  
 ATCTGCACAC TGTGTTCCAN 380

SEQ ID NO:3130

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03698

## SEQUENCE DESCRIPTION:

GATCTGCTAG TGCTGTAATA TTGTAAATAC TGGACTCAGG AACTTTTGTT AGGAAAAAAT 60  
 TGAAAGAACT TAAGTCTCGA ATGTAATTGG AATCTTCACC TCAGAGTGGA GTNNNNNCTG 120  
 CTATAGCCTA AGCGGCTGTT TACTGCTTTT CATTAGCAGT TGCTCACATG TCTTTGGGTG 180  
 GGGGNGNGAN GANGAATTGG CCATCTTAAA AAGCGGGTAA AAAACCTGGG TTAGGGGTG 240  
 TGTTACCTT CAAAATGTTT TATTTAACAA CTGGGTCATG TGCATCTGGT GTAGGAAGTT 300  
 TTTTCTACCA TAAGTGACAC CAATAAATGT TTGTTATTTA CACTAGTCTA AA 352

SEQ ID NO:3131

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03699

## SEQUENCE DESCRIPTION:

GATCGTGGGT TGCCGAGAGG ACCTGAGCGC TGGGCTCTG CTGAATGGAN CCGGGTCCCT 60  
 CAGGCCGTGG ACGCCCTCGG AAGGGGGGTG ACTGTGGCTT GTNTCTGGAC AGGAATGTGT 120  
 CATTTCCACAT ATCTTCTAGA GGGCTGCCAG CTGGGAAGAC AGTTATNAGG GCAAGCTGTG 180  
 CTCTGAGTTT CGGGTTCTGC TCCTACAAAG AACGTGCGGT GCTGCGGGCN AGGGCCCCGG 240  
 CACGGACAAG GGCCACTGCA GAGTGTGTTT CTNCTCGTNA GCTGCCCTGG GCANGGAATG 300  
 GGCTGGNTNA TGCAGTTGGA TGCACATCTN ATTCTGTCAT GAATGTCCAG TAAAAAATCT 360  
 GAAATTGGTT GCAAA 375

SEQ ID NO:3132

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03701

## SEQUENCE DESCRIPTION:

GATCCAAACC AAGGGCAAGG GCATCCTGGG AAATACCATC AAGTGGAAGT TCACCAAGTN 60  
 CCTCATNGAC AAGAACGGCT GCGTGGTGAA GCGCTACGGA CCCATGGAGG AGCCCTGGT 120  
 GATAGAGAAG NACCTGCCCC ACTATTTCTA GCTCCACAAG TGTGTGNCC CGCCGAGCC 180  
 CCTGCCACG CCCTTGGAGC CTTCCACCGG CACTCATNAC GGCCTGCCTG CAAACCTGCT 240  
 GGTGGGGCAG ACCCGAAAAT CCAGCGTGCA CCCC GCCGGA GGAAGGTCCC ATGGCCTGCT 300  
 GGGNTTGGCT CGGCGCNCCC ACCCCTGGCT ACCTTGTGGG AATAAACAGA CAAATTAGCC 360  
 TGCTGGAAG 369

SEQ ID NO:3133

SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03702

## SEQUENCE DESCRIPTION:

GATCTTGGGA AAATTGCGGA GTGTACATTT ACAAAGATGC GTTCAAATAG TGCTCTAAGA 60  
 GTTTTGTCA GTGGCTCACT TCGGCTAAAA TGCAGAAATG NATGCTGTCA GCGTTGGTAT 120  
 TTCACATTCA ATGGAGCTGA ATGTTGAGGA CCTCTTCCCA TTGAAGCTAT AATTTATTG 180

GACCAAGGAA GCCCTGAAAT GAATTCAACA ATTAATATTC ATCGCACTTC TTCTGTGGAA 240  
 GGACTTTGTG AAGGAATTGG TGCTGGATTA GTGGATGTTG CTATCTGGGT TGGTACTTGT 300  
 TCAGATTACC CAAAAGGAGA TGCTTCTACT GGATGGAATT CAGTTTCTCG CATCATTATT 360  
 TGAAGAN 367

SEQ ID NO:3134  
 SEQUENCE LENGTH:366  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03703

## SEQUENCE DESCRIPTION:

GATCAAGAAA TGCATTGACA TTCTAATTGA GAAAGAATAT TTGGAGCGAG TGGATGGTGA 60  
 AAAGGACACC TACAGTTACT TGGCTTAACC CTTCTGGAAG GGTCTGACTG TGTGACCCGC 120  
 AGCAAATAGT TCATGTTGGA AAGAATGAAA ACAACTCAAG TTCATAGCAG CCAGCCTGCC 180  
 GCCATTGGAC CTCCTTTTAA AAAACTGAGA CCAAGACTCC CATCAGCTGG TCTCGGGTTT 240  
 ACATCGGAAC TGCTCAGGAT TGATACATTT NAAGTCTGTA AATACGGACA CCAACGCCAT 300  
 TTACCCTAAT TTNANGAACA GCGGGGNCCTG TCCNTCCGGT GCCGAGGGGC TTGCATTGCT 360  
 TACCGN 366

SEQ ID NO:3135  
 SEQUENCE LENGTH:364  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03704

## SEQUENCE DESCRIPTION:

GATCCCTGAT TAAGCTGATG ACTAGACCTA CAATTAATTT TCCTGCAGTA TATGAAGTAT 60  
 TGTACCAGAG TATTAAAAGA TATGTAATAT TTNATTGATA AATCTATCCT TTTAAAGGAA 120  
 TACGTTTTAG GATGTCATCA TTTTGATGTG AATCATGTAA ATGTTGATAA TATGCTGTTT 180  
 ATTATACATT TAGTGTTTCA AGAGATTAC TTAATTGCCT TTTTGCCAC GTATATTATG 240  
 TAGTCTATTT GCAACTGTTC TTAAAAAANT GNCATTAAAG GACTAGTTTA TGNGGGAAC 300  
 CATTAGTGGN TGTTATTNGN CTCCCCCCT NTNTTTTGG GGTGTTAGCG CACCTGCTTT 360  
 GCTN 364

SEQ ID NO:3136  
 SEQUENCE LENGTH:363  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03705

## SEQUENCE DESCRIPTION:

GATCCTGACC AGCAAGCCCC CCCCAGCCC CCCTTCCAAG TGAAGCCGTG NCTTGAGTGT 60  
 GTCTGCGTGT TTACACCCGT CCCTCTGCTG GCCGCCCCCG TGCGAGCGGC ACCCCTGCCC 120  
 TGCCCTCCAC AGAATTGGGT TCCAAGGGCT GTTCCAGACA ACTGCCAAG TCACTGAGGG 180  
 CCCTGCCCCA GCGGNCCTGG CCCCAGGCTC TATTAACCTA AAATGTAGCT CCCTAGCGNT 240  
 AACCTAGGAA CCGGCGTTGN CTGCTTGGGG GGTACGCCC TCATGNCCTT GTTCCCAGGG 300  
 CCGGGGGCCT TNAAGCGGTT NGAACAATTC NTTGGCTTTT TTTCANANTG TTTAATNGGA 360

ATN

363

SEQ ID NO:3137  
SEQUENCE LENGTH:359  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03707

## SEQUENCE DESCRIPTION:

GATCTGGTGG TCAGCCCTAG GATAAAAAGC CAGGGCTGGA GAACAAGAAA GGGCCAGGAG 60  
ATGGAATTCC TTCAGGCCGG CACCCACACC CTAGGACATG TAAGCCCTCA TGTCCAAGGG 120  
AGCCTCATGC AGATAGTAGG AAATCAGGTC TGGAAATTTA AAANTAAAAG GCATGAGACT 180  
AAGGCTATCT GCTTCCNTTA TGCCCTGACT GGAGAGGGGA GGGTGGAGAG GCANGGCCCA 240  
CAGTGGGCAT CCCNGCTNGG TCTTNGGATG NCTGCNGTGN GGTGAATTCC CGGGAAC TNG 300  
TTTTGGCACA ANGNTNNTTT TTGGCACTTT GTTTTTTTTG GTATTTAAAG GTTTTGCTN 359

SEQ ID NO:3138  
SEQUENCE LENGTH:358  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03708

## SEQUENCE DESCRIPTION:

GATCAGGGGA TAGTGAAGTT TACCAACTGG GTGATGTCAG TCAAAAGACA ACATGGCACA 60  
GAATATCAGT ATTCCGGCCA GGCCTCAGAG ACGTGGCATA TCAATATGTG AAAAAGGGGT 120  
CTCGAATTTA TTTGGAAGGG AAAATAGACT ATGGTGAATA CATGGATAAA AATAATGTGA 180  
GGCGACAAGC AACAACAATC ATAGCTGATA ATATTATATT TCTGAGTGAC CAGACGNAAG 240  
AGAAGGAGTA GAAAGGATGA TTCTTCTTTG GCCATCATTT GGTACAGTCT CATTTCCAAG 300  
TCATGTATAA TCTTTATGGC TTCCAGGGAC ANGGNTTTAA AATACTCTTT TACGTAAA 358

SEQ ID NO:3139  
SEQUENCE LENGTH:356  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03709

## SEQUENCE DESCRIPTION:

GATCTCAGTC TCTCTGTCTC TCTTTCTCTC CTTTTCCTTT TGGTGTATCA AATATTTNAT 60  
TGACAAAGTA AGGGCCTTGA TTAGGACCAA ATTCTCGTGT GTTGCTATGG TCTTTATTTA 120  
GGACAACAAT TAACAATGCA GTGGCCCATC CTTGTCACTC TACACATATG ACTATACGGG 180  
ACATATGTAA TATATAAATA TATATATAAA NCATTCCCCT CTGTCCCCTT GGCTTCGGAT 240  
GGAGGCCTTT CTGTTGAGCT GAAATGCACC TGCAGCTGGG TGCTGCCAGC AGCTTG CAGG 300  
CCCCAGCCCT GTTCCANTCA ATGCAGTTGN CAATAANTGG NATGAGTATC GTCAAA 356

SEQ ID NO:3140  
SEQUENCE LENGTH:354  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear



CLONE:HUMGS03710

SEQUENCE DESCRIPTION:

5 GATCTTCAGC ATGTGCGGCC TCATGCTTAA GCTGAAGTGG TGTGCTTGGG TCGCTGTCTA 60  
 CTGCTCCTTC ATCAGCTTTG CCAACTCTCG GAGCTCGGAG GACACGAAGC AAATAATGAG 120  
 TAGCTTCATG CTGTCCATCT CTGCCGTGGT GATGTCCTAT CTGCAGAATC CTCAGCCCAT 180  
 GACGCCCCCA TGGTGATACC AGCCTAGAAG GGTACATTT TGGACCCTGT CTATCCACTA 240  
 GGCTTGGGCT TTGGCTGCTA AACCTGCTGC CTTGAGCTGC CATCCTGGAC TTCCCTGAAT 300  
 10 NAGGCCGTCT CGGTGCCCC AGCTGGGATA GAGGGAACCT GGGCCCTTTT NCTN 354

SEQ ID NO:3141

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03711

SEQUENCE DESCRIPTION:

20 GATCTTGATG AGGGCCAAC TCCCTCTTC CACAAGGGAT TAATCTTAGA ACTATAGCCA 60  
 ATTTATTATA AGTACTATTT AGCTACTCTG TGCTCCACAC ATCACGGAGT AATATCTTCA 120  
 AACTATGAGG TTAGTAACA CTTGACTGCT GAGGTTTATT TCCTCAGCTC TGATGCTTCC 180  
 TGGGTGAAGA TGTAAGTNAT TAAATTAAC CAAATTTTAA AGCTAACACT TCATTCCATC 240  
 TAGACCAGGT AGCTCGTCAT TTGTACGTCT GATAGGTGCT TCAACATCTC AGAATTGGCT 300  
 TTATTTTCA TGCATTGCAT ATTGTACTCN TTTGTAATAT TGGGNATGTA AN 352

SEQ ID NO:3142

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03712

SEQUENCE DESCRIPTION:

30 GATCTGACCA CTGTTCTCCA GCAGGCCTCT GCTGCAGCTT TTNCTCTCAG TGTCTGGCC 60  
 CTCTCCTCTC TTGAAAGTTC TCTGCTTACT TTGGTTTTC CTCTGCTTGT AAAACATTGA 120  
 GTCCCCCTCC TGCCCTGGTT AATTGACTCA CACCAGCTGT GCGATGCCCG CTTTACAAT 180  
 35 TAAAGGAAAA CTGTTTGTG CAGTGTCAAC TTGTCAGCAA CACTGTGTCC CTTGCCCCCA 240  
 CCGTTCTTCT CTGCTGCATT TGGACATGAG CCAAATTTGA ACCCAATCAA ATATAACGTG 300  
 TCTGACACTG ATTTGTNTT TACTCAANTA AANGTATAGA CTACAGAAA 349

SEQ ID NO:3143

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03713

SEQUENCE DESCRIPTION:

40 GATCTGTTCC AGCTGCAGGT GAACACCCTA CGACGTTATA AACGACACTA ACAAGTTGCA 60  
 GACCAGACCA GGCTTCAATA AGGCCAGTT AGCAGAACT GTGAGTCGAC ACTTCAGGAA 120  
 CATACCTGTG AATGAAAAAG AGACCTTGC CTACTTCATC TACATGGTGA AGAGTAACAA 180  
 50 GAGTAGACTG GACCAGAAAT CGGAGGGNGG CAAGCAGCTT NAGTGAGGAT GAAGCACATC 240

TTAAAGGAAT GAAGTGTAAT TGCTTGATGC ACAGGTNGAT ATCTACTACA TTTAAGCCCA 300  
TAAAGACTGT TTAAATATTA TTGTAAATAA AAAAGTTTGT ATGATTGN 348

5 SEQ ID NO:3144  
SEQUENCE LENGTH:348  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS03714

## SEQUENCE DESCRIPTION:

15 GATCCAGATG CAGAGGCCAG GATGTGGGCC CAGCCCTGTG CCAGGAGGCT NGCTGGAATA 60  
AAGGGATGGG CAGGCTGGCA TGGGGGCAGC CGCTGCCCTT GCCTNNNTGT TGCTGTGTAT 120  
TCCTGCCGGC CAGGGGCCAC TGCCAGGACC ACGCCTCCCT TTTNATATCC CGATTCTTAA 180  
GTTCTGCTAT TGTGGTATTC TGGTGGAGAA AAAAGAACCG CGTGGCTGTT TTTNAACTGC 240  
CTGGAACCTA AGACCCTGAA TTCTTTTCCC CCCCAGGGG AAAATCTATA TGGAAANCAT 300  
TTATTTTAAA ATACAGGATG AAGTGAATTA AAAGATTTTA AATGCAAA 348

20 SEQ ID NO:3145  
SEQUENCE LENGTH:379  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03715

## SEQUENCE DESCRIPTION:

25 GATCACACCT GAGCTTATGC TAAAAGGTGG GATGACTCAG AGCTGGGGCT GGTCACCAGA 60  
CAGACTGACC ATGTGATTAG AGGTTTGAGG CTTTGAGTCA GCCTGACCTA TGGGGCGGGG 120  
GACTGGAGGC TGAGTTTAAAT CATCTGGCCA GTGCTTTAAT CAGTACATCA TGAAACCCTA 180  
30 ATAAAACTC TGGACACTAA AGCTCAGCAT AGCTTCCTGG GTGGTGAAGC TGTGGCTATG 240  
CCGGCAGGGC AGTGTGCCCT AATTCCACGA AGAGGGGGCA TGGGAGCACT GTGCTCAAGA 300  
CCCTTCCAGA CCTTCCCTG TGTCTTCCTT GGCTTGTGGA GCTGATTGT ATCCTTTATA 360  
ATAAACCTAA TCATAAGGN 379

35 SEQ ID NO:3146  
SEQUENCE LENGTH:371  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03716

## SEQUENCE DESCRIPTION:

40 GATCTGACCT GTGACAAGTC TGTACTATCC ACTATGTAAT TGGCTCACAA GTCAATTGCA 60  
AACAACCTGA ATGTACAAAT CTTAGTGCTG GTGCTGAAAT CTCTTCAGAA TAGTNATCAT 120  
GATTTAAAAG TTTGTTTTAA AATTTGCAAG CATCAAGTGT CAATCAAAAC TGAAGATGAA 180  
45 AACTAATGA ATGTTGAATT CTCATGCTTT TAGGTGTACT TCCTTTTATG AATTTTCAGT 240  
TTTCTGCTAT TTTTACCGTA ACTATTTTCGTT TTAANTTGG TTTCATTTAN GTTTCCTACA 300  
TGCTAACTTC GTTTGTGCGN TTGANTAAAN TTGCCGGTAT ATATNTGGTG GCCTTGTGTTG 360  
TGACACTTTG N 371

50 SEQ ID NO:3147

SEQUENCE LENGTH:346

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03717

SEQUENCE DESCRIPTION:

GATCACAGGC AAACCCATCA AGCTGACTCA GGTGGAACAC GAAGCTGGCA NNTAAGTGG 60  
 ACATGGATGG GGC GGGAACC ACCCCAGCC CAGGGCTGCA GCCTNNCCCA CCTNACCTTC 120  
 CCGCTGGACT ATNACCTTAA CCAGCCTTTN ATCTTCGTAC TGAGGGACAC AGACACAGGG 180  
 GCCCTTCTTT TCATTGGCAA GATTCTGGAC CCCAGGGGCC CCTAATATCC CAGTTTAATA 240  
 TTCCAATACC CTAGAAGAAA ACCCGAGGGA CAGCAGATTC CACAGGACAC GAAGGCTTGC 300  
 CCCTGTAAGG TTTCAATGCA TACANTAAAA GAGCTTTATC CCTAAA 346

SEQ ID NO:3148

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03718

SEQUENCE DESCRIPTION:

GATCTNCTGC CGAGTGAATG GGGAAAGTGNT CCAGAGCGGC AACACCAAAT AGATGGTATT 60  
 CAAGACAGAG GACCTGATAG CCTGGGTCTC CCAGTTTNTN ACCTTTNACC CAGGGGATGT 120  
 NATCCTAACT GGGACCCCCC CAGGTGTCGG TGTATTCAGG AAACCTCCTG TTTTNTCAA 180  
 GAAGGGGGAT GAAGTCCAGT GTGAGATTGA NGAAGTAGGT GTNATCATCA ACAAGGTGGT 240  
 GTGATGGCTC CTGCACAGGC CCTGCACATA GGTTGAGGGC ATCTGCTCCC ACTNAGCCTA 300  
 GCCCAGGGAA AGGCCANTG ACAGGNTGTG GACAGGTTGC CAGN 344

SEQ ID NO:3149

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03719

SEQUENCE DESCRIPTION:

GATCTTTGAA GTCTATTTAA ATATTCATTC CATTACATCT AGACTCACCN AGAACTACAT 60  
 GTTATGATGT TAAGTTGAAG TTGAAACATG ATGTTTTCGA TTAAATTTAA GATATGCAAA 120  
 TTTATGTAGA GAAAATAAAT GTTATATACC CTATAATCTT TCACCTAATT AGTATTTAAT 180  
 TATATGGATT TGNNTTATAT TATAAAAGAT GTTTTGATTT TGTCTNTNGA TATTGNCAAA 240  
 ATTGTTTGGA TATNCTTATG TTCTCAAGTC TGTATCTGCC TCCCCTGCCT TATNTCTNAT 300  
 GTTTTGCCAC AGTTAACCCA TTGTGCTTCT TTGTAATCAA N 341

SEQ ID NO:3150

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03720

SEQUENCE DESCRIPTION:

GATCTNATCA GTCCTAAGCG GGTCATGGGG CAACACGGTT AGCGGGGAGA GCACGGGGTA 60

EP 0 679 716 A1

GCCGGAGAAG GGCCTCTGGA GCAGGTCTGG AGGGGCCATG GGGCAGTCCT GGGTGTGGGG 120  
 ACACAGTCGG GTTGACCCAG GGCTGTCTCC CTCCANAGCC TCCCTCCGGA CAATAAGTCC 180  
 CCCCTCTTGT NTCCCACCCCT NAGATTGGGC ATGGGGTGCG GTGTGGGGGG CATGTNCTGC 240  
 CTGTTGTNAT GGGTTTTTTT TCGGGGGGGG NTTGCTTTTT TNTGGGGTCT TTGAGCTCCA 300  
 AAAAATAAAC ACTTCCTTN AGGGAGAGCA CACCTTAA 339

SEQ ID NO:3151  
 SEQUENCE LENGTH:337  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03721

SEQUENCE DESCRIPTION:  
 GATCCTCTCC CTGGGATAAG CACTCCCAGC CCGTTTATC AGAAACACAG GCAAGGAAAT 60  
 TGGAACTGCC ACCCAGCCCA GCATGATGGC TCAATTGGTT GGTTCGTTG TNAGTTGTCT 120  
 CTNGTTTTG TTAAGNNTT TAATAAGTA CGTTTTGCAT AATTGCCTT AAATGGTTT 180  
 TAATATTTGT AACGGTTTTA GCAGCCTATA ACTTTTCAGC TGGTGCTTT ACTTAGGGNA 240  
 AAAACAATT TGTAATACA GNACATTGT TAAAAGGCAT AACCNTAGAA CATAGCTTCC 300  
 TGTTTGTGG ATTTGGTTTC CTNTATATTC AAAGTAN 337

SEQ ID NO:3152  
 SEQUENCE LENGTH:336  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03722

SEQUENCE DESCRIPTION:  
 GATCAGAGGC AGACAATGAC GAGTGAAGAT GGTGTAAAG CCCTCTTCAT TCCTGGAGGA 60  
 GCCTGCATCT AATCTNTAG GCCCTCTTC TCTGTGGTC TCATGAACAG CAGTGGGGAC 120  
 CATTGAGNAC TTGAATGGCC TGTTGTNTA TGGGCTTGA AAGGACAAGC AGAGTTCACA 180  
 GAGCTCAGGA TAGAAACATC AGAGCCTCCT CCACGGGCTT CAGTGNAACT CCGATGAACT 240  
 GTACCTGAGG GAATTTTTT NTAATCAAC CCCTTGTGTG GATGAATACA GGACCACAAA 300  
 ANTTNGTNTA CGTTGAAAA AAAANAANNT NTNNNN 336

SEQ ID NO:3153  
 SEQUENCE LENGTH:334  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03723

SEQUENCE DESCRIPTION:  
 GATCTGCATT CCGACTGCCT ATNAACGGGT GTGGGGGCCG GGGGCTGGAN TTGCTGAAGT 60  
 NTTCAACTTG CACTCGGAGC TCCTTNATA CCTCAAAGCT GGCTGTNAGG TGGCAGCTCA 120  
 CACCCAGACT CACTGGCCAC ACCTCAGCAG GGGGGGAGTC GAGTGTCACT NTCTTTCTGT 180  
 GAAGGCTTTT TTTTCTTTT GGCCTGGGAA TTTTCCCAT TTAAATGAAG GGGTTTTAAA 240  
 TTGTTTCATT TTGTGTGCTG TGCTCAAAG CCTTAACTGT CAAATCTTGC ATTATCTNGT 300  
 TTGTACAGAA ATATACTGGC CTAGCAGNGG CAAA 334

SEQ ID NO:3154

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03724

SEQUENCE DESCRIPTION:

GATCAAAATT TGTGACTTG CAGGGCTTTC TTTCTTTTNN TTCAAATTTA CAAGGGTTCA 60  
TTTTGGAAAC TACATTTTAA ACTTTGGAAT CAAATTGTTT CTTATTGGG AGGATAATGT 120  
ATATACATTG GTATTATGTT AAATAATAAA ATTGTNCTAA TTTGGTGCCA TTCCTGAAT 180  
CACAACGTGA TTTTGNATC TCANGCTATT TTCATATGTN ATGTGTCAAT GTATCATCTC 240  
TCAGAAAGGT TTTACANTCC AACATTATA TGTNCTCTGT GTAACGAAT TTNACTTATC 300  
TNTTNTAAAC CAGNAACATT AATTGAGAAA 330

SEQ ID NO:3155

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03725

SEQUENCE DESCRIPTION:

GATCTTCGCA AGCCAGCTTC TTCTGCATCT NAGGGGCTGC TGGCGCCCAN AGGAGGCAGA 60  
CAGATGTCTN NTAGCTGAGT TTCTAACCGC ATGATGAGAC TCAGACCTTC CGCTGCACTA 120  
GAAAATCTGC AACAGTGTCC CTGAGTCACT TCTCCTTAGT GGGCAGACTC GTGTTAGATT 180  
TGTGGAACCC AGCTCTCTGA TTTACTCCTT TTGAAAAACC CATGGAATTT CATGTATAAG 240  
GCTTTCATTT GTATTNNAAG GTTTTCTGT TTGTTTGTAG TATATACATG GTGCTCAATA 300  
GCAACATCTT AGCAGATGAA GCAGTTTATN 330

SEQ ID NO:3156

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03726

SEQUENCE DESCRIPTION:

GATCTACTGC AAATCCTGCT ACGGAAAGAA GTATGGGCCA AAAGGCTACG GTTATNGCCA 60  
GGGCGCTGNC ACGCTTAAAC TGGACCGTGG CGAGAGGCTG GGCATCAAAC CAGAGAGTGT 120  
TCAGCCTNNA CAGGCCTACA ACAAATCCAA ACACTTCTAA ATTTNCTCAG AAATATGGAG 180  
GTGCNGNGAA GTGTTCCAGG NGTGGGGATT CTGTATATNC TGCCGAGANG ATAATTGGAG 240  
CTGGAAAGCC CTGGCACAAA ANCTGTTTCC GATGTGCAA GTGTGGGAAG AGTCTTGANT 300  
CAACANCTCT GACTGNAAAN AGAAGGTGN 329

SEQ ID NO:3157

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03727

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCGGGCGC ACGGNCCGCT TTGGCAAGAG GGGCCTGGCA GTGAACATNN TGGACAGCAA 60  
GCACAGCATG ANCATCCTGA ACAGAATCCA GGAGCATTTT AATAAGAAGA TAGAAAGATT 120  
GGACACAGAT GATTTGGACG AGATTGAGAA ANTAGCCAAC TGAGAAGCTC CACCAGCCAC 180  
TGATGCCAGC CCTGGCACTG CCCCTGCACA GGAGACAAGT GCGTTCAGGG CACAGGCCCC 240  
GACATCACCC CAAGGNAAC GGCACAAGTA GAGAGANACT ACCTACCTCA NTTCANATTA 300  
TGTTTGGCCT TGACAAAATT GTATGCAAN 329

SEQ ID NO:3158  
SEQUENCE LENGTH:327  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03728

SEQUENCE DESCRIPTION:  
GATCAAATTT ACTNGAACAA TTGTTAATTT ATCCATTGTG CTTAGCTTTG TGACACAGCC 60  
AAAAGTTACC TATTTAATCT TTTCAATAAA AATTGTTNTT TGAAATCCAG AAATNATTTA 120  
AAAAGAGGTC AGGTTTTTAA CTATTTATTG AAGTATGTGG ATGTACAGTA TTTCAATAGA 180  
TATGAATATG AATAAATGGT ATGCCTTAAG ATTCTTTGAA TATGTATTTA CTTTAAAGAC 240  
TGGAAAAAGC TCTTCCTGTC TTTTAGTAAA NCATCCATAT TTCATAACCT TATGTAAAT 300  
ATGTNGTNCC TGTTTCCAAT AGGTGAN 327

SEQ ID NO:3159  
SEQUENCE LENGTH:324  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03729

SEQUENCE DESCRIPTION:  
GATCTGAATT TGGACCATT CACTAAAGAG AACATGAGTT TGCTCAGCCC TTTCTCACA 60  
AGAGGGAGGG CCCCAGTTCC CCAGACTTCT CCACGCGCTG GCTCCATAAA GGCCAGCTTT 120  
GGCCAGGCTG CCACAGGGGC CTNAGGAGCT CACTCTGGGC CTACCTGGTT TCAGTTAGAG 180  
GGTCCTCCTG TTATTTTCC ATTTAAAAAG TATGTCCTCA GAAAACTGTA NTGGAAGGAT 240  
GGGTGGCAGG AACTTGTATA GTTCAGCTTC CAACACTTTG GAACAGATTA AAAAGGGAAT 300  
CTTTTAAATA AAAACGTATA NAAA 324

SEQ ID NO:3160  
SEQUENCE LENGTH:322  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03730

SEQUENCE DESCRIPTION:  
GATCTTGGTT TTAATTAAC TATTACTCTA TTAATATAAC CTTGGAATTC TATTCTAATN 60  
ATGTTGTTCT GGCTGCTTGT AGTATCAGTT CGCCCCCTCTT GTTAGGGAGA TATGTAACAA 120  
TCTGTCATTT AATTGAGCAG TCTTTTTTAC ATAACAGTAA TAGCAAAAAT CCTACCTACT 180  
CAGAATCATC TNCTTAGGTT GTCTCCTAAA TCTGAACAAT ACAGTTGTTT TATAAANTNN 240  
CATTTNGTCT CTTGAGATTN AATCAATTAG AACTCTTTAG GGAGAAAATA AATANTAGAN 300  
GAAANTATAT GCCTCANATT GN 322

SEQ ID NO:3161

SEQUENCE LENGTH:320

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03731

SEQUENCE DESCRIPTION:

GATCTGACTT TTTTCCTTCT CAAAAGAATC ATACTTGGGA TTACAGGTAC ATTTNATGTT 60  
ATATNATGGA TAAGTGAAAA NTTTTTAAAG GAGATTTTAT ACCTTTTCAC ATTAAAAAAG 120  
GTATTATAT TATNACTTTG TAGTGATTGT CTTAAGAAAA AATATAGCCC AAATGTATAG 180  
TAAATCAGC AGCTCAAGAA GAATTTCTGC TTCTNTTGT AGTTGATGCT TTGTTTTTNC 240  
CTGCAGTCAG AAATTCCTTG TATTTGTCAA ATGTATAATC AGCTTGATT GTTTTTAAAT 300  
TAAAAAATAA TTTGANTAAA 320

SEQ ID NO:3162

SEQUENCE LENGTH:320

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03732

SEQUENCE DESCRIPTION:

GATCTGAAAA NAAACCTTAA TACGCTCATA TGGTTGGAGT GTTAAGTGAA CCTNTGATTT 60  
TTTNAGGGTT TTTNTACGTG TAGGCGTGAA TAGGGGGCAC CCCTTCAAAA CTGTACAAAG 120  
AAGACGACTG TTTTCATTT CCATTTAAAC ATTTTtagcc ACTTCATTTT TATTTATTGA 180  
ACAGGTCAAA TTTGTNTTGT TATTTGTGAG TACAGTACAT TTAaaaaaca TCCTTATCGG 240  
TTATTTTTTT TTCAGTCGGA GTTTGACGTA TAAATNGTTT ATGCTTTTGG TGAATCTCT 300  
TAATAAACTG GTTCTTCAA 320

SEQ ID NO:3163

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03733

SEQUENCE DESCRIPTION:

GATCAGCTAG CTTGATTCTT GTGTACTTTT TTNAACTGT GGGTTTTTCCT AGTAAATTTA 60  
ATTTACAGAA ATNAATGGTA GCATTTAGTA ATCTACAAAG GAAATATCAA AGTNTTTTNN 120  
AAGCCTGTNA TATTCAGTGT GTGCCACAGG ATTGAAATAA ATGACAATGT AATTATGAAA 180

SEQ ID NO:3164

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03734

SEQUENCE DESCRIPTION:

GATCAGAATT CCGATTTGAC GGGCAACCAA TCAATGAAAC AGACACACCT GCACAGTTGG 60  
AAATGGAGGA TGAAGATACA ATTGATGTGT TCCAACAGCA GACGGGAGGT GTCTACTGAA 120

EP 0 679 716 A1

AAGGGAACCT GCTTCTTTAC TCCAGAACTC TGTTCTTTAA AGACCAAGAT TACATTCTCA 180  
ATTAGAAAAC TGCAATTTGG TTCCACCACA TCCTGACTAC TACCGTATAG TTTTCTCTAT 240  
TCTTTCATTT CCCCTTCCC CATTCTTTA TTGTACATAA AGTAACTGGT ATATGTGCAC 300  
AAA 303

SEQ ID NO:3165  
SEQUENCE LENGTH:311  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03736

SEQUENCE DESCRIPTION:  
GATCTAGAGC CAGGCTGGTC AAGACAAGAA TTGGCTGGAA TAGGCTGCTC TTCCCCCATT 60  
CCATCATGTG CTGTCCCCAC CCCTTTGGCC ACCTGGGCTG ACTGTGTCTT AATACCTCAA 120  
GTGCAAGTAT ATAGGAGTAA GAAATNAACA ATGCCTGCCT CTTATACTC ATGCCTACAT 180  
TGTATGACAT CTAGTATGAA AGGGAAACAT TAAAGGAAAA CCCTTGTTTT GCTCTAAAAC 240  
CTGAGGACGG TAAACACTGA GAGTAACCTG GTGCTTGGTT TGAAGTAAAA CACAAATACT 300  
TCCCTTTTAA A 311

SEQ ID NO:3166  
SEQUENCE LENGTH:309  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03737

SEQUENCE DESCRIPTION:  
GATCAAGGGC AATGCCAATG AACATCGGCA TGGATTATAA TTATGCCCTC CTGGAACCTCA 60  
AAAAGCCCCA CAAGAGAAAA TTTATGAAGA TTGGGGTGAG CCCTCCTGCT AAGCAGCTGC 120  
CAGGGGGCAG AATCACTTC TCTGGTTATN ACAATNNCCN NCCAGGCAAT TTGGTGTATC 180  
GCTTCTGTGA CGTCAAAGAC GAGACCTATG ACTTGCTCTA CCAGCAATGC GATGCCCAGC 240  
CAGGGGCCAG CGGGTCTGGG GTCTATGTGA GGATGTGGAA GAGACAGCAG CAGAAGTGGG 300  
AGCGAAAAAN 309

SEQ ID NO:3167  
SEQUENCE LENGTH:309  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03738

SEQUENCE DESCRIPTION:  
GATCTTGATA TGTTTAAACA TTATCATGGC AGGGAAATAT ATAAAGAAGA AAAATATTTT 60  
NACATTAAAC CTTTTCTAAA ANTTGTAAAT AGAAAAATAA TTTGGTTTTT NATCAAGANC 120  
AACACTTATC GTTATGTATT GTGTAGTTA TATTGCCAGT CTGTTGCGAC TGACTCAAAA 180  
AGTTAAATGT TGCCACTGCT GANGATGATT ATGNGCATCG CANACTTTGT TTCTGNCCCA 240  
TTTTGGCAGT TTTNATATAC TCCNTTAAGA TGTGAATGT TACAGGTAN TAAAGTTAAT 300  
ACCTTTAAA 309

SEQ ID NO:3168



SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03739

SEQUENCE DESCRIPTION:

GATCCTTTAC AGAAAAAGTT TTCTGACCTC AATTCTAAAG TAATTGTAGT AGGGAGCTGG 60  
 AGGACTTTCT TTCCTTTTAT GGTAATTTT TGAGCTACAA AAGAGCCTTG CAGAAATGGG 120  
 TGAAGGGATT AANCTTTTAA AAATAAATGC TATATATTAG GAAAATAAAA AATATTTTAG 180  
 AGCCAAGTTA ACAAGTACTT CAGCAAAACA TGCTAGTTT ATGCAGGGGA TTCTGTATTC 240  
 CAAATGGATA CANTCCGACA TATATAAAG AATCAGATTC TTAATATTG ACTCTTATTT 300  
 NGCAAN 306

SEQ ID NO:3169

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03740

SEQUENCE DESCRIPTION:

GATCATACCC AGAATTCAAT GTTTGATATT TTAAGAATGT ATGTTCTAGT GTTTTNNAGA 60  
 GTGAGTCTAC CATCTGTATA AAAACACCTT GGGGGCAGGC AGGGGCATTT AAAAATGTAG 120  
 GACCTATCGT CCAGACTCAC AGAGTGGGGC TCCAGAATCT CCATTTTAA CAAACTCTCT 180  
 TAAGTAATTC TGATGTGTAC CAAAATCAGT GCCATTGGTG TGTGTGTACG TAACTATATA 240  
 CATATGTGTG TGTGTGTATA TATATAATGT GTCATAACCG TAAACAATAA ACAATATCAA 300  
 GNTAAA 306

SEQ ID NO:3170

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03741

SEQUENCE DESCRIPTION:

GATCTGTCAT GTTTAAACCC CCTACTTCTA AGGGAACCTC TCTAATCTCT TATCCTCATC 60  
 CCCAAATAGT GTTTTCTTCC TCTGGGTTCT TATAATNTTG GTATCAATCT CACAGCATT 120  
 AGTGCTTCTT GCCTGGTGTG ACAGTTACCT GTGTGCATGT GCAATTTCTA ATTTCCACG 180  
 CTAGACTGTG AGCTTCCTAA GGCAAGAATC ATGCCTTGTG GGTTCCTGTA TTCCTCATGG 240  
 TGCCAAACAC AGTGCCTTCT ACATTGCAGG CGCTGAATAA ACATTTTAA AGCAAAAAA 300  
 TTNAAA 306

SEQ ID NO:3171

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03742

SEQUENCE DESCRIPTION:

GATCTCCAGT GGTCAAAAGA CATTTACCCT TAATATCAGA CAACATTTAT ATTTTAGTGA 60

AGAAACAAGT TCTCGGGTGG GGAATCTATG TTCTACTCAG ATTTATATGT TTGGAGGAAA 120  
AAAGCCTTTT TTTGTAAAAT ATTTAAATTT ATATANGAAA ATGTTAGAAA AAAATATGGG 180  
GGAGTGTATT ATAAANCCTG CTTTATTTGC CATGGGGCCN GGGGGAGGCC NGGCCTAATA 240  
CTCCTAAAGT ANGTGTTNGG GNCNTNTTT TCTTCCAATC CACCTGGTGC TGTTCNTGT 300  
AANGN 305

SEQ ID NO:3172  
SEQUENCE LENGTH:303  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03743

SEQUENCE DESCRIPTION:  
GATCTCCGGG AGGGACAGAT GGCCAATNTC TCCCCTTCCA AAGCAGGCCG TGCTCCCCGG 60  
GCAGCCTCCC GCCGAGGGGC CCAGCCCCCA ACCCAGGGC AGGGAGGGGC ATCCCTCCCT 120  
GCGGACCTCA GGGAGCGAAC GTGGATGAAA ACCACAGGGA TTCCGGACGC CAGACCCCAT 180  
TTNATACTT ACTTTTCTCT ACAGTGTGTG TTTGTTGTTG TTGGTTTTNA TTTTNTATAC 240  
TTTGCCATA CCACAGAGCT AGATTGCCCA GGTCTGGGCT GAATAAAACA AGGNTTTTCT 300  
AAA 303

SEQ ID NO:3173  
SEQUENCE LENGTH:306  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03744

SEQUENCE DESCRIPTION:  
GATCACTTTT GAGCTCTGAA GCTTTGAATC ATTCAGTGGT GGAGATGGCC TTCTGGTAAC 60  
TGAATATTAC CTTCTGTAGG AAAAGGTGGA AAATAAGCAT CTAGAAGGTT GTTGTGAATG 120  
ACTCTGTGCT GGCAAAAATG CTTGAAACCT CTATATTTCT TTCGTTTATA AGAGGTAAAG 180  
GTCAAAATTT TCAACAAAAG TCTTTTAATA ACAAAGCAT GCAGTTCTCT GTGAAATCTC 240  
AAATATTGTT GTAATAGTCT GTTTCAATCT TAAAANGAAT CAGTAAAGC AAACAAGGGG 300  
TTTAAA 306

SEQ ID NO:3174  
SEQUENCE LENGTH:301  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03745

SEQUENCE DESCRIPTION:  
GATCAGCAAA CACGATAGAG GAGACCAGTC AGTACTTCTT GGAGGGGGCN GGAGGAGAGA 60  
GGAAAAGGGA GGGCGAGAAT NACCACACAA CACAGCCNTT NGACCATGAG CAGAAGCGTC 120  
CGTGGGAAC CCACTGGGGT NGATGGGCTG CCTGCACAGC CCCTGGAGAG GGGGCCAGGC 180  
ACACCCTCAG AGGAGCTGCA ACCCGTGGCC TGGCCTGCTA CATGCCCTGC TTCCACGTGG 240  
NTGCCACGGT GACACANCCA CATTNACCAA TCCCNCCGG GTCCTGGGGA CGNAGNCACG 300  
N 301

SEQ ID NO:3175

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03746

SEQUENCE DESCRIPTION:

GATCAAAGTT GTCATGAATA CTGACTTGGG CGTGGGACCC ATCCGAGATG TGCTGCACCA 60  
 CATCTACAGT GCGCTGTATG TGGAGCTGGT GGTGAAGAAT CCCCTGTGCC CGCTGGGCCA 120  
 AACTGTGCAA AGTGAGCTCT TTCGCTCCCG ACTGGACTCC TATGTTGCTT TTCTGCCCN 180  
 NTTCTCCGCC CGGGCTGGCT GAAGCAACCT ACCTCAAGTN TCAGGAGAAT TCATGTCTNC 240  
 CTGGGGCCCT TCCGAACCTT GTGCCAACTA AGGGCCCCCA NTGTAAGCCC CCGTACCTN 299

SEQ ID NO:3176

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03747

SEQUENCE DESCRIPTION:

GATCTGAATT ACTACAGAAA AATAATTATG TTGCTTGCTT AATNATTCCC AGGAAACTTC 60  
 GTTGTAGGCA TATATTTTAT AAGAGTATTA TACAGTGTTA ACTATGCAAG TAAGTTCTAA 120  
 AATNACACAA TNATCTGTGT AATGTTTTAG TCCAATNACT GTGATTTATT CAACTCTGTT 180  
 CTAAGATTAT CTGGAATTGT CATGCTGCCT CAATTTACAG AAATCTATAA TAGATTTCTA 240  
 TAGAAATGTA TAAAGACGTA GCAGTCATTT TGTGTTTCT AAATAGATAA CATATAAA 298

SEQ ID NO:3177

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03748

SEQUENCE DESCRIPTION:

GATCAGAGTA TGGGTTCTCC ATGTAGCAAT ACTTCAGTGA GATTAAGTAT AAACAGTTTT 60  
 TGGCAAAAAA CAACACAGTC TACTCTTTCT GCTTACAAAG ACAAAGCCTT ACAAACCTCAC 120  
 TATGAAGGTA AAGGGAGGAC AGCTTGCTTC TTTGCCCAGA CATTTACAAA GTTGTTTTTA 180  
 AANCACACTC ATAAGTAAGT TTGGCAAGTT GTTTAAAAAA TGTCTCTTTG TTTTGTACAG 240  
 TTCTGTTAGA TGTTGTNATA TTTTAANAGT TTAATTTANA ANNTTNATT TNGTCCN 297

SEQ ID NO:3178

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03749

SEQUENCE DESCRIPTION:

GATCTNATTA CCTTCACGGA AGGAAGCGGA CGCTCACCAC GCTATGCCCT CTGGTTCTNT 60  
 GTGGGGGAGT CATGGCCCCA NNACCAGCCG TGGACCAAGA GGCTCGTNAT GGTCAAGGTT 120  
 GTGCCCCAGT GCCTCAGGGC CTTGGTAGAA ATNGCCCGGG TAGGGGGTGC CTCCTCCCTN 180

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GAGAATACTG TNGACCTGCA CATTTC AAC AGNCACCCAC TCTCNCTTNA CCTCCGACCA 240  
GTACAAGNCC TACCTGCAGG ACTTGGTGGA GGGNATGGAT TTCCAGGGNC CTGGGTN 297

5 SEQ ID NO:3179  
SEQUENCE LENGTH:295  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03750

10 SEQUENCE DESCRIPTION:  
GATCATCACA TTTCGTGAAT TGAGGCCATG TTCAGGTGCT AAGGAAGTAT GCCTTTNACA 60  
CAGAAGATTG AGAAAATTC CTAGATATAA ATACAGATAA ATCAGACGTT ACAGTGGTGA 120  
CGTAGTAACC ATCATGGCAA TGGAAAGNAG TCCAATTCAT AGCCTAAAAC TTCAAATGTA 180  
15 TTCTTAGGAG TCAGATTTTA CTGAATATTT TACCCACAAT AGCTGCCTAT TTTGTTATAA 240  
TAAATATAT ATAANTNTAT NTCTNNNCCT TCCTTTAANC TGTA AAAANNA NNNAN 295

20 SEQ ID NO:3180  
SEQUENCE LENGTH:295  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03751

25 SEQUENCE DESCRIPTION:  
GATCCCAGCA CTACTTTTTA TTACTGGAGA AATGGGGGGG ATAGAAAATT CTACTTTGAA 60  
TTATTTAGTT TTTTAAAG AGTGGGTTGT GTTTGTNCTT CTCCACCTT TCAGCATTTA 120  
TAGAACATGC TGCCCCACAT ACAAAGTCAA GACCACTTAC TTTATGTGA CACTAGTAGT 180  
TTGGGGTTAA TGTTTTGTGT AAGANCAGCT GCATATGAGT AAAGTTACCC CAACCACAGT 240  
30 GAGGAGGAAG ATGTTACAT ACTGGAAC TGCTGCCAAA TAAATTTTGC CCCTN 295

35 SEQ ID NO:3181  
SEQUENCE LENGTH:294  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03752

40 SEQUENCE DESCRIPTION:  
GATCAGTTAA TGCCTAAGAG TGAAAGTAGT TCTATTGACA TTCCTCAAGA TATTTAATAT 60  
CAACTGCATT ATGTATTATG TCTGCTTTAA TCATTTAAAA ACGGCAAAGA ATTATATAGA 120  
CTATGAGGTA CTTGCTGTG TAGGAGGATG AANGGGGAGT TGATAGTCTC ATAAACTAA 180  
TTTGCTTCA NGTTTCATGA ATCTGTAAC AGAATTTNAT TTTCACCCA ATAATGTTCT 240  
ATATAGCCTT TGCTAAAGAG CAACTNATAN NTTANCCCTA TTCTNTCTGT GAAA 294

45 SEQ ID NO:3182  
SEQUENCE LENGTH:293  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03753

50 SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

GATCCGTGCT GGAAACTCGC AGGGGGACTT TTACATTAGG CAAATCAACA ACGTCAGCGC 60  
 CATGCTGGTC CTCGCCCCGC CGGTGACGTG CCCCCGGGAG TACGTGCTGG ACCTGGAGAT 120  
 GGTCAACCATG AATTCCCTCA TNAGCTACCG GGCCAGCTCT GTACTGAGGC TCACCGTCTT 180  
 TGTAGGGGCC TACACCTTCT GAGGAGCAGG AGGGAGCCAC CCTCCNTGCA GCTACCCTAG 240  
 CTGAGGAGCC TGTGTGAGG GNCAGAATGA GAANGGCAAT AAAGGGNGAA AGN 293

SEQ ID NO:3183

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03754

SEQUENCE DESCRIPTION:

GATCTGTGGA CTTTNAATTT TTTAAGAGAC TTAATCAATT TNATGACTGT ACTACCTGAA 60  
 ACAAAGTGAG AAAGGACAGG TGTATTTTTC TAAGTNATCA AGATAAATCC TTAANAATTC 120  
 AGTCTAAATN AGCAACCAGG AAGGAAAAAT ATATTAAAA CAACAAAAAA GTGGCACATG 180  
 TCCAGGCAGT GTGAGGATTT GCTGTATATA AGTTGCCTGC TTTGTATTNT TNAAATCTCT 240  
 GCATCACTCA TTGGAAGTGC TTCTNAAGAG AGCTGCTCTG TGTTCAGTTG AAA 293

SEQ ID NO:3184

SEQUENCE LENGTH:395

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03755

SEQUENCE DESCRIPTION:

GATCAAGATG ACCAAGATGT ATAAAGGGTT CCAAGCCTTA GGGGATGCCG CTGACATCCG 60  
 GTTCGNTAC ACCCCCGCCA TGGAGAGTGT CTGCGGATAC TTCCACAGGT CCCACANNCC 120  
 GCAGCGAGGA GTTTNTCATT GCTGGAAAAC TGCAGGATGG ACTCTTGAC ATCACTACCT 180  
 GCAGTTTNT GGCTCCCTGG AACAGCCTGA GCTTAGCTCA GCGCCGGGGC TTCACCAAGA 240  
 CCTACACTGT TGGCTGTGAG GAATGCACAG TGTTTCCCTG TTTATCCATT CCCTGCAAAC 300  
 TGCAGAGTGG CACTCATTGC TTGTGGACGG ACCAGCTCCT CCAAGGCTCT GAAAAGGGNT 360  
 TCCAGTCCCG TCAACTTGCC TGCTGCCTN GGGGN 395

SEQ ID NO:3185

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03756

SEQUENCE DESCRIPTION:

GATCAGCACT TNANTCGGAA AGTTGGAACC TCTGACAAGA CCAAGTACTA CCTTCAAGGT 60  
 AATCCGTGGC TTCCCACAAA GTTCCACATT TAACTTCCTC CAAGGAAGGG GATTAAAATT 120  
 TNAAACTAAC TCCCTTCAGT TGAAATCTCG GACCACTNNN NAAAAACAAA ACCATGGTCT 180  
 AATTNTTNC TTTGTTATGA ATTTNTTGAC AGTGGATTGA GCGATACGTG TCAGANCTAN 240  
 GCATTCACT GTAGGCAAAT TGTGTCTTAG TTATCANGTA AATGTACAAA 290

SEQ ID NO:3186

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03757

SEQUENCE DESCRIPTION:

GATCCAGATG ACTGAATTTC AGATAGCATT TTTATGATT CCAACTCATT GAAGGTCTTA 60  
 TTTATATAAT TTTTCCAAG CCAAGGAGAC CATTGGCCAT CCAGGAAATT TGGTACAGCT 120  
 GAAATATAGG CAGGATGTTC AACATCAGTT TACTTGCAGC TGGAAGCATT TGTTTTTGAA 180  
 GTTGACATA GTAATAATAT GTCATTGTAC ATGTTGAAAG GTTCTATGG TACTAAAAGT 240  
 TTGTTTTATT TTATCAAACA TTAAGCTTTT TTAAGAAAAT AATTGGGN 288

SEQ ID NO:3187

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03758

SEQUENCE DESCRIPTION:

GATCCCCAAA AAGTGAATAT CAATGGAGGA GCTGTTTCTN TGGGACATCC AATTGGAATG 60  
 TCTGGAGCCA GGATTNTTGG TCATTNACT CATGCCTTGA AGCAAGGAGA ATACGGTCTT 120  
 GCCAGTATTT GCAATGGAGG AGGAGGTGCT TCTNCCATGC TAATTCAGAA GCTGTAGACA 180  
 ACCTCTGCTA TTTAAGGAGA CAACCCTATG TGACCAGAAG GCCTGCTGTA ATCAGTGTGA 240  
 CTACTGTGGG TCAGCTTATA TTCAGATAAG CTGGTTTCAT TTTTNATN 288

SEQ ID NO:3188

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03759

SEQUENCE DESCRIPTION:

GATCAGCAGC TGTGGAAATA AAGCTTGTA GCCCTCTGCT GGCCACAGTA NAGGAAAGTA 60  
 GCACAAATAG GATACAGTTG TATGTAGTCA TTGGCAACAA TTGCATACAA TTTTACTACC 120  
 AAGAGAAGGT ATAGTATGGA AAGTCCAAAT NACTTCCTTG ATTGGATGTT AACAGCTGAC 180  
 TGGTGTGAGA CTTGAGGTTT CATCTAGTCC TTCAAACTA TATGGTTGCC TAGATTCTCT 240  
 CTGGAACTG ACTTTGTCAA ATAAATAGCA GATTGTAGTG TCAAA 285

SEQ ID NO:3189

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03760

SEQUENCE DESCRIPTION:

GATCTCACCA TTATGACATC CATCCCCCTA GTCACCACA TAGCACATAG AATGATATTT 60  
 TTAATTTGTA AGAGGCCATC CAGGTACTAA GGNCCCAAGG CATACAGATT CACAAAATNA 120  
 ACTAATCTTT TTGCCTCAGA ATACAAAAC ANCAAAANTA TAAAGCTGTA TTTGGACANC 180  
 TANAAAACAC CAACTATCTT CATTGCAATT NGTATTGTAG CAGATGTTCA GCACTATCC 240

TAATCANTGT TATTGTGTTC CANTTTAACT GGGTTAAATG TTTN

284

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SEQ ID NO:3190

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03761

10

SEQUENCE DESCRIPTION:

GATCTCGACT CCCCCCTGGC CACAGACCCC CAGGTCATTG TGTTCACTGT ACTCTGTGGG 60

CAAGGATGGG TCCAGAAGAC CCCACTTCAG GCACTAAGAG GGGCTGGACC TNTGCGGCAG 120

GAAGCCAAAG AGACTGGGCC TAGGCCAGGA GTTCCCAAAT NTGAGGGGCG AGAAACAAGA 180

15

CAAGCTCCTC CTTGAGAAT TCCCTGTGGA TTTTAAAC AGATATTATT TTTNTNATTA 240

TTGTGACAAA ATGTTGNTAA ATGGGATATT AAATAGAATA AA 282

SEQ ID NO:3191

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03762

20

SEQUENCE DESCRIPTION:

GATCTGGAGA AGTAAGATGG CCAAATAAAA GCCTCTACCA ATCATCCTCC CCACAGGAAC 60

ACCAAATTTA AGAACTATCT ACACAAAAAA GCACCTTCAT AAGAACCAAA AATCAGAGAG 120

AACAAGGATA AAGAAGTATC CAAATACAAA GAAAATGTTA TGCAAGTGAC CTTTAGAGAT 180

GTTTTAAAGA TGACAAAATA TTGATGANGA TGGGCCAACA AGTGTTACTG TTACCTCTAA 240

TAAAGTTTCA TCACTAGTTT CACCATGGTT AATTGGAAA 279

30

SEQ ID NO:3192

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03763

35

SEQUENCE DESCRIPTION:

GATCTGCTCA AATGCACCAA CACTGCCAAG TGACTAAGGT AGAAAAGAAA AATAACAGGT 60

ATCGTCATCT GAAGGACAGA TGAATCTTTT TCTGCCCCTT CTTACAATG GAATATAAGG 120

40

AACAATTATG GGATGTCATC AGAATGGATG CCATAGGACC TACAGCTCCC TTTCTNTTTA 180

TTGTNATTAT ACTTTAAATA TGACATTGTC TTTNATGTGT ATGTTCTCTAT ATTTTCAATG 240

TATCTTTTTC CTTCAGTAAA CCTGATATTC AAATAAA 277

SEQ ID NO:3193

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03764

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SEQUENCE DESCRIPTION:

GATCAGAGG AGCCTGTGTT TGTTGGAGGT GTTCCAGAAT CTNCTACTGAC ACCACGCTTG 60

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GCCCCAGCA AACCN TTCAC AGGCTGCATA CGCCACTTTG TGATTGATGG ACACCCAGTG 120  
 AGCTTCAGTA AAGCAGCCCT GNTANGCGGC GCCGTANGCA TCAACTCCTG TCCAGCAGCC 180  
 TGACATGACA NAGCACAGCT GCCCAANTAC AAAGTTCTTT AGNGCAATGN AAGNAACACA 240  
 AAAGCCAGNC CAGGAGGCNC CAGTTNCTTA TTCCTTN 277

SEQ ID NO:3194

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03765

SEQUENCE DESCRIPTION:

GATCACAGAA GCCACTGCAC TCCAGCCTGG GTGACAGAGT GAGACTCTGT CTCAAAAAAA 60  
 AATTAAATAA ATTATTATAA CCTTTCAGAA ATGCTGTGTG CATTNNATG TTCTTTTTTT 120  
 TAGCATTACT GTCACCTCTCC CTAATGAAAT GTACTTCAGA GAAGCAGTAT TTTGTTAAAT 180  
 AAATACATAA CCTCATTCTG ANTAATGTCC CTCATTTTGA CTATAACTGT GCTTGGTTTC 240  
 AAANGCAAAN TTAANCAAAA ATCTCAGTCA AA 272

SEQ ID NO:3195

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03766

SEQUENCE DESCRIPTION:

GATCTCCTGC TGGTCAGTGG GGCGGCGGCA GCACTACCGT GGCCTGGTAC CAGGTGAGCC 60  
 CGCTGGCCGC CCGCCTGCTC TACCCTACC TGGCCTGGCT GGCCTTCGCG ACCACACTCA 120  
 ACTACTGCGT ATGGCGGGAC AACCATGGCT GGCATGGGGG ACGGCGGCTG CCAGAGTGAG 180  
 TGCCCGGCCC ACCAGGGANT GNAGNTGNAC CAGNAGGTGC CATNANGTTT NTAATNTAGT 240  
 GGCCGTNANG TTTTAATGAC CANTGGGNCT GN 272

SEQ ID NO:3196

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03767

SEQUENCE DESCRIPTION:

GATCCCATCT NTTTTCCCTT CTTTCCTCCT GGTTCGGGTC AGTTCAGAGG ATTTAACAAT 60  
 CACAAGTGTC CTGCAAAAAT GCCTGAACAT TATTCTTAGG CCCTCGTGGA TTTTTTTTTT 120  
 CAGAAAACCT AAACAAAAAA NGAATTACTA NGAAATATGT ACAGCTACCC CTGTTTTTCTAG 180  
 GCACTATGTT TGNGANCATT TTNGCCATTG ANGTCACAC GTGGCATCAG CCCATGCAAG 240  
 ATAGGTTTCT GTATTNNTAT ATNANNNTN 269

SEQ ID NO:3197

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



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CLONE:HUMGS03768

SEQUENCE DESCRIPTION:

GATCCAGCGA GGGGTCCAGG CCCTCTGCAT CTCCTCAGGC TCCAACCCTG CTTCTCAGC 60  
AATNAGCTCT CCTCCAGCTT TGGCTTTGGG AAGCCAGACT CCAGGGACTG AAAAGNAGCA 120  
ACAAGGAGAG GGTCTGCTTG AGAAATGCCA GATGCTTGGT CCCCAGGAAC TAAGGCGACA 180  
GAGTGCAGGG TGGGGGCAAG ACTGGGCTGT AGGGGAGCTG GACTACTTTA GTCTTCCTAA 240  
AGGACAAAAT AAACAGTATT TTATGCAAA 269

SEQ ID NO:3198

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03769

SEQUENCE DESCRIPTION:

GATCCCTTGG AGCCCAGGAG GNAGGTGTGT NAGCTCAATC CGGACTGTAN CGAGTTGGCT 60  
GACCACATCG GCTTTNAGNA GGCCTATCGG CGCTTCTACG GCCCGGTCTA GGGTGTGCT 120  
CTGCTGGCCT GGCCGGCAAC CCCAGTTCTG CTCCTNTCCA GGCACCTTC TTTCTCTTC 180  
CCCTTGCCCT TGCCCTGACC TCCCAGCCCT ATGGATGTGG GGTCCCCATN ATCCCAGCTG 240  
CTCCCAAATA AACTCCAGAA GAGGAAA 267

SEQ ID NO:3199

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03770

SEQUENCE DESCRIPTION:

GATCTGAACC TGTCATTGTA AGTACAGGTT AAAGACTGTG TCCACTTTGG GCATGAAGAG 60  
TGTGGAGACT TTTCTTCCCC ATTTTCCCTC CCTCCTTTT CCTTTCCATG TTACATGAGA 120  
GACATCAATN AGGTTCTCTT CTCTTTCTTA GAAATATCTG ATGTTATATA TACATGGTCA 180  
ATAAAATAAA ACTGGCCTGA CTTAAGATAA CCATTTTAAA AAATTGGGCT GTCATGTGGG 240  
AATAAAAGAA TTCTTTCTTT CCTAAA 266

SEQ ID NO:3200

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03771

SEQUENCE DESCRIPTION:

GATCTGACTT GGGGAAAGGG TTATCAGAGC CTAGAGGGGC TAAAAAGTA ATCATTTGAT 60  
GTACATACCA CACTCCTTGG CTTCTTTCT CTTCCCTTAA CCCTTTCTGC TTTTCATTAA 120  
CCACATTCTT GCACAACTCA TTTCTGAAAA CCTACCATGT TTCTTTACAG AGCCATCCAA 180  
AAATTTTTTG TCCCTACATA GCAATTTTCT GTGGCACTGA GAAACCATGT ATGACCACAA 240  
TAAAAATCCA TTTTGTGAAA GGAAA 265

SEQ ID NO:3201

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SEQUENCE LENGTH:262

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03772

SEQUENCE DESCRIPTION:

GATCTCAGCT CACTGCAACC TCTGCCTCCT GGGTTCAAGC GATTATCCTG CCTCAGCCTC 60  
CTGAGTAGCT GGGATTACAG GCATGCGCCA CTATGCCCAG ATAATNTTTT TGTATTTTAA 120  
GTAGAGACAG GGTTTTACCA TGTGGCCAG GCTGGTCTGG AACTCCTAAC CTCAGGTTAT 180  
CCACCCACCT TTGGGCTTNC CAAAGTGCTG GGATTATAGG CATGGANCCA CCGTGNCTGG 240  
NCANAGATGT AAGTNTAAAT TN 262

SEQ ID NO:3202

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03773

SEQUENCE DESCRIPTION:

GATCCACCTG CCTCGGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCAC CATGCCCANC 60  
CACCTTTTCT ATNTTTAGAT ACATAAACAC TCACCACTGT GTCACAGTCA CCTACAGTAT 120  
TCAGTACAGT AGCATATGCT GTACAGGCTT GTAGCCTAGG AGCAATAGGC TATACCATAT 180  
AGCCTAGGTG TGTACACCAT CTAGGTTTTT CTAACACAC TCTATGGNGT TCACACAATA 240  
AAATTGCCCA NCGACGCAAA 260

SEQ ID NO:3203

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03774

SEQUENCE DESCRIPTION:

GATCCCAGCT TATGGCCTTG ACCCAGCCGT CCTCACAGAT GCCGGGTGAC CCTCTAGCTC 60  
TCTCTGCATC TCCCACCCCG CGACACCCTG GGACCCTCGA CCCCACCCCT CTTTCCTACC 120  
AGCCCAGAGC CTTGTGGCTT GTACAGTTTT GAAACTCCCG TTCTATTTTA TGATGGTTGA 180  
TAATAGTCAG TAACNNAATA AAGGAACGTT TGTAAAATA TCAAA 225

SEQ ID NO:3204

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03775

SEQUENCE DESCRIPTION:

GATCTGCCCCG CGGCGNACCC GTGTTATGTT TTGTGCTGTG TCCACGCGCT AAGACGACCC 60  
CCTCCCCCGT ACTGACTTCT CCTATAAGCG CTTCTCTTCG CATAGTCACG TAGCTCCAC 120  
CCCACCCTCT TCCTGTGTCT CAGCAAGTT TTNACTCTA ATATNNNNAT GGCTTTTTTT 180  
CTTCGGCAAA AAAATAATAA AACGTTTCTT CTGAAA 216

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SEQ ID NO:3205  
 SEQUENCE LENGTH:256  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03776  
 SEQUENCE DESCRIPTION:  
 GATCTGACAC TTCCTTTCCA TTGCTTGGCC TGAACAGACT GACCTTGTNA ACTTAAGCCT 60  
 GGAGTCCATG CCTCGTCTTC CTTTGTTC TGTCTGTAC CAAGAAAGCC AAGGAAGAGC 120  
 AGCCTGACTC ATTCTTCTTG GCTGCAGCCT CTTCCCCACT TCCTGGGAGT GACCCAGCGT 180  
 TATTCCTGCC TCCTCACTCC TATTCTCTTT GCCTTTGTGT AAAAATAAAA TGGAAATAAA 240  
 CAAGTTGCAC AGTAAA 256

SEQ ID NO:3206  
 SEQUENCE LENGTH:256  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03777  
 SEQUENCE DESCRIPTION:  
 GATCTCTTTT NATCATATAT GACATTAAGG CTACAGAAGT TTTGTGCAAN AATCTTAATT 60  
 CATATTTATN AATTTCAAGG GAATATTGAA AGGTTTAAA ATGGCATACA GATAATGGAA 120  
 AATAAGCTTT ATGTTTCAAG AAGGGCAGAC TCACGAATTT TTTAGAAAAC AGTGCTTCTT 180  
 AATGATATGC TATTATNCTT ATNAGTTATG TGCAAGCTTT GTATATNCTT ATATNTATAT 240  
 NTAACNTAA CCCTCN 256

SEQ ID NO:3207  
 SEQUENCE LENGTH:253  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03778  
 SEQUENCE DESCRIPTION:  
 GATCCCAATT CGAGAGGTTT TAACCCAGAG ANCGGACATC TCGATTGCAC ACGTTCTGGT 60  
 TGCCCGAGCC GACCTGTCTT GTCTCGTCCC AGCCACCAGC GTGGCTGTGC GNAGAGGGAC 120  
 CTGCTGTGCC ATCAACAAGG TGCTTATGGG NAACGTTCCA TACCGGGGGN GCCGCCCAA 180  
 TNAGCTGGAG CCTCCCATGC CCACCTGGAG NAGCNGAAGA GAGGATGGAG GCGCCCAAGT 240  
 NNGGNNTCGC ANN 253

SEQ ID NO:3208  
 SEQUENCE LENGTH:252  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03779  
 SEQUENCE DESCRIPTION:  
 GATCATGNTT CATGTGCTAA AAATAAACTT GAAACACGGA AGTAGTGGTT GGTCCAGTTT 60  
 GAAAGCTCTT ATNAGTATTC TTCATCCTGG CTGTAATAAT AGCCATNATT TGTNATGCCT 120  
 TTGTTATGTA GCAGACACTC TTAAGNATTT NATGTGTATN ATTCAAATG CTATNACTGT 180

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TCTTTTATA GTTGAGAATC TCAGGATACC TACATTTATC ACTTTTCAA TATATATGTA 240  
TTTCTTATTA AA 252

5 SEQ ID NO:3209  
SEQUENCE LENGTH:251  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS03780  
SEQUENCE DESCRIPTION:  
GATCAAGCTG TCCGAACCTA CCAAGAGCAC AAAGCAAGCA TGCATCCCGT GACTGCAATG 60  
CTGGTGGGGA AAGACTTAAA AGTGGATTAA AGACCTGCGT ATTGATGATT TTAGAGATTT 120  
CTCTTTTTTA AATGGAATTC GTAAAGAAAT ATAAACTTC AGCTCACAAT TAAAACTGTC 180  
15 TTTTtagTTT TGGCTTTTAA TTGTTTGTG GGTGATTTTA CTGAAATAAA GTTGAGCTAC 240  
TTCTTCTTAA A 251

20 SEQ ID NO:3210  
SEQUENCE LENGTH:250  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03781

25 SEQUENCE DESCRIPTION:  
GATCTTGTGT TCAGATGAAA GTGCAAGTTT TTATTAATTT GGATTGCCTG AACAGTGTAT 60  
CCCATGATGA TGAAGGAAAA TGGAGAGATT TTTCTTTTAA ACTCTGNNNN NTCAGAGATG 120  
AAGCCACGCC TTTCCATTTT TCAATGCTGC ATATTTAATC TGCAACAAAA ATGTTAAGCC 180  
ATAACAGCCT TTTTATATTT TAGTTTGTCA CCTTTGCATT GCAGAATAAA TACTGGNTAA 240  
30 CCATTTTAAA 250

35 SEQ ID NO:3211  
SEQUENCE LENGTH:251  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03782

40 SEQUENCE DESCRIPTION:  
GATCTTACTT GCTCCTGCTT ACGAAGATTN CCCAATNACT GGTCATCTGA CCCTACTTGA 60  
ACACTCCTGA ACAGTCATGT TTTTNAAAAT NTTCTTTTAT ATCAAGTCAG AGAGTATACT 120  
TCTATAAATT TNACTCATGG ATGTTAGGAA ATCTAGTCAT CTTCCCTGTG ATTGCCCTGT 180  
TAAGTATTTA ACCATAGCTA TCATGTGTTT CCCAAATCTT CTCTAGATTA AATATCTTCA 240  
GTTACTTCAA A 251

45 SEQ ID NO:3212  
SEQUENCE LENGTH:250  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03783

50 SEQUENCE DESCRIPTION:

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GATCTAGACT GAGAATCAGC CTGAGCTTTA CACAGCTGGG GTCTGTTACT CGCGTTTTGT 60  
 AGACTTTTGT GTAACATTTT GTACCGTAGA CAGAAATGTGA GGAGGAAGTA ACACACAGAG 120  
 GAGGATGTGT GTGTATGCAT GTGTTTGAAT TCACAAGGAA GAAATTATTT ATCTTGAGCT 180  
 TTTTCCTTTG TTATTCAATT TCTATTGATT TATTAGTAAT AACAAATGATA ATAAAAATGTA 240  
 AATGAGCAAA 250

SEQ ID NO:3213

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03784

SEQUENCE DESCRIPTION:

GATCTAACGT GTTCCAGTGT CTGTCTGAGG TGTCTTAAAA AATCAGAACA AAACCTTCTAT 60  
 TATCCAGAGT CATGGGAGAG TACACNCTTT CCAGGAATAA TGTTTTGGGA AACACTGAAA 120  
 TNAATCTTC CCAGTATTAT AAATTGTGTA TTTAAAAAAA AGAAACTTTT CTGAATGCCT 180  
 ACCTGGCGGT GTATACCAGG CAGTGTGCCA GTTTAAAAAG ATGAAAAAGA ATAAAAACTT 240  
 TTGAGGNAAA 250

SEQ ID NO:3214

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03785

SEQUENCE DESCRIPTION:

GATCATAGGT CTGGACACTC CATCCTTGCC AAACCTCTAC CCAAAAGTGG CCTTAAGCAC 60  
 CGGAATGCCA ATNAACTAGA GACCCTCCAG CCCCCAAGGG GAGGATTTGG GCAGAACCTG 120  
 AGGTTTTGCC ATCCACAATC CCTCCTACAG GGCCTGGCTC ACAAAAAGAG TGCAACAAAT 180  
 GCTTCTATTC CATAGCTACG GCATTGCTCA GTAAGTTGAG GTCAAAAATA AAGGAATCAT 240  
 ACATCTCAAA 250

SEQ ID NO:3215

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03786

SEQUENCE DESCRIPTION:

GATCAAACTG CCATTACAG TGTAAGGCAG CACTTAAATT TCGAACCTAA AGTTTAGATG 60  
 CATTGTATAA AAAAACCTAA AAGCAGTATC TGTTNNTNNN GCTGTAAACC AAGTTGGAAG 120  
 CTATTCGGAT AATTCTTAA ATATTGATGA NCTTTGGAGT ACTGTTTCTN CCTTCAAAC 180  
 GAATGTAATT AATNCATGAT TAAATGCACC TNATATGTTT AANCAATCTT TGTATACTTN 240  
 TGGGNTTTTN 250

SEQ ID NO:3216

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03787

SEQUENCE DESCRIPTION:

5 GATCGCCACA CTGCCACTCT GCTGCCCAGC CACCAGGATT TCTGCCTGGA GCCCTTTGCC 60  
CTGTCCCTGC TGCCTGAGGT GGCCTAGAGC AGAGGAGAAG AATTGCTCC AGGCCAGGAG 120  
CACAAATCGT TGTTCATGA ATTTNTCTCC AACTCGACCT TGGTAAACGG AAATNTTGGG 180  
GGTGAAGAGA AACAATCACT ATTTTNTNCT TTTTATCTG GTAAATAATT AAAAGAAAAA 240  
10 CCGAACACTA AA 252

SEQ ID NO:3217

SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS03788

SEQUENCE DESCRIPTION:

20 GATCTGTATT GGATAAGGAC CAATGNACAG CAAAGCAAAA ATGGCTTTAA AGCTTGGTGT 60  
TACTTTTNTT AAGTTGTTTA ATTATAGTTA AGCAATTTCA AAAATGCTCC AAAGAAATGT 120  
GAAAGGACCT TTTGTCACAG CACTTCAGAA AATACACAAC AGCCCCTTCT GCCCCGCAC 180  
AGAAATGCTG CAGAGTATAT AAAACTTGAG ACATTTTGT AGGATGCCTG ACGAGGTGTN 240  
GCCTTTTATC TTGTTTCCGG ATGCATATTT ATTACGAGTA CTCTGGTTAA ATATTGAAAA 300  
GTTATATGCT GTAGTTTTTA GTATTTTGT TTTGTN 336

25 SEQ ID NO:3218

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS03789

SEQUENCE DESCRIPTION:

35 GATCTCGAGT GTTATTTTCT GATTGTGGTG TTGAGAGTTG CACTCCCAGA AACCTTTTGA 60  
GAGATGCATT TATAGCCCTA GGGGTGGTAT GACCCAAAGG TTCCTCTGTG ACAAGGTTGG 120  
CCTTGGGAAT AGTTGGCTGC CAATNTCCCT GCTCTTGGTT CTCCTCTAGA TTGANGTTTG 180  
TTTTCTGATG CTGTTCTTAC CAGNTTGGGA AAAAAGTGTG GATTAAT 227

40 SEQ ID NO:3219

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03790

SEQUENCE DESCRIPTION:

45 GATCTGCATA GAAAATTTN ATACAATTTT TTGAAAGTCC TAGGTGAAA CATTACCCA 60  
TTAAAAAGGA AGCAGAAATA CTGAGACATG AAAGGCATTA TCAACTAACT CTAGACTCTA 120  
GAACCCATTC TNGCATATCT CACGTGCAAT TTTTAAAAAT AAGTTAATAA TTCANCTCAT 180  
ATCAACAAAA GCCTTTGNNA CATGGGTTTN CACTNGATAT CACCTAGTGC TNANGNTAGA 240  
50 NGCCAANN 248

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SEQ ID NO:3220

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03791

SEQUENCE DESCRIPTION:

GATCCAGTGC TCTCCCATCT AACAACTAAA CAGGAGCCAT TTCAAGGCGG GAGATATTTT 60  
AAACACCCAA AATNTTGGGT CTNATTTNNA AACTTTTAAA CTCACTACTG ATGATTCTNA 120  
CGCTAGGCGA ATTTTCCAA ACACATAGTG TGTGTNTTTT GTATACACTG TATGACCCCA 180  
CCCCAAATCT TTGTATTGTC CACATTCTCC AACAAATAAG CACAGNGTGG ATTTAATTAN 240  
GCAAA 245

SEQ ID NO:3221

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03792

SEQUENCE DESCRIPTION:

GATCCACCCG CGTTGGCCTC CCAACGTGCT GGGATTATAG GCGTGAGCAC CACGCCCCGC 60  
CTAAAATCCA TATTCAAAGA AGCAATTTC AATCCTTTCT AAGCTTTGTC AGTCAAGGGG 120  
CTCCACTGAC TTCCTAGGCC CTGTAATTTA ACCAGTCTTT AAGGTTTTGC AGGAAAGTCC 180  
CTTCTTCCAA GTGGTTTTTC CAAATCGCAC AATGGCAAAG CCAAACAGAG GAAGAAACAT 240  
TAAA 244

SEQ ID NO:3222

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03793

SEQUENCE DESCRIPTION:

GATCAGATTG CTGAAACACT ATGGGAACAG GTATTGAAGC CCCTGGGTGA TAATNTAATG 60  
GAGGAAAACA TAAGGCAGTC TGTAACAAAC TCTATCAAAG CAGGCCTGAC TGACCAGGTG 120  
TCTCATCATG CCAGATTAAA GACAGACTGA CAGTTCATCT CCTCACGGAC TCCACTCTCT 180  
TTTTTTTNA TGCTTGCTGT ACAATGAGAA CTCAAATAAA ANTAAACCAA AGTTTACAAT 240  
CAAA 244

SEQ ID NO:3223

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03794

SEQUENCE DESCRIPTION:

GATCCAGGAG GAGCAGCACC CGAGCCCTGG AGTGGCCCAG TACCCTTCCA AGAGGCCACA 60  
GTCCCAGCCA GGACAAAGTA TGCGGCCCAT CCTGGTGCN CAGGTGGGAC AATGTGAACA 120  
TGGACTCGAA GACATGGCCC TTTCTCTGTA GTTGATTTTT TAAATGTGCC ATTATTGTTT 180

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TTAAAAAANN CGGNAAAANG AAANGCANAC AAATAAAACA CCTTTAAGAG GCTTGAANGC 240  
GNCAAA 246

5 SEQ ID NO:3224  
SEQUENCE LENGTH:243  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03795

10 SEQUENCE DESCRIPTION:  
GATCATAACT CATGAATATG TTTGTAATCA TGGTAATTTA GATTTTATG AGGAATGAGT 60  
ATCTGGAAAT ATTGTAGCAA TACTTGGTTT AAAATTTTGG ACCTGAGACA CTGTGGCTGT 120  
CTAATGTAAT CCTTTAAAAA TTCTCTGCAT TGTCAGTAAA TGTAATATAT TATTGTACAG 180  
15 CTACTCATAA TTTTAAAAAG TTTATGAAGT TATATTTATC AAATAAAAAAC TTTCCNATAT 240  
AAA 243

20 SEQ ID NO:3225  
SEQUENCE LENGTH:241  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03796

25 SEQUENCE DESCRIPTION:  
GATCTGACCT TTTTTTCCA GTTGAAATGT ATTAACACAC CTTCCACAAT NATTTTATAA 60  
GAGTCAGCAT AACATAGTGG ATAAGAACTG TGAGATGTTT AACCTCTCAG TAACTCGGTT 120  
CTCTCATTAT AAAATAGGAA TAAATCAGT ACCTGTTTCA TATGAAGGTC GTTCTGAGA 180  
ATTAATGGA CTAATGTATG CAAAAAGCCT GGCAACAAT AAACACTCAT CTGACTTTAA 240  
A 241

30 SEQ ID NO:3226  
SEQUENCE LENGTH:240  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03797

35 SEQUENCE DESCRIPTION:  
GATCAAAATA TATTTGTCCA GAAACTCTTG GGCCAGTTCT CTGAGAAGGA ACTGGCTGCT 60  
GAAAAGAAAC GCATCCTGCA CTGCCTGGGG CTTGCAGAAG AAATCCAGAA ATATTGCTGT 120  
40 TCAAGGAAGT AAGAGGAGGA GGTGATGTAG CACTTCCAAG ATGGCACCAG CATTGGGTTT 180  
TTCTCAAGAG TTGACCATTA TCTCTATTCT TAAATTTAAA CATGTTGGGG AAACAAGAAA 240

45 SEQ ID NO:3227  
SEQUENCE LENGTH:239  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03798

50 SEQUENCE DESCRIPTION:  
GATCCTCCCA CCTNCAGCCT CCCAAGTAGC TGGGACTACA GGCACATGCT ACCATGCCCA 60

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GCTAATTA AAAAATTTT TTTTGTAGA GACGGAGTTT CACTGTGTTG CTCAGGCTGG 120  
TCTTGAATC CTGAGTTCAN GCAACCTCC ACTTCAGCTT CCCAAAGTGC TGGGATTACA 180  
GGCATCACTG GCCCAGGCAG AGCCAATTNT GTATAATAA TCTGTNTCTC TCTGTCAA 239

SEQ ID NO:3228

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03799

SEQUENCE DESCRIPTION:

GATCAAATTT NATTGAATGG TTTGAGGTTG TAGCTCTATA AATAGTAGTT TTTAACATGC 60  
CTGTAGTATT GCTAACTGCA AAAACATACT CTTTGTACAA GAGGTGCTTC TAAGANTTTN 120  
ATTGACATTA ATGACACTGT ATACAATAA NGTGTAGTTN CTNAATCGCA CTACCTATGC 180  
AACACTGTGT ATNAGGTTTA TCATCCTCAT GTATTNTNNT GTGACCTGTA TGTNTATN 238

SEQ ID NO:3229

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03800

SEQUENCE DESCRIPTION:

GATCCAAAGC CATCCCAGAC CTTCCCGGGC CCCTCTTCCT GGCAGATGAC TCTCCCGCT 60  
TCTGCGTCCT GCCTGCCCCT TCATACCAGT TTGAACTGCA ACAGCCTAGC TCCTCACCTG 120  
TGCACCTCCT TCCCCAGGTG TGCACGTCTC CAGCCCCGAG CGCGTGTCTT CCTGCTCATC 180  
TGGGTTTCCT GGGCAAATAG TGGCCCTCAA TAAATNTTGT CTGAGTGAGA ACATAAA 237

SEQ ID NO:3230

SEQUENCE LENGTH:515

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03801

SEQUENCE DESCRIPTION:

GATCGCCAGA GCCCAGGAGT TTGAGGCTGC AGTGAGCTAT GAGGGTGCCT CTTTGCTCCA 60  
TCCTAGGCAA CAGAGTGAGA CGCTGTTTAA AAAGGAAAAA ATCCTTCCNT AGAGCTAGTA 120  
TCCTAAAGCT GCAGAGCTAG CCCATGACCT CATTGGTTTC NTTGTCCTTG GGGTGCTTTT 180  
CCTGAATCTT TGGGGGTGAA GGGAGTNTTG CTCCCAGTCC AGAGGCCTGA TTCTTTTCGG 240  
ACTGGGTTCT CAAGACACGA CCAGGTCTC AAGACACGAG TCCCCTTNTT CCTNCCCATT 300  
AAAGGGGGTT TNTNAGAAGC AAGANCAGCC CCTTTCCCA AGTCACAGCC TGAAGGGAGG 360  
CCCCNGAGAN GCTTCCCTCC TTTCCCNCA CCCTGNTTCC TTAACCTTNT TTTGNCCCTG 420  
NTTTTTTTAG GAANCTGGNA GTTTCAATTN GTTTTAAANG GGGGATTGGG GGGGAAGGGA 480  
AGNCTTNGGG GGACAAAAA NNTTTTNTT NCAAN 515

SEQ ID NO:3231

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03802

SEQUENCE DESCRIPTION:

5 GATCAGTGTA TGCGAAAAGG TTTTtagGAA GTATGGCAAA AATGTTGTAT TGGCTATGAT 60  
GGTGACATGA TATAGTCAGC TGCCTTTTAA GAGGTCTTAT CTGTTCAAGT TTAAGTGATT 120  
TAAAAAATA ATAACCTGTT TTCTGACTAG TTAAAGATG GATTGAAAA TGGTTTTGAA 180  
TGCAATTAGG TTATGCTATT TGGACAATAA ACTCACCTTG ACCTAAA 227

10 SEQ ID NO:3232

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS03803

SEQUENCE DESCRIPTION:

20 GATCACTAGC TAATNCTCAT ATCCATGCCT TTTGTCCTG TTTACAGTCT TAAAAGAGGT 60  
AAAACAGCAA ATATTTTTTN AAGGGAATA TAACCTTAGG ATTCCTGAAA ANAATTTCAA 120  
AAAAAATA AAGACACTGT TGCCAATGTG NCCCAAACT TAAGACCATA CTAATGGCAT 180  
ATATTTGTNA CAATNAAAAA TTAANTTTAC TACTTAATCC TAAA 224

SEQ ID NO:3233

SEQUENCE LENGTH:310

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03804

SEQUENCE DESCRIPTION:

30 GATCGGTGCT TTGTGTAAAT ACATCTTTAA CATTTGGGTG GAGAGGGGCC TTAAGAAGGA 60  
CAGTTCATTG TAGGAAAGCA ATTCTGTACA TGAGTTTAAG CATTCTGTT GCATTGTCTC 120  
TGCAGATTCT ATTTTGTGTT ACAATATTAA AATGTATGTN AGCAAAATGG GTGGATTTTC 180  
AAATAAAATG CAGCTCCAC AAAAGTTTG TNATGGTATT CTGGTCTGAG ATGCATTTNC 240  
ATTTNCCTN TCTCTNTTA TTATCAATAT TGTNATTTT CCCTAATAAA ATATACCCAG 300  
35 GTGNATTAAA 310

SEQ ID NO:3234

SEQUENCE LENGTH:220

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03805

SEQUENCE DESCRIPTION:

45 GATCAAAATTT TTNAGACAAT CCTTGGTCTG GATTGGTTAA TGAAAATNTN TTGTTTAAGA 60  
GGTCTATTA AAAAATATTT CTAGTGTATT AGTCATAATT NTTTTGTGG AGTGGGGGTA 120  
AACCACACCA TTAAGGGAAT AAAATGTAAT TTGAAAGAGG TGATTATAAG ATTTGTTTCA 180  
GGCCCCAAA TATAAATAAA AATTGGTGTG GAATCTCAA 220

50- SEQ ID NO:3235

SEQUENCE LENGTH:219

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03806

SEQUENCE DESCRIPTION:

GATCGATACA GAGCATCTGC ACTGGGATTG TCCGCCCCGC CTGTCAGGGA GGCCTCGGGG 60  
GCTAATNGAG CTGAGGGTAT AGTCGGCCTT GGACCCTCGC TTTTTCCTT TCCTGTACTA 120  
TNAAGATAAC TGCCTTATCT CCCCCTCAGG ACTGTTTTGG GGATTAAATA GGACGTTTAA 180  
ATNACCAACG CTCTTTGAAA TAAACATTTT AAAATTAAA 219

SEQ ID NO:3236

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03807

SEQUENCE DESCRIPTION:

GATCAAAAAA ACTTTTCTTC TTTTGCAAAG AAAGCTTTTT GTTTTAAACN GCAACGTACT 60  
TTTCCCTAC CTTGAAGAGA CATGGTGGTC GCAGCTTCTN ATCTATATGA AAAAGTTTTT 120  
GATGTATTGG AATNATTTGG GAATGCTTTT AAAACAATTT GTAATTATTT CTTTACAAAC 180  
CAAAACAGAA CAGAAAGGTG TGGTGCTGGA ACATCGAAA 219

SEQ ID NO:3237

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03808

SEQUENCE DESCRIPTION:

GATCTGCATT TTCAGAAGAG GACAATCAAT TGAAACTAAG TAGGGGTTTC TTCTTTTGGC 60  
AAGACTTGTA CTCTCTCACC TGGCCTGTTT CATTTATTTG TATTATCTGC CTGGTCCCTG 120  
AGGCGTCTGG GTCTCTCCTC TCCCTTGAG GTTTGGGTTT GAAGCTGAGG AACTACAAAG 180  
TTGATGATTT CTTTTTATC TTTATGCCTG CAATTTTACC TAGCTACCAC TAGGTGGATA 240  
GTAAATTTAT ACTTATGTTT CCAA 265

SEQ ID NO:3238

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03809

SEQUENCE DESCRIPTION:

GATCTACTAT AAGGTATTCT ATATTTATAT NACTTCAGAG ACGCGTATGT AATAAAGNAC 60  
GCCCTCCCTC CAGTGTCCAC ATCCAGTTCA CCCCAGAGGG TCGGGCAGGT TGACATATTT 120  
ATTTTGTCT ATTCTGTAGG CTTCCATGTC CAGAATCCTG CTTAAGGTTT TAGGGTACCT 180  
TCAGTACTTT TTGCAATAAA AGTATTTTCT ATCCAAA 217

SEQ ID NO:3239

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03810

SEQUENCE DESCRIPTION:

GATCGGTGCT ACCAAGGAAG AGAGCACACA GATAAGACAG AGGGGAGGAG GTGGGCATTT 60  
CCTACATTCC TCCTTGTTN CCGCTGCTGA NATTGCACTA TTTATTGCAA TNTAAATNTA 120  
TCCTGAAGGT GGGGAGGAAT GTTTAANCTA CCATNTCCGT GTGTCATCTT GGTNTGTTTT 180  
TNTCCCTGTT TGTAGCAAGA CTCTNATGAT AATNCTN 217

SEQ ID NO:3240

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03811

SEQUENCE DESCRIPTION:

GATCTATATG AAGTGGGAAT ACAGCATATA TCTGGATATT CTTATAGTTA TCTTTTAAAC 60  
ATCTTATTTT TTTCATTAAT TACATATCAA CATTAATNTT GTATCTNGAA GCAAATNGAT 120  
TTTGTATAAT TAAATGTGTC AAGCATCTGT ATTAATTGAT TNGATGGCAT AAGGTATGAA 180  
ANTANTGTAC TGCCCCATGT ATNACTGTTC CAACCAN 217

SEQ ID NO:3241

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03812

SEQUENCE DESCRIPTION:

GATCATAAGA CCAGGAGTTC AAGACCGGTC TGGCCAACAT GGTGAAGCCT CATTTNTACT 60  
AAAAATACAA AATNAGCCAG GTGTGGCGTC ACATGCCTGT AATCCCAGCT ACTCAGGAAG 120  
CTGAGGCAGG AGAATTGTTT GAACCTGGAA GGTGGAGGTT GCAGTGAGCC GAGATTGTGC 180  
CACTGCACTT GACAGAGCGA GACTCTGTCT CAAA 214

SEQ ID NO:3242

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03813

SEQUENCE DESCRIPTION:

GATCATCGAG GACGAGAAGA TGGTGGTGGT GGCNTGCAG CCGACTGCAG AGCTNGAGGT 60  
GGGCTCGGCG GAGGTCATTG TGGAGTCCCT GGCCAGGGN GGCCTGGCCT CCCAGCTCCC 120  
CGGCCAGAGA CTGTGTGCAG AGNAGAGCTT CACCGGCCAG GTGTCCTGGA GCCCTCCCTC 180  
ATNATNACAG CTGCTGTCCC CGAGGACTGT GATN 214

SEQ ID NO:3243

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03814

SEQUENCE DESCRIPTION:

GATCTGGGGA GCTNTGACTG AAGGGGCTTG GTCTTCCACT CAGCATCAGC NTGGCAGTCA 60  
 CCACCCAGT NAGGACCTCG ATGTCCAGCT GCTGTCAGGT CTGATAGTCC TCTGCTAAAA 120  
 CAACACGATT TACATAAAAA ATCTTACACA TCTGCCACCG GAAATACCAT GCACAGAGTC 180  
 CTTAAAAAAT AGAGTGCAGT ATTTAAACCA AA 212

SEQ ID NO:3244

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03815

SEQUENCE DESCRIPTION:

GATCTCTGTA GACTAGAGTC TTGCAGCAAC ACAGAATGTA ATATAAGGCA AATGCATCTG 60  
 GGACTTGACC AAAGTTGTTT TGTGTTGTTT TTTTAACTGA AAGTAACAGA AGGACCTTTC 120  
 TTAAATGTGA CAGATGGTCC TGCAGTGTGA ACCTGAAGGA CAGTGTTAAA GCTGGGCTCT 180  
 AGTATATTGA TGATTCTGC ATAAGTGTGG N 211

SEQ ID NO:3245

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03816

SEQUENCE DESCRIPTION:

GATCTATTTT TGCACTGGAA TATCTGAGAA TTGCAAACT AGACAAAAGT TTCACAACAG 60  
 ATTTCTAAGT TAAATCATTT TCATTAAAAG GAAAAAGAA AAAAAATTTT GTATGTCAAT 120  
 AACTTTATAT GANGTATTAA NNTGCATATT TCTATGTNGT AATATANTGN GTCACAAANT 180  
 AANGCTGTGA CAGTCTGTT GGTCTACAAA 210

SEQ ID NO:3246

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03817

SEQUENCE DESCRIPTION:

GATCTTTTAC CACTAAAAGA GCATTATTCT CATGTCATAA TGAGAATAAT AATTTACATA 60  
 CTTGGCATAA TAAATGCCTA AAAGACATTT TATTNTCTGA ATCTATTTT TTCTTGCTAT 120  
 AATGGGGATA TTGTAAATAA TGCATTTGTA TTAATGGTAT TTCTTAAAGC AATCTATGTA 180  
 ACTGTAAATT AAACCAATCT ACAAACATAA 210

SEQ ID NO:3247

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS03818

SEQUENCE DESCRIPTION:

5 GATCAGAAGT GGCTAATTTA TTTNATTCT NATTTATTTA TCCAGAGGGT ACTTTTTTAA 60  
TGGATATTTG TAAATCTNCC ACTTAACCAC TGAAAATAAT NTTNTTTTAA TCCCACCCTT 120  
CCATCCATAC CTCTGCCTCC CCAAAAAGCT CCTATNAATT TNCTTATCCC CCTCATGTAG 180  
CTAGTTGAAT GTGAATAAAT AACATGGAAA 210

10 SEQ ID NO:3248

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03819

15 SEQUENCE DESCRIPTION:

GATCTCCATT CTTTGCCATG AGGGCCAACA CATGAGACCC CACCTCCCTC CCTGCCTGCC 60  
AGCCCTAGAC TTGTTGGAGC ATAGAGCCCT TCCTCCCAG GCCTAAGTAT GTGGAGCTCT 120  
GCTTTGGCAC TGCCCCGAG AGGCCACGCC TATTTATTCT GTTCTNTTG TTTTGT TTTT 180  
20 AACAACTATA CTTGCACAC ATGAAA 206

SEQ ID NO:3249

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS03820

SEQUENCE DESCRIPTION:

30 GATCCCCAGA GTTGGTCCAA GGAGGGAGAG TGGGTTCTCA ATACGGTACC AAAGATATAA 60  
TCACCTAGGN TTACAAATAT TTNAGGACT CACGTAACT CACATTTATA CAGCAGAAAT 120  
GCTATTTTGT ATGCTGTAA GTTTTCTAT CTGTGTACTT TTTTAAAGG GAAAGATTTT 180  
AATATTAANC CTGGTGCTTC TCACTCAA 209

35 SEQ ID NO:3250

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03821

40 SEQUENCE DESCRIPTION:

GATCTGTGTG GTCCCCGACG TAACATCTGG CGAGACCCTG CCCTCTGCTG TTACCTGAGT 60  
CCTGGGGATG AACAGGTCAA CTGCTTCAAC ATCAATTATC TGAGGAACGT GGCTCTAGTG 120  
TCTGGAGACA CTGAGAACGC CAAGGGCCAG GGGGAGCNGG GCTCAACTGG AGGAACAAAT 180  
45 ATCAGCTCCA CCTCTGAGCC CAAGGAAGAN TGAGTCACCC CAGAGCCCTA GAGGGTCAGA 240  
TGGGGGGAAC CCACCCTGCC CCACCATCT GANCACTCAT TACACTAAAC AACTTTTTTG 300  
GNAANTNTNA TNTATGATGN GNNGNGNGTG GGGAN 335

50 SEQ ID NO:3251

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS03822

SEQUENCE DESCRIPTION:

5 GATCTAATTC TNCACCTCTG CTCCAAGGGC TGGGCTGTGG GTGGGATACT GGGATTTTGG 60  
GCCACTGGAT TTTCCCTAAA TTTGTCCCCC CTTTACTCTC CCTCTATTTT NCTCTCCTTA 120  
GACTCCCTCA GACCTGTAAC CAGCTTTGTG TCTTTTNNCC TNTNCTCTCT TTAAACCAT 180  
GCATTATAAC TTTGAAAGCA AAACAAA 207

10

SEQ ID NO:3252

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS03823

SEQUENCE DESCRIPTION:

20 GATCTCATTT NAATGATTTA TAGGTAAATA CTAATCAGAC ATTATTAAAA GCAAAACAGG 60  
AAAAAGGTAA ACTTCTTAAA TTTAGTTACC TATAAAAATT GTCAATNTTN ATTCTTTAAA 120  
AACACATGGA CTTACTATAA AAGCCTTTTT GTACTAGTGA AAAGAATCTT CAGCTATATA 180  
GAAATAAAGT TATACTTTAA A 201

25 SEQ ID NO:3253

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03824

SEQUENCE DESCRIPTION:

30 GATCCCTAAA AGACAAAAGA GTCTTGGAAG GACTGCTGG CTTCGTCTTG AACGTTGCGC 60  
CCATACCAG TGTGAGTCCG TGGGGAAGTC TTCCTCAAGT GGGGTTGAGT CTGTAATTTT 120  
CCTGTCTGTT CTTAGCANNNG TTCTGAGTTA TTTTGGATTT TNTTCTTTAG CCAAATAAAG 180  
GCAGTGTGGT TTTACCTGAA A 201

35

SEQ ID NO:3254

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS03825

SEQUENCE DESCRIPTION:

45 GATCCTAATG GTGCTGCCCT ATTTATACCT GGGTCTGCAT TAAAAGGGAA AGCCCCCCT 60  
GTTGTAGATT TCATCTGCTT CCTCCTTAGG GNAGGCTGGG ATATGATGAG AGATTCCAGC 120  
CCAAGCCCGG CCCCCACCG CCAGGCCATA GGGCATANTT TGCATCTCAA ATCTGAGGAA 180  
TAAACTGATG ACCTGTGAAA 200

50 SEQ ID NO:3255

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

CLONE:HUMGS03826

SEQUENCE DESCRIPTION:

5 GATCAAGCAT TTGCGTTTGG ATGGCAATCG CATCTCAGAA ACCAGTCTTC CACCGGATAT 60  
GTATGAATGT CTACGTGTTG CTAACGAAGT CACTCTTAAT TAATATCTGT ATCCTGGAAC 120  
AATATTTTAT GGTATGTTT TTCTGTGTGT CAGTTTTCAT AGTATCCATA TTTTATTACT 180  
GTTTATTACT TCCATGAATT TTAAAATCTG AGGGAAATGT TTTGTAAACA TTTATTTTTT 240  
TTAAAGAAAA GATGAAAGGC AGGCCTATTT CATCACAAGA NCACACACAT ATACACGGTT 300  
10 AGACATCAAA CTCAATGCTT TATTTGTNAA TTAGTGTT TTNTATTCT ACTGTCAAAT 360  
GATGTGCAAA ACCTTTTTNC CGGGTTGCAT N 391

SEQ ID NO:3256

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03827

SEQUENCE DESCRIPTION:

20 GATCTTTAAT TTGNATGGTG ATGAATGTCT TAGTCATGAA GAGTTTCTAT GGGGTGTNAA 60  
AAACAGAAT GCATCGAGGT TNATGGGTAC CACAACATCA GAGTATACAA GAATACTGGA 120  
AGTGTGTGAA GAAAGAAAGC ATTAAAGGAG TAAANGANGT CTGGAAACAN GCTGGAAANG 180  
GTCTTTTNA ATNN 194

SEQ ID NO:3257

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03828

SEQUENCE DESCRIPTION:

30 GATCTAGTAG GTTCTATTT TTCCTTTCTC TTTACAATGC ACATAATACT TTCCTGTATT 60  
TATATCATAA CGTGTATAGT GTAAAATNTG AATNACTTTT TTTGTGAATG AAAATCTAAA 120  
35 ATCTTTGTAA CTTTTTATAT CTGCTTTTGT TTCACCAAAG AAACCTAAAA TCCTTCTTTT 180  
ACTACACAAA 190

SEQ ID NO:3258

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03829

SEQUENCE DESCRIPTION:

45 GATCCCTTT TNTNCTGGAG CTTCCGTGCC TCCCCTGCCT CTTCCCAGCC CTTGTAATCC 60  
TCCTTCACAG GCCAGCCAGA TACCTGTNTG GCCTNTGGGC CCATTTTNTT CCCTGTCTGT 120  
CCCCACCCCA CAAGAACCAG GTTCTNTAA TAAATTCTCT CCCTTCTTTA GCCAGGACTT 180  
AGCCCGCAAA 190

SEQ ID NO:3259

SEQUENCE LENGTH:189



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03830

SEQUENCE DESCRIPTION:

GATCTNAGAG CCTGCCCAAC AGCAGGGAAG CCAAGCACCC ATTCATCCCC CTGCCCCCAT 60  
CTAACTGCGT ANTGANAAAG GGAACAGTGC CATGTACCAC ACAGATGTTT CTGTCTCCTC 120  
GCATGGGCAT AGGGACCCAT CATTNATGAC TGATGAAACC ATGTAATAAA GCATCTCTGG 180  
GGAGGGAAA 189

SEQ ID NO:3260

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03831

SEQUENCE DESCRIPTION:

GATCCCCTTC CTATCAATCA CCTGATAGCA ACAGGGACAG CTGCCAATAC CCTGCTCTTT 60  
ACTCAATGGT ACCCAGGGAG GGAGCATGGG AAGAGGGTGA GCTGAGGGCT GGAGGAGGGC 120  
AACAGCCACT GGGTGAGCTG TTCACGGTCT TATACTATTG TTTGTNATTA AAAGTGCTTC 180  
AACCCAAA 188

SEQ ID NO:3261

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03832

SEQUENCE DESCRIPTION:

GATCAACAAG GCCACGCCCT ACAACTACCC AGTGCCCGTC CGTGATGATG GGAACATGCC 60  
CGACGTGCCC AGCCACCCCC AGGACCCTCA GGGCCCCAGC CTGGAGTGGC TGAAGAACT 120  
GTGAGCACCT CCACTGACAG AGGCGGCCCC TCCCACGGNT CCCAATAAAA ATGTGAAAAC 180  
CAAA 184

SEQ ID NO:3262

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03833

SEQUENCE DESCRIPTION:

GATCCACCAA TGTTTCAAAT AGGACTATAA CTTATTCAAA GGCCAATNAT ACTTCGCATA 60  
ATTCAATTTT AATATTATTC ACATTTTCATG TCACAAATTT AGTAAGTTAC ATGTGTTATG 120  
TGATGTTTTG TTTTGATAGA TTATATCTTA CTCCTAAATA AAANGTCAAG ATTTTGTAG 180  
CAAA 184

SEQ ID NO:3263

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03835

SEQUENCE DESCRIPTION:

GATCTCTCTG TGTGGAATGC CTTGGTGAGA GAGATGCTTA TAATNACTAT NATNATTTCT 60  
AACCAAGCTT CTATNAATNT AATTCTAAT AATACACTAT CTTGATTGTA CTCTCCAGAA 120  
AATTTTCTG TCAGTGAAAA TAAAAGAAAA ATTAAAGTAA AGCTAAGGAA CTGTCTATAA 180  
A 181

SEQ ID NO:3264

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03836

SEQUENCE DESCRIPTION:

GATCCCTGGA CCATCTGCAT CCAGAGGACC GTCCGTAACG GCCGGGGGTC CAGGCGGACC 60  
TTGTGGTGAC CCGGCTCGG CNTNTCCTCG GTTTCNTTGC CTCACCCGCG GAGAGCGCTG 120  
AACCTGGACA AGCAGCGGCT GGNAAGNACA GGTCCAATAA ACGCCCTCTG CGCCAGAAA 180

SEQ ID NO:3265

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03837

SEQUENCE DESCRIPTION:

GATCTAGTTC AGAAGGAAGC AAAATCCCTT AATCTATGTG CACCGTTGGG ACCAATGCCT 60  
TAATTAAAGA ATTTAAAAA GTTGTAATAG AGAATATTTT TGGCATTCTT CTAATGTTGT 120  
GTGTTTNTT TTNGTGTGN CTGGAGGGAG GGGATTTAAT TTNAATTNA AAATGTTTAG 180  
GAAATTTNTN CAAGGAANCT TTTTAATAAN GTATATNGAA AGNTAAA 227

SEQ ID NO:3266

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03838

SEQUENCE DESCRIPTION:

GATCACTTCT CCTTGGCTTC CTTCTTTTCT GTGCTTGCAT CAGTGTGGAC TCCTAGAACG 60  
TGCGACCTGC CTCAAGAAAA TGCAGTTTTC AAAACAGAC TCAGCATTCA GCCTCCAATG 120  
AATAAGACAT CTTCCAAGCA TATAACAAT TGCTTTGGTT TCCTTTTGAA A 171

SEQ ID NO:3267

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03839

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCACTTTA TTTGCTAGGG AGGGAAGTCC TAGGGTGGTT TCAGTTTCTC CCAGACATAC 60  
 CTAAATTTTA ACATCAATCC TTTTAAAGAA AATCTGTATT TCAAAGAATC TTTCTCTGCA 120  
 GTAAATCTCG CAGGGGAATT TGC ACTATTA CACTTGAAAG TTGTTATTGT TAACCTTTTC 180  
 GGCAGCTTTT AATAGGAAAAG TTAAACGTTT TAAACATGGT AGTACTGGAA ATTTTNCAAG 240  
 ACTTTTACCT AGCACTTAAN TATGTATAAN TGTACATAAN GACAANCTAG TAAGCNTGGC 300  
 CTGGGGANAT GGTCAGNCCT TGTNTTGTGT TTTTGGCN 338

SEQ ID NO:3268  
 SEQUENCE LENGTH:170  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03840

SEQUENCE DESCRIPTION:  
 GATCATAGGA GAAAACCATT TCANATGACA AGAGCACCTC AAAGGCAGCA GCCTCAAGGA 60  
 GCAGCCATGG CCCCAGACTT GTCGCACGGA TGCAGAAAAC TTAATGGAGG AGGCTGAGGT 120  
 CAGAATGGGA AGAGTTTSTA AAAAATAAAA AGGGGAGCTA ATATGTGAAA 170

SEQ ID NO:3269  
 SEQUENCE LENGTH:168  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03841

SEQUENCE DESCRIPTION:  
 GATCAAGGGC AAAAAGTGGT CATTAAGTNA TCTAANATTA AATNATTTAG CCACTAAGTA 60  
 ATTTNTTTAC TCTNACTTTA AACTCACCAA AGAAGATTCT TTAAAGAAA TTATGAAAAA 120  
 TGTACAATTT AACATTTTAA ATAANTAGTG ACAGANGTTG TTTATAAA 168

SEQ ID NO:3270  
 SEQUENCE LENGTH:167  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03842

SEQUENCE DESCRIPTION:  
 GATCCTCCTG CCCCAGCATT CCAAAGTGCT GGGATTACAG GTGTGAGCNA CTGCCTGGCC 60  
 TGGCCGTAGG TTTGTAAGT TTTTCATAGAA GAGCCCTGGA GAAGACAGTA GAATNAGCCT 120  
 ATCTAGTTTA AAAAATAAAG AAGCACGTTG ATTCACCAC CGCCAAA 167

SEQ ID NO:3271  
 SEQUENCE LENGTH:167  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS03843

SEQUENCE DESCRIPTION:  
 GATCAGCTTT GTTTTCCCA GAGTTCATGC AAATAGAATC TGGCTTCTNT AAGTNAGCAT 60  
 CATGGACTTG GTTNAAATC GCCCGTNTTG CTGAGTGTAT CTTAGCTTG TCCCTTTTAA 120

CTGACGAGTA GTATTCCACA GTNTGGATGC ACTGTATTNN NTTTATN 167

SEQ ID NO:3272

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03844

SEQUENCE DESCRIPTION:

GATCAGAGCA TTGTGCAATA CAGTTTCATT AACTCCTTCC CCCGCTCCCC CAAAAATTTG 60  
AATTTTTTTT TCAACACTCT TACACCTGTT ATGGAAAATG TCAACCTTTG TAAGAAAACC 120  
ANANTAAAN TTGAAAANTA AAAACCNTAA ACATTTGCAC CAGAAA 166

SEQ ID NO:3273

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03845

SEQUENCE DESCRIPTION:

GATCTNTTTT TTTCCCTTCT TGTATCATCC CTTTGGGTTT TTCGGTTTGC TTTGGTTTTT 60  
AATTTNCTT TGTTTTNCT ATAAATCCTG TTTTAATCTT ATAAGGGAAA ATNCATTTN 120  
TTCAACTGTN CTAGTTAATA ATGAGAACTC AATTNCTGGA AATNN 165

SEQ ID NO:3274

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03846

SEQUENCE DESCRIPTION:

GATCTCAGGA ATNACATTTT CCAACAGACC AAAAAATGTT TTCATGTAGC AGCAATGCAG 60  
ATTTGGTGAA TATTTAATAT ATATTTAAGT ATGTATTCA CTTTATNACT GACAATNAAA 120  
AAATATTGTT TGGCCAAATA GTAAACACCC TTTTGAAACC AAA 163

SEQ ID NO:3275

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03847

SEQUENCE DESCRIPTION:

GATCCCTTNG TTTGCTTAAT AAATTATAAA ATAATGGCTT GGAAAAGCAG GCTAGTCTAA 60  
CCATGGTGCT ATNATNAGGC TTGCTTGTTA CACACACAGG TCTAAGCCTA GTATGTCAAT 120  
AAAGCAAATA CTTACTGTTT TGTTTCTATT AATGATTCCC AAA 163

SEQ ID NO:3276

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03848

SEQUENCE DESCRIPTION:

5 GATCTGTTCT TGGTATTTNN TTTTGTGTTG TTTTGGTTTT TAAATGTAAT CACCCATTGG 60  
 TCAGGCCAG GACTGGTCAC CATGAGCTCT GCTAGCCACG GCCCAACGA TGCTTCGGC 120  
 TCTCATGGAT TCCACAGCAA ATAAACTGT GCTGACAACA GAAA 164

10 SEQ ID NO:3277

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03849

15 SEQUENCE DESCRIPTION:  
 GATCTGGGGT CCCTAAGTCC CTCTCTTTAA AGAACTTCTG CGGGTCAGAC TCTGAAGCCG 60  
 AGTTGCTGTG GCGGTGCCCG GAAGCAGAGC GCCACACTCG CTGCTTAAGC TCCCCCAGCT 120  
 CTTTCCAGAA AACATTAAAC TCAGAATTGT GTTTTCAGCA AA 162

20 SEQ ID NO:3278

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS03850

SEQUENCE DESCRIPTION:

30 GATCCTAGGA ACTCCTATNT TCAGAAAAGA ATTTTNTTCC TACTATATAA TTACAGTATT 60  
 TAGCTGTCAA TTTTAAGATG AATTTGGTAG AGCCTTAGT TAAAGNATGT ATCTTGGTCA 120  
 CACACAAAGC TTGGA AAAAG TAAAAGATGT CTAAACCATA AA 162

35 SEQ ID NO:3279

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03851

SEQUENCE DESCRIPTION:

40 GATCAAGAAG TAGCCGAGGT TGATAAAAAC ATAGAAGTTT TGAAAAAGAA GGATGAAGAA 60  
 CTCAGTTCTG CTCTGGAAAA AATGGAAAAAT CAGTCTGAAA ACAATGATAT CGATGAAGTT 120  
 ATCATTCCA CAGCTGCTCA ATAAAGTACA AGAGCTTAAA 160

45 SEQ ID NO:3280

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03852

50 SEQUENCE DESCRIPTION:

GGGTGGGATG GAGAGAATGC TGAATCTTTT TTTNACGGG ATGGGGTTTT CNTCTTTGTA 120

ATTATNNCTT TAGTTTAATT AACCTTTTGG TTGTTTGTNC AATATTATAT ATNNNAN 177

SEQ ID NO:3281

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03853

SEQUENCE DESCRIPTION:

GATCAGGACT ATAATATTGT ACAGTTATTA TAGGGCTTTT GGGGAAGGGG AGGATAGCGA 60  
 GAAGATGCTC TGGGGGTTTT GTTTTGTCTT TTCCTTCAGG GTTTTATTTT TGA CTGTTTT 120  
 GTTTTCTNGT NGGCCATTTT TGTATTGCTG GCATCTGTGC TAAGCTTTAC AGTGGCAAAA 180  
 ATAATGACAT GTAGCAAAGA TTTTCAAACA AAATATTTT NCCTTTTGTA AA 232

SEQ ID NO:3282

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03854

SEQUENCE DESCRIPTION:

GATCGATGGT GCGGCTTTCT CCTGTGCCCA CCCGTCTTCA ATCTCTGTTT TGCTCCCAGA 60  
 TGCCTTCTAG ATTCATGTC TTTTGATTCT TGATTTTCAA GCTTTCAAAT CCTCCCTACT 120  
 TCCAAGAAAA ATAATTAAAA AAAAACTTC ATTCTAAA 158

SEQ ID NO:3283

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03855

SEQUENCE DESCRIPTION:

GATCTCATCA CAAGATGACC AAAAGAGTTT GAACTGTGTG TGCTATTTAG AAGATTTAAC 60  
 TTTNATGTAT CTATAGATAC CACAGCTGTT GCTTCTAATA AATTACCTA CCTTTNAACT 120  
 GAAAGTTTAA TAAAGCCAAA TCAATTTGAA ATACCAA 158

SEQ ID NO:3284

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03856

SEQUENCE DESCRIPTION:

GATCTGCCTC ACGTGCACTG TGGTGGCCGT GTGCTACGGC TCCTTCTACA ATCTCCTCAC 60  
 CCGAACCTTC CACATCGAGG AGCCCCGCAC AGGTGGCCTG GCCAAGCGGC TGGCCAACCT 120  
 TATCCGGCGC GCCCGAGGTG TCCCCCACT CTNATTCTNG CCCTTTCCAG CAGCTGCAGC 180  
 TGCCGTTTCT NTCTGGGGAG GGGAGCCCAA GGGCTGTTT TGCCACTTGC TCTCCTCAGA 240  
 GTTGGCTTTT GAACCAAAGT GCCCTGGACC AGGTCAGGGC CTACAGCTGT GTTGTCAGT 300  
 ACAGGAGCCA CGAGCCAAAT GTGGCATTG AATTGAATT AACTTTAGAA ATTCATTGTC 360

TCAACTTGTT AGTGGCCACC TCTTATATTN 390

SEQ ID NO:3285

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03857

SEQUENCE DESCRIPTION:

GATCTCAACA CCTATGCCTC CACGTAAATT ATTTTTCCTA GCCTTATTC CCTCAAAATT 60  
GTAGAGTCCT AATCTTCTTC TATCTTGTGG TGTGAGACCT TGGATAAGTC TCCCTTCCAC 120  
CTTTTCCTAT TACTTAAAT GGTGAATTG CATAAA 156

SEQ ID NO:3286

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03859

SEQUENCE DESCRIPTION:

GATCAGGTGA TTTGTAAAT TGTATTTATC TGTACATGTA TGGGCTTTTA ATTCCCACCA 60  
AGAAAGAGAG AAATNATCTT TTTAGTTAAA ACCAAATTTC ACTGTTCAAA NTATCTTCCA 120  
ACTTATTTAT TGGGTTGTCA CTCAATTGCC CTGTN 155

SEQ ID NO:3287

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03860

SEQUENCE DESCRIPTION:

GATCTTGCAA CTCCATTTCG GAAGACACCG AGGAAGAGGA GGAAGATGAA GACCAGGACT 60  
ACAGCTTTCC TATATCTCCT ATTCTAGAGT GGTAACTCT CTNTAAGTNT TCAGTGTGTA 120  
CATAGCCTTT GTGCAA 137

SEQ ID NO:3288

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03861

SEQUENCE DESCRIPTION:

GATCAGTGGG CACAGTTCTT CAGCTACATT GAGACCCTGA AATAACAAT NATATTCTNA 60  
CTCGACATCT TGTCCCAAT CCTTCAAAA ATATTGATGG TGATTTGTGC TACCATTTAC 120  
TCGTTTATTT AATAAGACA TTCAATCCCA AA 152

SEQ ID NO:3289

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03862

SEQUENCE DESCRIPTION:

5 GATCAGNATT GTACGTATTC AAGGTGTAAA ATNTGATAAT TTGTCGTACA CGTACATTGT 60  
GCAATAACAG TCACAATNAA TTCCTCAGCG CACCCATCAC CACGAATACG ATACATTAGA 120  
TATTCTGAAC TTGCTCATCT TAGGACTTCA AA 152

10 SEQ ID NO:3290

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03863

15 SEQUENCE DESCRIPTION:

GATCATAATA GTGACCAAAA TATACATGCA GACTTGTTTT TTATTATTGT TGTTTAAGCA 60  
TAATTTAAGA AAAAAAATTT TTACCTGGTG AACTTGCTAT CTGCTCTGTT TCTAGTTAAA 120  
ANATAATANA TNTTATCTNC CCTGTGCTGT AAA 153

20

SEQ ID NO:3291

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03864

SEQUENCE DESCRIPTION:

25 GATCTTCTTT CTTTTTACAG GAACAATTGG CTTCTTTGCA TGCTTTTGGT TTGTNACCAA 60  
AATATACAGT GTGGTGAAGG TTGACTGAAG AAGTCCAGTG TGTCCAGTTA AAACAGAAAT 120  
30 AAATTAAACT CTTCATCAAC AAAA 144

SEQ ID NO:3292

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03865

SEQUENCE DESCRIPTION:

40 GATCATGGTG AACTTACCAA AGCAAACAAT GCCTGTAAGA TGGTCCTGCA GCAGCCAACC 60  
AGTGAACCTCT TTTGGTGACA TCCTGTTCTT GTTGATAAAC TTTATATTCC TATAAATCCA 120  
TTAAGGCCCC AATAAAGTTT GTCTCTAAGC GCTGTGTTAG AAA 163

SEQ ID NO:3293

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03866

SEQUENCE DESCRIPTION:

50 GATCCAAAAT TAGAGCTCAT CAGANTTGTG ATTGAAAGTG TTAACAAAAG TAATATCAA 60  
TGACATTTGA AAAATATCCT TGTAATAATGA CTATATTAAT AGGTATAAGG NTTTTCTTA 120

55



TTAATCTAAT AAAATNCCTT AATAGGAAA

149

SEQ ID NO:3294

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03867

SEQUENCE DESCRIPTION:

GATCAGGACA CTTAGCAAAT GTAAAAATAA AATCTAACTC TCATTTGACA AGCAGAGAAA 60  
 GAAAAGTTAA ATACCAGATA AGCTTTTGAT TTTGTATTG TTTGCATCCC CTTGCCCTCA 120  
 ATAANTAAAG TTCTTTTSTA GTTCCAAATT TNAGAAA 157

SEQ ID NO:3295

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03868

SEQUENCE DESCRIPTION:

GATCCGNTAG GAGTAGTAAA TGNGAGACAC AATNGCTTGA TTATACCTCN TATNTGGTTT 60  
 AGCTTCAGTA TTTAAACAAG GAAATAAACT TGAAAATTAT TTGTCATCAT AAAAATGAAA 120  
 CAAANTAAAA TATTTATTGC CAGGNAAA 148

SEQ ID NO:3296

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03869

SEQUENCE DESCRIPTION:

GATCTCAGAG GCTCAGAGAC TGCAAGCTGC TTGCCCAAGT CACACAGCTA GTGAAGNNCA 60  
 GAGCAGTTTC ATCTGGTTGT NACTCTAAGC TCAGTGCTCT CTCCACTACC CCACACCAGC 120  
 CTTGGTGCCA CCAAAAGTGC TCCCCAAAAG GAAGGAGAAT GGGATTTTNN TTTTGAGGCA 180  
 TGCACATCTG GAATTAAGGT CAAACTAATT CTCACATCCC TCTAAAAGTA AACCTACTGG 240  
 TTAGGAGCAG CAGTGTCTC ACAGTGTGGG GTCAGCCGTC CTNCTTNATN NNNGGCCAAT 300  
 GGNTATTGAC ACGTGTNCNN NGTTTGGGCA GN 332

SEQ ID NO:3297

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03870

SEQUENCE DESCRIPTION:

GATCTNCTGT CCTCCTTTCA CTACATACCA ACAACCCTCT GGCATTAAAC TTCCAGTGAT 60  
 AGTGCTATNA ACTTTGTGTC CTCAGGTCAA CAAGGGACCT CAGTAATTNG TTCTNTACAT 120  
 AAGTATATAT ATGGGTATTA NTNNGTN 147

EP 0 679 716 A1

SEQ ID NO:3298

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03871

SEQUENCE DESCRIPTION:

GATCGCCCTC TACATGGCTT CGCAGCCCAA AAACAAATNA GTTAGGCTGC AGAGGACTGG 60  
 TTTGTTTTTT GGCATAAACC CTTTGAAGTT CCTTTTTCAT TGTTAAATTA AAATTTTTTT 120  
 NTTNACTTGG ATGGCTTAAC ATTTTNNCAA GAAAANTNGG AAGNTATGAA GATGNTGTTT 180  
 TGGTTTGTTC ATGAAANGCA TATGGCTTGN CAGAGCTCAT TCGACAGTTA AGGCCATTGT 240  
 TTAAAGAANC GGTGCTTTC TCTGTGTTT TNCTCCTGAT TTCCCTGGAG GTTCTGGATG 300  
 AGGGCTGANC ACAGGCTTNG TTANTGTNCA GTCTGTGCTG GGGGNCCTCA GGGGN 355

SEQ ID NO:3299

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03872

SEQUENCE DESCRIPTION:

GATCACCAGG GTCAGTTTNT TTAATAATGG TTTCCAACCTG GCCTAATACA TTAAGTAAGA 60  
 NTGGNTGATA ACATGACCAG ACAGACATAA AGACCCTGTT GGGGAATNACA TTGAACTCTC 120  
 AAAGTCAAGA TTTNTTACAC AANTNTN 147

SEQ ID NO:3300

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03873

SEQUENCE DESCRIPTION:

GATCCGCTAC TAAAAGTAAA AATAACCGGT TTGTAAAACA TTAAGAGAAA AANTAGGATA 60  
 TTTAATACAT GTGGTGAGTG GAGANCAGGG TAACTTTAAN TNAAAGTTTA AGGCAAATTG 120  
 TAAGCNCCAC AAGANATATC ANATTTN 147

SEQ ID NO:3301

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03874

SEQUENCE DESCRIPTION:

GATCTAAAAA AATTA AAAAG AAATATGAAT GAAAGNAAAA AAAATGCNAA AATNAGCAGT 60  
 TTCCTGGAGG AGCAGTTCCA GCAGGGCAAG CTTNTTGCTT GCNTCGTTTC AAGCCGGGA 120  
 CANTTTGGCC GAGCAGATGG CTATNTN 147

SEQ ID NO:3302

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03875

SEQUENCE DESCRIPTION:

GATCATNTTA TTTTACAATC ATTTATAATG AATNAATGTT NCAGTTAGCT TTAAAAGGTA 60  
TACGGTGCTA ATNAGTAAAA TATTGAAGGC AATATTTTAC TGCTAGCTTG CAAAGTTATG 120  
AGAGTTTAAA AAATAAAATA TATGAAA 147

SEQ ID NO:3303

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03876

SEQUENCE DESCRIPTION:

GATCTAGGGT CCTGGGTNTC TTGCATTTAT ATGTCAGAAA AGGGGCGATA TGCTGCTGAG 60  
GGGTGAGTGC ATATAANTNT GGCCCTGAGG ACCAGGGCTG GCAGATNTTG TCTACCTGCT 120  
GAAGAATAAA ANATTTCTTT TGGTAAA 147

SEQ ID NO:3304

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03877

SEQUENCE DESCRIPTION:

GATCTNACCC CCAGCATGAT TGTATTCTT TCCCCTCCAG TCAAACCGTA ATACAGTTTC 60  
CAGAAAATTC GACAGTCTGC AATGCCAAAA GGGTAAAAAT CTGTATTCA CAGTTGTATA 120  
GAATAAAGGC TTTAGTTAAA ATATTTCAAA 150

SEQ ID NO:3305

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03878

SEQUENCE DESCRIPTION:

GATCTAAAAA TAACTGTAAT TATTTAAATG ACTAANAGGA AAGTACATTT TTAAAAATNC 60  
TGAAAATTGC CTTNNTGTGT TTATNCAAAAC TGAAAAGCTG AGACCAAGAG CAAGGAAGGT 120  
AAAANGTTAA CAGGCAAACA TTTNCN 146

SEQ ID NO:3306

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03879

SEQUENCE DESCRIPTION:

GATCCTCACC AACCTAAGCA AGAGGAAGTG CCCCTCTCAA CCTGTGCGGG NTGCTGCGTC 60

CCAGGACTGA GACGCAGGCC AGCCCCGGCC CCTAGCCCTC AGGCCTTCTT TTTTATCCAA 120  
ATAAATATTT CTTAATAAGG AAA 143

5 SEQ ID NO:3307  
SEQUENCE LENGTH:143  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS03880  
SEQUENCE DESCRIPTION:  
GATCAACAAG AGCACTGTAC TCCTGGCAAT NATTACATAT GTNAGAACAT GGATTTTGCA 60  
CTGTAGACAA CATTAAACAC CAGTCTATGG GGTACTGCAT TGCTTTTNAT AAAGTTCAAA 120  
ATAAAGATTT ATTTTCAAAC AAA 143

15 SEQ ID NO:3308  
SEQUENCE LENGTH:142  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS03881  
SEQUENCE DESCRIPTION:  
GATCCCTTTA CTGGAGCCCA GTATGTGCTG TGTGAGTTAG AAGTCATTCT TGCTGAGAAG 60  
GTGAATAGGT AGGGATTTGC CTTGTTTTGT AAGTCTACAA TTTGCCAAGA GTAAATAACA 120  
25 CTGGACCAGC TGTAAGTA AA 142

SEQ ID NO:3309  
SEQUENCE LENGTH:142  
30 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03882  
SEQUENCE DESCRIPTION:  
35 GATCTGCACA TTTAATCGTG GCTGTTTCTG TATAGCCTAT ACTGCATTAG CCNAAGANAT 60  
TGTTGCTTTG TAACTTTTGT CACTATTGTT TTGGCTGGAT TTGTATTACA CACAGTTTAA 120  
AAAAAAACAA TTCCACACTA AA 142

40 SEQ ID NO:3310  
SEQUENCE LENGTH:141  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS03883  
45 SEQUENCE DESCRIPTION:  
GATCCCTAAG CCCCCAGCT GTAAATAGGC TGTGGCCAGT GCCTGGTCAT NAGAAGAGNG 60  
AGGAGGAGCC CAGGCGTCTG TTTATGTATT TATTTATTTA TTTATTATAC CTATTAATAA 120  
AAAAGGTGCT CAGCCTCCAA A 141

50 SEQ ID NO:3311  
SEQUENCE LENGTH:139

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03884

SEQUENCE DESCRIPTION:

GATCTTGGCC TTCGCAGTGC CCAGTGATGG CATTACTCTG CACTATAGCC ATTTNCCCCA 60  
 ACTTAAGTTT AGAAATNACA AGTTTCAGTA ATAGCTGAAC CTGTTCAAAA TGTTAATAAA 120  
 GGTTTCGTTG CATGGTAAA 139

SEQ ID NO:3312

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03885

SEQUENCE DESCRIPTION:

GATCTGGAAG ACAAGTAACA TCTTCCTTTT NTTGGTGCTC GCCTGCCGTG CTCTAGGTGC 60  
 TTTTAGAGAT GCTGGTCTGT GTGCTAGGGA AGCGATGAAC CATACTGTTA GTCTATTAAA 120  
 CATAACTCAA CCTGGAAA 138

SEQ ID NO:3313

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03886

SEQUENCE DESCRIPTION:

GATCTATCTC TGTGTCCAAG TCTCCTCTTT TTATAAGGAA ACCAGTCATA ATGGACCCAC 60  
 CTGAATNACC TCATTTTAAC TTGATTACCT CTGTAAAAAA TGTATTTCCTA AATAAAGTGA 120  
 CCTTATGAGG TATTGAAA 138

SEQ ID NO:3314

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03887

SEQUENCE DESCRIPTION:

GATCAACAAA TCTCCTAGGC CTNTNACCAC ATACATTTAC ACCNACTACC NCAACTATCC 60  
 ATAAATCTAA GTATAGCCAT TCCACTATNA GCTGGAGCCG TAATTACAGG CTTCCGACAC 120  
 AAATAAAAA GCTAAA 136

SEQ ID NO:3315

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03888

SEQUENCE DESCRIPTION:

GATCCACCT TCAACACCTT ACAAGTAAAG CCAATGAAGN ACAGTTGAAA CATGCAAAAT 60

ATGGNGCTTT TCATGTAATT ACTCTTTTAC TGTTTACCAT TCACTATAAT TCACAATTAA 120  
AATTGTGTGN CTANACAAA 139

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SEQ ID NO:3316  
SEQUENCE LENGTH:133  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS03889  
SEQUENCE DESCRIPTION:  
GATCTGTGTA GTTAATGTAT TTATTAATGC TTGACTTTTA AAATCCTGGG CATAAATAGT 60  
GCAGAGCCTC GTATGTTTGT CAGTTCATGC CGAGATGAAA TAAATCACGC AGAAAGTGCC 120  
AGTCCTCCTG AAA 133

15

SEQ ID NO:3317  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear  
CLONE:HUMGS03890  
SEQUENCE DESCRIPTION:  
GATCTGTGGA GTGTGTGTTT CAAAGAGAGA ACTACAGAAA TNTTAAAGCA GGAAAACCTG 60  
AATGTNATGT GCACATTTTC ATCCCACATG GACAATGTAT GTGTTTTAAT AAATGGAATT 120  
TTCAGATTCA AA 132

25

SEQ ID NO:3318  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear  
CLONE:HUMGS03891  
SEQUENCE DESCRIPTION:  
GATCAAATGT GGGCCCGTTT TTGGCCGCCG CCGCCCTGCC CCGTCCCTNC GGCCACCACC 60  
TAATTANTTG CCGTGCTTCC TGCTGCTGTA ACTGCTTTNT TACCTTTCCA ATAAAGANTT 120  
TCTTGGTTTA AA 132

35

SEQ ID NO:3319  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid

40

TOPOLOGY:linear  
CLONE:HUMGS03892  
SEQUENCE DESCRIPTION:  
GATCATTATT ATTGTAATAG TCTCATGTTT AAATGGGATT ATATAATGAN AACAGTTTAA 60  
AGAAAATNAT AATCTTATAT NTCAAATGTG GATGCATATA ACCTGTNAGT GAAAAANCAC 120  
TGANTGATTT AN 132

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SEQ ID NO:3320  
SEQUENCE LENGTH:131

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03893

SEQUENCE DESCRIPTION:

GATCATATTG CTGTAAGTTC TTTTAAGTAG TTGATGTGGA AAACATTTTA AAGTGAATTT 60  
NTCAAAATNC TGGTTTTGTG TTTTATCCAA CTTTTGTGCA TATATATAAA GTATGTCATG 120  
GCATGGTTAA A 131

SEQ ID NO:3321

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03894

SEQUENCE DESCRIPTION:

GATCCTCAGT GTAGTTCTGA AACTAAGACT ATAGATATTT NNITTCTTTT AATTTCTCTT 60  
TATACTAAAG AATCCAGAGT TGCTACAATA AAATAAGGGG AATAATAAAC TTGAGAGTGA 120  
ATAACCATAA A 131

SEQ ID NO:3322

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03895

SEQUENCE DESCRIPTION:

GATCTTAGAG TTGACACAGC TTAATAAAT GGAAATATTG GAATCTGAAT CCAAAACAGC 60  
CTGACTCAA ACAATGTNCT TNCCATTATG CAAGGGGAAA AAAAAANGGT TGGGTNTCAG 120  
NGNGAGGGTA N 131

SEQ ID NO:3323

SEQUENCE LENGTH:433

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03896

SEQUENCE DESCRIPTION:

GATCATAGTC TTAGGAGTTC ATTTAAACCA TAGGAACTTT TCACTTATCT CATGTTAGCT 60  
GTACCAGTCA GTGATTAAGT AGAACTACAA GTTGTATAGG CTTTATTGTT TATTGCTGGT 120  
TTATGACCTT AATAAAGTGT AATTNTGTAT TACCAGCAGG GTGTTTTTAA CTGTGACTAT 180  
TGTATAAAAC CAAATCTTGA TATCCAGAAG CACATGANGT TTGCAACTTT CCACCCTGCC 240  
CATTTTTGTA AAAGTGCAGT CATCTTGGAC CTTTTAAAAC ACAAATTTTA AACTCAACCA 300  
AGCTGTGATA AGTGAATGG TTAGTGTGTTA TACTGTGGGT ATGTTTTTGN NTTACAGCAG 360  
GTTAATGCTT TCTTTTTCCA GGTCGNCCTT TGAGGATTNA GGGAAAATTA NATAACTCTT 420  
TGTACAGTTC AAA 433

SEQ ID NO:3324

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03897

SEQUENCE DESCRIPTION:

GATCCACCCA CCTCGGCCTC CCAAAGTGCT GGGATTATAG GTGNNAGCCA CCGCGCCGGG 60  
CCGGTTGCTG GCATCTTAAT GTTCTGTAGG TGGAATATTT CCAATAAACA CAAGGTGCCG 120  
TAATTGAAA 129

SEQ ID NO:3325

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03898

SEQUENCE DESCRIPTION:

GATCTGGTAA ACTTNNAATC AATTAAATTA ATGCANCAAT AGATTATNAA TATTAAGTGA 60  
CCATTTAAGT TTTTNAATAA GTTTTTTACA AAGAAAAGTT AAACATTAAA AAGAATTACA 120  
GCTTTCAAA 129

SEQ ID NO:3326

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03899

SEQUENCE DESCRIPTION:

GATCTGGAAA TTTTTTAATC AGTTAAATTG TGCAGCAATA GATTTTTTAAC TTAACTGAC 60  
CATTTAAGTT TTTNAATAAG TTTTTTACAA AGAAAAGTTA AACATTAAAA AGAATTACAG 120  
CTTTCAAA 128

SEQ ID NO:3327

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03900

SEQUENCE DESCRIPTION:

GATCCTGTAG TGCCTCTATA GAAGTACCCA CAGAAAGTAA AGTATCACAT TTATAAATAC 60  
CAAAGATGTA ACAATTTTAA AATTTTNTAG ATTACTCAA TAAAGTGTTT TAAGTTTTC 120  
TATGAAA 127

SEQ ID NO:3328

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03901

SEQUENCE DESCRIPTION:

GATCCATCGC GATACTATGT GTGCATTATT TGAAAGTTAT TGGAATTTT ATTCAAACCG 60



TGGAACAAAT GTATGTNATT TTTTATACT TCTTAATTTA AATAAAATAT TTAATGCACT 120  
 ATTAAATAA A 131

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SEQ ID NO:3329  
 SEQUENCE LENGTH:123  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS03902

SEQUENCE DESCRIPTION:

GATCAGCCCT TTGTACAGAA AAATGTGTCT ATAAAAATTA TGTGTTATTT AATTCTGATA 60

CTTTTGGCT TGTAATAGC TTCTTGAAC TTTTACAATA AAAATGTTTT AGAACTGTT 120

AAA

123

15

SEQ ID NO:3330

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear

CLONE:HUMGS03903

SEQUENCE DESCRIPTION:

GATCATGACC GGAACATGGN CTGGGTTTCC ACCCAGCTCC AGGCCACATG CAATGTCCAC 60

AAGTNTGCCT TCAATNACTG GTTCAGTGGA CACCTCAACT TCCAGATTGA GCACCATCTN 120

NNN

123

25

SEQ ID NO:3331

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear

CLONE:HUMGS03904

SEQUENCE DESCRIPTION:

GATCGATTCA ATGCCCGATG CTTCTGTTTC ATTCCCGACC CTTTCTACTA TGCATTTCCT 60

TTTTATCAGG TGTATAAAGT TAAATACTGT GTATTTATCA CTAAAAAGTA CATGAACTTA 120

AGNGNAACT AAGCCTTTCG TGTTTTTCCA NAGGNCNGCN NGGCTTCTNT GTACAGTTGG 180

AATAAACAGA CAGCAAAATG GTAAA

205

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SEQ ID NO:3332

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS03905

SEQUENCE DESCRIPTION:

GATCCTCAGG CGGCCCCAC CAGGGCACAC CCTACTGTCC TTGTGCCTCA CGCCCCCTCC 60

TCATCCTGCA CCCCTTCCAT CCCACCTTCC CTTTCAATAA ACAGCTGGGA TGGATACTGA 120

AA

122

50

SEQ ID NO:3333

55

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03906

SEQUENCE DESCRIPTION:

GATCTGATTT TTTCCCCCTT TACCTAGCTG TGCCCCCTCT GGTTATNTAT TTCCTTAGTG 60  
CCAGGAGGGC ACAGCAGGGG AGCCCTGATT TTAAATAAAT CCGGAATTGT ATTTATTAAA 120

SEQ ID NO:3334

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03907

SEQUENCE DESCRIPTION:

GATCACCAGT GCATCCTTCA TCACAGCATG TGCAATATGC CAAGATTACC CTCGGTCATT 60  
CCTGTCAACA AGGGGTCAAT GTCATAAATG TCACAATAA ACAATCTCTT CTTTTTAAA 119

SEQ ID NO:3335

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03908

SEQUENCE DESCRIPTION:

GATCCATGAG GAAAAGATGC TCTCCACCT AAGGCCAGGA ATCTGAGAGC AGGACTGGCT 60  
GAGCTCCAG GGCAAGGGGT TACTAATGC TTATCAATAA AGAATATTGA GCCTGGA 119

SEQ ID NO:3336

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03909

SEQUENCE DESCRIPTION:

GATCAGATTG CATGTNACTC TNAAGCTGAC GAACTTCCAT GGCCCTCATT AATGACACTT 60  
GTCCCCAAAT CCGAACCTCC TCTGTNAAGC ATTCGAGACA GAACCTTGTT ATTTCTCAGA 120  
CTTTGGAAAA TGCATTGTAT CGATGTTATG TAAAAGGCCA AACCTCTGTT CAGTGNNNNT 180  
AGTTACTCCA GTGCCAACAA TCCTAGTGCT TTCCTTTTNN AAAAATGCAA ATCCTATGTG 240  
NTTTAACTC TGTCTNCACC TGATTCAACT AAA 273

SEQ ID NO:3337

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03910

SEQUENCE DESCRIPTION:

GATCACCATG AACAAAGNTA TATTTCTAT TTATTTATTA TATGTGCACT TCAAGAAGTC 60

ACTGTCAGAG AAATAAGNN TTGTCTAAAT GTCATGTTGG AGATNCCTTT GCATNCTTN 119

SEQ ID NO:3338

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03911

SEQUENCE DESCRIPTION:

GATCAGGACT TCAAGGGCCA GACCACAGAC TACTTATAGG AGCATCTTCA AGGCGGTCAC 60  
AGTGAAAACC TTGAAATGGC CTTTTNAAT ATATATAANT AANTGTNAAT ATTATTNN 118

SEQ ID NO:3339

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03912

SEQUENCE DESCRIPTION:

GATCCAAATN ATGGCCACAG ATGAACTTCC ATGCAAGCNA TGGCTGAGTT TCATTGCTTA 60  
AAATNCTCCT CTGTTTAGAG GGGCCTGGTA GAAATAAAAA CCCACCTAT ATCTTAAA 118

SEQ ID NO:3340

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03913

SEQUENCE DESCRIPTION:

GATCCTCCTG GCCGCCCGC AGGTCTNTGG AAGGGCTGGA CGGCAAGTCC GTNTAGCTCA 60  
CGGGCCCCTC CAGTGGAATG GNTCTTTCCG GTGGAGATAA AAGTTGATTT NCTCTAAA 118

SEQ ID NO:3341

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03914

SEQUENCE DESCRIPTION:

GATCCCAGGT GCGTGTNTCT CTGTCTCTCC TAGCCCCTCT CTCACACATC ACATTCCCAT 60  
GGTGGCCTCA AGAAAGGCC GGAAGCGCCA GGCTGGAGAT ANCAGNCTCT TNCCCGTCGG 120  
CCCTGCGTCG GCCCTGGGGT ACCATGTGGC CACAACCTGCT GTGGCCCCCT GTCCNNAAGA 180  
CACTTCCCCT TGTNTCCCTG GTTGCTCTC TTGCCCCTTG TCCTGAAGCC CAGCGACACA 240  
GAAGGGNGNG GGGCGGTCT ATGGGGGAGA ANGGGAGCGA GNTCAAGAGG TGGGCATGGG 300  
TTTGNAAGG GTNGGCGTTT GGGGGGCTN TNATGNTGGC TTTTCAANC N 351

SEQ ID NO:3342

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03915

SEQUENCE DESCRIPTION:

5 GATCATGCCG CTGCACTCCA ACCTGGGCAG CAGTGCAAGA CTCTGTCTCA AAAGGGGAAA 60  
AAAAAAANT TNCTGATGTG NCCCATGAAG GGACCTCATT TNCCTCGNAA TTTTGGN 117

SEQ ID NO:3343

10 SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03916

SEQUENCE DESCRIPTION:

15 GATCGGCCGT ACCAGCCGCC CCGCCCGCCG GTGGGCGCTC TCGGACTACT CGCTGTACTT 60  
GCCGCTCTGA GTCAGTGGCC CCTTCGTTCC TTGTAAATAA ATCCCGCCCC CGGAAA 116

SEQ ID NO:3344

20 SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03917

SEQUENCE DESCRIPTION:

25 GATCCAGACA AGTGGGAGAG CCCGTGGGGG CAGGGGACCT GGAGCTGCCA GCACCAAGCG 60  
TGATTCCTGC TGCCTGTATT CTCTATTCCA ATAAAGCAGA GTTTGACACC GTCAAA 116

SEQ ID NO:3345

30 SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03918

SEQUENCE DESCRIPTION:

35 GATCTCATAA GAAATGTAAT ATGTAAATAA TATCTTGCTT TATGTTGTAA AATATACATT 60  
GTTTGCNCTA GAATAGAAAT AATTTCTTTT CAATAAAAAG AAAGAAGGAC TCTAAA 116

SEQ ID NO:3346

40 SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03919

SEQUENCE DESCRIPTION:

45 GATCGTTGTG TTGTTATTTT ACTGCACTTT TACTTTTTT NCGTGTGGAG CTGTATTCCC 60  
GAGACCAACG AAGCGTTGGG ATACTTCATT AAATGTAGCG ACTGTCAACA GCGAAA 116

SEQ ID NO:3347

50 SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS03920

SEQUENCE DESCRIPTION:

GATCAAGGCC AAATAACCCG ATTTGGTTTG GGCACCTCAAG CAATAGTAAA GCCTGTAAGA 60  
CATGATAGGA TTATNTTCCC CTTTGGATT AAATNTAATA TAGCAGTTGG ATTAAA 116

SEQ ID NO:3348

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03921

SEQUENCE DESCRIPTION:

GATCCTGTAG ACCCTTTCTT TTGGCCAATT TCCCCCTTTT TGGGATGGAA ACATTTACCC 60  
AATCCCTATA CCCCATTGT ATCTTGGAAG TAAATAATTT GTTTTGGATT TTTAAA 115

SEQ ID NO:3349

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03922

SEQUENCE DESCRIPTION:

GATCTCTTCA CTGTNAAAAG TTGCCCGGGT GCAGCGCCTT TCCCTTCTAN CATGGGAAAT 60  
GCAGGCTGGG CCCTTGGGNT NAGCCTGCGG GGCTCTGGTG CTGTCCCCGA CCCNN 115

SEQ ID NO:3350

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03923

SEQUENCE DESCRIPTION:

GATCCACTGT TTGCAGCAGA ATTATATATA TGTATAGGAA AAATCCACTT TGAATAATCC 60  
ATGTTTTGTA TTTGGAAATT GTTTTAAAA ATAAAAAGGA AAGGAAATAT AAA 113

SEQ ID NO:3351

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03924

SEQUENCE DESCRIPTION:

GATCTAGGCA GTGGGTAAAG CCAGACCCCT AAAAGTGACC CTTTCCTCTT CTGCCCTATT 60  
CTNCTNAGAC CCTCAGAAAG NNNTCCAATT TTTTAAATC CCTGTAGCTC CAN 113

SEQ ID NO:3352

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03925

SEQUENCE DESCRIPTION:

5 GATCTGATGA ATTGGTTTT GAATCCCAGA AANGGTCTGC CATGGAGTTG GCAGTCATCA 60  
CGGTAGATGG CGTATGATTT TCCTGAATTT TAAATAAAAT GAAAACCATA AATTAAA 117

SEQ ID NO:3353

10 SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03926

SEQUENCE DESCRIPTION:

15 GATCAGAGCT GTTAGGTAAA GGCCTAACCA CCTCCCTGCA GNCTCTTAAN TCTCAAGCTT 60  
TAGGAACCCA TTTCTAAANG TACACTAGCG GAGANTTTAT ATTGTCAGCC NN 112

SEQ ID NO:3354

20 SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03927

SEQUENCE DESCRIPTION:

25 GATCACGTA CGTCCATAAA GCCAGTATTA CACTTAAATN NAGTATTCTT TTTTGTATC 60  
GTTTTTTTGA GAAGGTAAAC AAATTTAATA AAGCTACCAA TAATGTTGAA A 111

SEQ ID NO:3355

30 SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03928

SEQUENCE DESCRIPTION:

35 GATCTAGAAA NTGCCCTCCT TATACCCCTA CCATGAGCCC TACAAACAAA AAACCTGCCA 60  
CTAATAGTAT GGTATCCCT CTNANTAAAN CATCATCCTG GCCCTAAGGN N 111

SEQ ID NO:3356

40 SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03929

SEQUENCE DESCRIPTION:

45 GATCTTTGCA ATTNAAGGNT TAGCCACGTG GCTTGCTTCA GCNAGTAATG TGAATGGAAA 60  
TAACGTGTAT CANTGCTGGA TAGAAAACCT AANAGCCAAC ACATGGTTCC N 111

SEQ ID NO:3357

50 SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS03930

SEQUENCE DESCRIPTION:

5 GATCCCGTAG AATATATATT TAATAATCCC ACAAACGGAG GCCAGACTTC TGC GTTAACT 60  
TCAGTAACAC AAGCTTCTTT AAGCCAAATA CATCACTTGC CACTACCAAA 110

SEQ ID NO:3358

10 SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03931

SEQUENCE DESCRIPTION:

15 GATCTCCGTG GTGGTCGTGG GCCGCCAGGT GAATNANCCC CACATCCGCN TCCTGGTCAC 60  
CGGCAAGACG GCCGAGTACG ACGTGGCCTA CGGCGAGAGC ACCTNTNCCN 110

SEQ ID NO:3359

20 SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03932

SEQUENCE DESCRIPTION:

25 GATCCTTCGA AGCACTCAGT TCACTCTTCC CCACCACAGT GGTTAAAAGG CGTTTGTATC 60  
TGCCACTATG TGTGTGTTTT AAAATAANCT TTTGGAAACA TGTTTGNGN GNAAA 115

SEQ ID NO:3360

30 SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03933

SEQUENCE DESCRIPTION:

35 GATCCACTAA TG TAGCTTAA GGTTATTAGN TTTGGGCTTT TAATCATGGN ATAATCTTAT 60  
GTATTGGTGT AAGAGTTGAT GAATGACTTT AGCTGTGTGA ATATATAATA GTCAAACCTGC 120  
AAACATTTTG CATCCCTTTT GTGACCTAAT TTACAGNCAT TTAAATTGTG TTGCAGTTCT 180  
GCTTTGCCGT TTAATAAAAA GCTATTTTCA NAAA 214  
40

SEQ ID NO:3361

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS03934

SEQUENCE DESCRIPTION:

GATCANAGAT TTCAATNACA GTGCAGGAAA GCAGCACTGA GAAACTTTTA ATTGTNTTNA 60  
ATTTCTNCTT TAATGTTTAC ACCACCACAT TCCCATTCAC TTAAATTTN 110  
50

SEQ ID NO:3362

55

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03935

SEQUENCE DESCRIPTION:

GATCTTCCCC TGACCTGCTC CCAGGGCTAT AACAGATACG GACTTTGAAA CTGTATGGAG 60  
TATAGAGCAG TGCTCTATAA TTAAAAATAT ACATATATTG CAACCAAAA 108

SEQ ID NO:3363

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03936

SEQUENCE DESCRIPTION:

GATCTTCAGC TTGGTAGATT TAATTGCCCA GTGAATGGCA CTTACGTTTT CATTTTNNAC 60  
ATGCTAAAGC TGGCAGTGAA TGTNCCACTG TATGTCAACC TCATGAAGAA TGAAGAGGTC 120  
TTGGTATCAG CCTATGCCAA TNATGGTGCT CCAGACCATG AAAGTCTAG CAATCATGCA 180  
ATTCTTCAGC TCTTCCAGGG AGGCCAGATA TGGTTACGNC TGCACAGGGG AGCAATTNT 240  
GGAAGTAGCT GGGAAATATT CTACGGTTTC AGGCTATCTN CTTTTATCAA GGTTCGAATG 300  
TCAGTNCAGT NTTTGACNAC TAAAAGGNNT NGGGGTNCTA ATTANGTNGG GTTTGAAGGG 360  
TAN 363

SEQ ID NO:3364

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03937

SEQUENCE DESCRIPTION:

GATCTGGGGA GTNTNAGGAG AGGGTGGCAT CAGNAGCTGC TCAGGCTTGG CGGAGGGAGC 60  
GGCATGGCCG ATGTCACTCA GCCCCTTCCC GGTCCGCCCN NTTCCN 106

SEQ ID NO:3365

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03938

SEQUENCE DESCRIPTION:

GATCGTTTT TCCAGAGTCG CGGGGACACA GGAGTNTTCC TACAGTACAT NCACGCCCGC 60  
NTCCACAGTT TGGAAGAGAC TTTTGGATGT GGTACNTGA NTGAN 105

SEQ ID NO:3366

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03939



## SEQUENCE DESCRIPTION:

GATCATCTAA AAAATGCCAT GANTGGAAAT NCGAAGGCC AGACACCAAT ATTCNTAGA 60  
AGTAAACAGC TCAAAGACAC TCTCCTATCT NAGGAAATNA ATGTN 105

SEQ ID NO:3367

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03940

SEQUENCE DESCRIPTION:

GATCCAGTGG GGTCCGGACA CTGGGCCCCG CAGCGAAAGC ACGNTCCAGC CACCAGGAGG 60  
CCACCTATTN TTTCAAAATA AAGACTGCGT TCCTCTCTTG GAAA 104

SEQ ID NO:3368

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03941

SEQUENCE DESCRIPTION:

GATCAAAAA GAAGAGTTAA AACAACACAT GTAAATNCCT TTTAATATTT NATGGGAATG 60  
CCTCTCATTT AAAAATAGAA ATAAAGCATT TTGTTAAAAA GAAA 104

SEQ ID NO:3369

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03942

SEQUENCE DESCRIPTION:

GATCCTTTAT CTTTCCATAT GGCACACGTA AGAAAGTGTT TTTCTACTAT TAATATTAAA 60  
TTAAACCTT TACTTNTGTA TAATAAATNA AAACCTCAGAA TAAA 104

SEQ ID NO:3370

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03943

SEQUENCE DESCRIPTION:

GATCTGGAAG AGGCTTGTA CCTGAACCTAN TATGTAGGAA GGCAGTACNA NCAGCCCACC 60  
AGTGTAATCT CCCTGNATTA AGGCATTCTT AAAAACTTAG GCNN 104

SEQ ID NO:3371

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03944

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCGCTCT GGTCAAACCC TTCCAGGCCA GCCAGAGTGG GGATGGTCNN TNACCTGCTG 60  
GGAAGGCANN CTGATGGGGC ACACCCTTGG CCTCTCGTCC ACGN 104

SEQ ID NO:3372

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03945

## SEQUENCE DESCRIPTION:

GATCAAAATT TTTGATAAT TTAATAATTG TGTGTGATTT TNAATTTNA AGAAATTGCT 60  
GAAACTTAG AAAATATAA TGGTATACAT ACAATAGNNA AA 102

SEQ ID NO:3373

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03946

## SEQUENCE DESCRIPTION:

GATCAATAAT TTAATGTAA CTAGTTGGGA TTTTATAGTT AAAATNATAT TTGTGTATAT 60  
AACATAACTA ATCTGTAAAT NGTAATAAAT ATATTTNCAA TTAAA 105

SEQ ID NO:3374

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03947

## SEQUENCE DESCRIPTION:

GATCATTTAG TACTTTTGTN TTCTCCCATG TGCTTGAAGG AAAAATAAAG TGCTACTACC 60  
GTATTTNTTG TTTTCATCAA AAAATAAAAA TAATTTAAA 99

SEQ ID NO:3375

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03948

## SEQUENCE DESCRIPTION:

GATCTTTAGC ACAGTGATAT NACCATGACT TCACAGACAT GGTCTAGAAT CTGTACCCTT 60  
ACCCACATAT GAAGAATAAA ATTGATTAAA GGTAAA 97

SEQ ID NO:3376

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03949

## SEQUENCE DESCRIPTION:

GATCAATAAT AATNAGGAAA GCATGATATG TATATTGCTG AGTTGAAAGC ACTTATTGGA 60  
AAANATTAAA AGGCTAACAT TAAAAGACTA AAGGAAA 97

SEQ ID NO:3377

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03951

## SEQUENCE DESCRIPTION:

GATCCCCCTC CTTCCCCCTC TCCCCATTGT ATTTATTTGC CTGCTGGAAA ATNACATCCG 60  
GAAATAAAAT AGAAATATGT CTTTNNATTT TAAA 94

SEQ ID NO:3378

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03952

## SEQUENCE DESCRIPTION:

GATCCTAAAC TTTTGGATA ATCTTTTATA TTTNTAACCT TTGAATTTAA TCATTGTNCT 60  
NAGATTAAAA TAAANATGC TATTGAACT AAA 93

SEQ ID NO:3379

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03954

## SEQUENCE DESCRIPTION:

GATCTGGAAA TCCCTGCTGT AATCTTTTAA AGGGAATCCA CTGGAAATAA TTAGTTTTTG 60  
TTTTAAATAA AACCATTCTT TACTTAACAA A 91

SEQ ID NO:3380

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03955

## SEQUENCE DESCRIPTION:

GATCTATGGC CTCTGGTGCT TTGTCCTGTA TTTGGTTTAA TTTTTTTGTC CTAATCTCTT 60  
CAATCAATAA AATTGTGCGT ATTAACTAA A 91

SEQ ID NO:3381

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03956

## SEQUENCE DESCRIPTION:

GATCAACTNA ATGTTTAAGA CTTTAGATGT CTTGTATTAA AAATTACACA AAAAAAGTAA 60  
AACTTTTAT ACTTACCCTT TTAACCTAA A 91

SEQ ID NO:3382

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03958

## SEQUENCE DESCRIPTION:

GATCTCTGTA ATNTTATNTA GAGTTTGAGC TGAAGCCCCG TATATCTAAT NTATTTTGT 60  
AAACATGAAA GTGCATCCTT TCCCTCCAAN 90

SEQ ID NO:3383

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03959

## SEQUENCE DESCRIPTION:

GATCATACCT ATTAAATATA TGCCAAACAC CAAATATGAA TTTNATGATG TACACTTTGT 60  
GCTTGGCATT AAAAGAAAAA AACACAAA 88

SEQ ID NO:3384

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03960

## SEQUENCE DESCRIPTION:

GATCAAGAAG ACGNNTAAGG GAAGAACGTA CACAGTGAAA ANCCAAAAAA AGAAAAAAAT 60  
GTTTATACAA CCCTAAGTCA ATAACCTN 88

SEQ ID NO:3385

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03961

## SEQUENCE DESCRIPTION:

GATCTAGGCA CACCTNGCTC TTNGCTGCAT GTGGTTATNA ACANCTTCCA GTGGAAGTCG 60  
AATAAACAGT TTTTGGTAAA TCTCAA 87

SEQ ID NO:3386

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03962

## SEQUENCE DESCRIPTION:

GATCCTGCCC TGAATCTCCA TAGTCTCCAC TGTGAACTGA GGAGGGGAGG GGTGTGCTGG 60  
GGAATAAATC TTGTATGAGA ACAAA 85

SEQ ID NO:3387

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03963

## SEQUENCE DESCRIPTION:

GATCCATTTA NAGGCCAAAT NTCATTCTGC AGGTGCCTTC CCGATGGATT AAAGGTGCTT 60  
ATNTTTTTTT AAGTTTNAAG TAAA 84

SEQ ID NO:3388

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03964

## SEQUENCE DESCRIPTION:

GATCGTGTTT ATTTTGNITT CCGATTCTAG ATATAAGTTT TGNATGGGCA GGAAGACTAA 60  
AATAAAAGTT TTAAGGTAA A 81

SEQ ID NO:3389

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03965

## SEQUENCE DESCRIPTION:

GATCTCCAGA TGTAATTTCC CCTCTTTAAT TTAAANTAAT NTAAAGATTA CTAAAACAAT 60  
AAAANCTCCT AAAAANTCAA A 81

SEQ ID NO:3390

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03966

## SEQUENCE DESCRIPTION:

GATCTTTCTT TCCAAAACAT TTCTGGACAG TACCTGATTG TATTTTTTTT TTAAAAATAA 60  
AAGCACAAGT ACTTTNGNGN TTGTTAAA 88

SEQ ID NO:3391

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03967

## SEQUENCE DESCRIPTION:

GATCCCCCA CAGCCCCTGG TCAGTCTGCC CTTGTCCTG GTCTGAGGTC ATTAAAATTA 60  
CATTGAGGTT CCTAAA 76

5

SEQ ID NO:3392

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

10

TOPOLOGY:linear

CLONE:HUMGS03968

SEQUENCE DESCRIPTION:

GATCACAATC ATTTGAATC CCTCTTCCTC ACTTTTTTTT CTAAGAAAAT AAACATTTTA 60  
CTGTTTTTAT GGAATAAA 78

15

SEQ ID NO:3393

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear

CLONE:HUMGS03969

SEQUENCE DESCRIPTION:

GATCACAGCT GACATTTACA AAATATTTTT NTACCTTAGA ATTTCTGCAT TAAATAAAAT 60  
ATTTTGTTTT AAA 73

25

SEQ ID NO:3394

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear

CLONE:HUMGS03971

SEQUENCE DESCRIPTION:

GATCTTTTGC TAATGCAATT AGNATTATGT TTTGCATGTA TGACTTAATA AATCCTTGAA 60  
TCATAAAA 68

35

SEQ ID NO:3395

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

40

TOPOLOGY:linear

CLONE:HUMGS03972

SEQUENCE DESCRIPTION:

GATCCTCTAA ATNTGGAATT TTGATGTAAT AACTGCTAAT AAAATNATAT TGAAACTGTT 60  
TTATAAA 67

45

SEQ ID NO:3396

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

50

TOPOLOGY:linear

CLONE:HUMGS03973

55

## SEQUENCE DESCRIPTION:

GATCAAAGCC CGGAAAGGCA AATGAAGCNT CATGTGTAGT GTAATAAAGN TGTCTGCTGT 60  
TCAAA 65

SEQ ID NO:3397

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03974

## SEQUENCE DESCRIPTION:

GATCGAAGCC TGTGTAAAT GCTACCAAAT GGCAAAAAGC AACATAAAC AGTTTGATT 60  
TTAAA 65

SEQ ID NO:3398

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03975

## SEQUENCE DESCRIPTION:

GATCCCCAAT ATATCTACCA TTGTATGTTA AATAAATNAC CATTTTTGTA GAAAAAATTC 60  
TAAA 64

SEQ ID NO:3399

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03976

## SEQUENCE DESCRIPTION:

GATCTGTAAA TNACTTTAAA AGCTATTTTA GTAATTTAAA TAAATTTACT TTCTTGTTT 60  
ATACTCTCAA A 71

SEQ ID NO:3400

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03977

## SEQUENCE DESCRIPTION:

GATCTCTATA NTTTTTTTA AATTTTCTCC AGCCTGGGTG ACAGAGCGAN ACTCCGTCTC 60  
AAA 63

SEQ ID NO:3401

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03978

## SEQUENCE DESCRIPTION:

GATCTCCTGC TGCCTTTCCT GGAGTTTGTA AAATTNTNCC TGAATACAAG CCTATGCGTG 60  
AAA 63

SEQ ID NO:3402

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03979

## SEQUENCE DESCRIPTION:

GATCCAAGCA TAGTAGAAAA GCTTCATGTG TTTTAAAAA TAAACAATAA CAAAAAATTA 60  
AA 62

SEQ ID NO:3403

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03980

## SEQUENCE DESCRIPTION:

GATCATGTGT TCTGGAGAGT GTTCTTTATT CAATAAAGTT TTAATTTAGT ATAAACATAA 60  
A 61

SEQ ID NO:3404

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03981

## SEQUENCE DESCRIPTION:

GATCTAATTT TTCAAACCTT CACTATTTTG AAAATATAAC CAAGGCCGGT TCGGGTGGAA 60  
A 61

SEQ ID NO:3405

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03982

## SEQUENCE DESCRIPTION:

GATCATGAAA CTGATTGTAA AGCTTTTGA CAACTAATAA ATGTCTTGGT AATTGCTAAA 60

SEQ ID NO:3406

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03984

## SEQUENCE DESCRIPTION:



GATCAATGGA TTTGTTTACA ATGTGATATT TTCTATTAAA TCCAGTATTT TCAAATAAA 59

SEQ ID NO:3407

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03985

SEQUENCE DESCRIPTION:

GATCTTGTAC TAACTTATGA TAGAATGTAT CAGAATAAAT ATTTTAAACA GTGTTAAA 58

SEQ ID NO:3408

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03986

SEQUENCE DESCRIPTION:

GATCATNAAA GTATACAAAA TAAATAAAGT AGGAGATTTT TTGCTGTTT AAA 53

SEQ ID NO:3409

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03987

SEQUENCE DESCRIPTION:

GATCTGTTTA GTGAGATTTA GCATGTGTGA ATAAAGTATA TGCAGGAGGA AATTGCTTTG 60  
TNTTCCCAAT CGGTAGAAAT TCGGGACCAT AAAAATTGTG TTTTACCATG TGGCCTACAA 120  
A 121

SEQ ID NO:3410

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03988

SEQUENCE DESCRIPTION:

GATCATTGTT AAAGGATTGC TGCAAATAAA TACACTTTAA TNTCAGTCAA A 51

SEQ ID NO:3411

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03989

SEQUENCE DESCRIPTION:

GATCTTTAAA ACATTTTAA TGAATAAGT TGAATAAAGG CACAATTAAA AACTGTCAAA 60

SEQ ID NO:3412

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS03993

SEQUENCE DESCRIPTION:

GATCAAACAG AAGCAGCCGT GGGCAAAATA CAATTTTCATT TAACAAATTG AAA

53

SEQ ID NO:3413

SEQUENCE LENGTH:521

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04020

SEQUENCE DESCRIPTION:

GATCTCATAG GACGGAGGGG GAAATGGTTT CCCTCCAAGC TTGGGTTAGT GTGTTANCTG 60  
 CTTATCAGCT ATTCAGACAT CTCCATGGTT TCTCCATGAA ACTCTGTGGT TTCATCATTG 120  
 CTTCTTAGTT GACCTGCACA GCTTGGTTAG ACCTAGATT AACCCTAAGG TAAGATGCTG 180  
 GGGTATAGAA CGCTAAGAAT TTTCCCCCAA GGACTCTTGC TTCCTTAAGC CCTTCTGGCT 240  
 TCGTTTATGG TCTTCATTAA AAGTATAAGC CTAACTTTGT CGCTAGTCCT AAGGAGAAAC 300  
 CTTTAACCAC AAAGTTTTTA TCATTGAAGA CAATATTGAA CAACCCCTA TTTNGTGGGG 360  
 ATTGAGAAGG GGTGAATAGA GGCTTGAGAC TTTCTTTGT GTGGTAGGNC TTGGAGGAGA 420  
 AATCCCCTGG NCTTTCACTA ACCCNTNTGG ACATACTNCC CACAACCCAG TTNGATGGGN 480  
 TTTCCCGTAA TAAAAAGGGN TNGGGNNTTN CCTTTTTGAA A 521

SEQ ID NO:3414

SEQUENCE LENGTH:501

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04021

SEQUENCE DESCRIPTION:

GATCAGAAAT NACTGTGTCA TGGTGCTCAT TCACTGCAAA CTCCCAGTTG NAAGCTCCTT 60  
 GGCTCCCCCG GAGGAGCAAG AATCTCATAG TTCAGAGACA CAGAGGGCCT TTAGCCCTA 120  
 ATNACCTTTT GGATGGGACT GCAACTCATG ACTATCCTGA TATTGGAAGA AAGGACTTTG 180  
 TTAATCTTCT CCCCATAGC TCTGCTGCGT AGGTCTACAT CTTACTCAGA ATCACTACAC 240  
 ATTCCTTTAG TCTTCCTCCA AGCTCCAGAG CCATTGGTAC AAATGCTTTA TTGAAACTAA 300  
 ATACATANTN NACACAATGA GATGAAGACA ATATAGANGT NCGCATAGTC ATCATAATCC 360  
 CGTTCCTTGG CCGGTTGAGG CAGCTCAGTG GCTGAGCCCA GTCAAGCCAA CCCGGNAGTT 420  
 TCACTCACGG CNTTCAAGGN TTTTGATGCT AATTCTTTTG GGTTTCCTAC AGTTTATTAA 480  
 ATAAGTNGTC TGNGTGGGAA A 501

SEQ ID NO:3415

SEQUENCE LENGTH:485

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04022

SEQUENCE DESCRIPTION:

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GATCTCAGTG AACTAATACA CAGCTTGAGC GTTTCCATGT GCTAATGTTG CACATTTACT 60
AAAAAACTTT GGAAATGGAA AATAATGTAT TAGTGCAACA GTTGATGTGC TTCTTTGGGC 120
AAAGATATAG TTTTGTTCCT CAATTTGTAC TTAAAAGCGA AAGAACATTG AAAACATAGA 180
CTTACTGGCT GTAGCAATGC TGGCCTGTTA ACTGATAACT AGAACTTAGG TTCACGTTTA 240
TGTAAGGTGT GTAAACCTA GTAGAGCTTG CATAGTCGGG CACTCAGTAA ATGGTTTGGT 300
TCCTTTTGCC CCTTGGTAAG TTTATTTTAC CCATCCNCCC ACCTGCCCAT TCTGACTTTN 360
TATTAAATC ANCCATGTGG GACCCAGNGG TGTTTAATGN GGATGTTATT NCCAGAAGGA 420
GGATTTGAGA AAAATTTGGG GATTNTCATT GCAGGTAAAC NATTCACAAA ATNCTTTTGT 480
GTAAN
485

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SEQ ID NO:3416
SEQUENCE LENGTH:471
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS04023
SEQUENCE DESCRIPTION:
GATCTGTTTT TTCATCGAGG TNCGAGGTA TNCTTTNAAA GATAGTGANA NGCAGACACT 60
GCTCCTGTG CAGCTCTGGT ACCTCCTGCC CACTGCTGTC ACTTCAAGCC ACTGGCAATG 120
CTTCTGTCCT CGTGTCTTGG AGGAAAATCA CCTGGGGGGA GGGGACTTCT TGTGGTAAGA 180
GCAAGTGCAG GTATGAAATG CGAAGATTGC CCCAGCTAAA AGTGGACAAG TCCGCTTTGT 240
GAGATGAATA CTTCTGAGA NNCNNNNCAA GTATCTCTCC ATTTTACCAT TATGAAAAC 300
ATCATTAAAA AAAACAGTTT AGATGCCTTC TCCTTTTGGG GGAAAAAGGG TGCTTTTAT 360
TGTATAAAGC AGCGTCTTAT GTATTTTGAT ATACCATTGT TTGAACTCC GTCTTTAGCT 420
GATAGATTCT CAAATATCCT NGATTTTGGG ATGTTTCAGTA TGTTTGTGAG N 471

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SEQ ID NO:3417
SEQUENCE LENGTH:466
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS04024
SEQUENCE DESCRIPTION:
GATCAAATAT ATTTCAAGCT ATAAAAGCAG GAGGTTATCT GTGCAGGGGA CTGGCATCAT 60
GTATTTAGGG GCAAGTAATA ATGGAATGCT ACTAAGATAC TCCATATTCT TACCCGAATC 120
ACACAGACAG TTTCTGACAG GCGCAACTCC TCCATTTTCC TCCCGCAGGT GAGANCCCTG 180
TGGAGATGAG TCAGTGCCAT GACTGAGANG GANCCGACCC CTAGTTGAGA GCACCTTGCA 240
GTTCCCCGAG AACTTTCTGA TTCACAGTCT CATTTTGACA GCATGAANTG TCCTCTTGAA 300
GCATAGCTTN MNNAATATCT TTTTCCTTCT ACTCCTCCNT CTGACTCTAA GAATTCTCTC 360
TTTCTGGANT CGCTTGAACC CAGGANGGCG GGAGGTTNCA GTAAGCCAAG GTCANTGCNA 420
CTGCACTNTT AGCCTTNGGT NANAANTNGA GGTTCATT TATAA 466

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SEQ ID NO:3418
SEQUENCE LENGTH:464
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS04025

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## SEQUENCE DESCRIPTION:

GATCGCCAGG CTGATTGAGA AGAACAAGAT GAGTGACGGG AAGAAGGAGG AGCTCCAGAA 60  
 GAGCTTAAAC ATCCTGACTG CCTTCCAGAA GAAGGGGGCC GAGAAAGAGG AGCTGTAAAA 120  
 AGGCTGTCTG TGATTTTCCA GGGTTTGGTG GGGGTAGGGA GGGGAGAGTT AACCTGCTGG 180  
 CTGTGAGTCC CTTGTGGAAT ATAAGGGGGT AGTGGGAAAA GTGGTACTAA CCCACGATTC 240  
 TGAGCCCTGA GTATGCCTGG ACATTGATGC TAACATGACC ATGCTTGGGA TGTCTCTAGC 300  
 TGGTCTGGGG ATAGCTGGAG CACTTACTCA GGTGGCTGGT GAAATGACAC CTCAGAAGGA 360  
 ATNAGTGCTA TAGAGAGGAG GAGAGGAGTG TACTGCCAG GTCTTTGACA GGTGTAATTC 420  
 TCATTCANTT AAAGGTTTCA GTGTTTTTGG TTAAGGTGGA TAAA 464

SEQ ID NO:3419

SEQUENCE LENGTH:457

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04026

## SEQUENCE DESCRIPTION:

GATCACCTTC CTGTCTGGAG GCCAGAGTGA GGAGGAGGCG TCCATCAACC TCAATGCCAT 60  
 TAACAAGTGC CCCCTGCTGA AGCCCTGGGC CCTGACCTTC TCCTACGGCC GAGCCCTGCA 120  
 GGCCTCTGCC CTGAAGGCCT GGGGCGGGAA GAAGGAGAAC CTGAAGGCTG CGCAGGAGGA 180  
 GTATGTCAAG CGAGCCCTGG CCAACAGCCT TGCCTGTNAA GGAAAGTACA CTCCGAGCGG 240  
 TCAGGCTGGG GCTGCTGCCA GCNAGTCCCT CTTCTGNTCT AACCACGCCT ATTAAGCGGA 300  
 GGTGTCCCA GGNTGCCCC AACANTTCAG GCCCTGCCN NNTNCCAACT NTTTGAAAGA 360  
 GGAGGNCGCC TTCTTNGGGG GCTTCCAGGT TNGGNTTNC CCGGGNTTTT TTTTTTCCC 420  
 TTGGGTGANA NATGGGTNGT TTNGGNGGCG GTNTTN 457

SEQ ID NO:3420

SEQUENCE LENGTH:452

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04028

## SEQUENCE DESCRIPTION:

GATCTGGAGG GGTCACGGA AGACGGAACA TGTCCACTTC CAGGCCCGAG CTTCTNAGCC 60  
 TGCCGTTTGC CACTCTCCAG CATCTGGCCC AGCCTGTCCA TCCTCATCTC TCTTCCTCCN 120  
 NNACTCCGTG CTCCCATCAC TNGGAACCAT TTGCATTTNT TTGTCTCAGC TATATTGTCT 180  
 CACCTCTGAG TTTTGTCCCA TGATGTTGGA TGCCATGGAA TGCCATATCN TCCCATTAT 240  
 CTCCCCCTTG TNTGGATAAT TCCTACTCAT CCTACAATAC TGATTTTAT CTGTGCAAAG 300  
 AAGGTCTTCC CCAAGTGGCC TCTGGGTTNG ANAAGGGGNG TTCCTCTGGC TTNTTCCAGA 360  
 CTTTTTTGTT TCCTNCAACC AAAAGGCTTT AGGCACCGTG GGGGAAGGAG GGGTNTTNNT 420  
 TNGTCCNAGG GAAAAAGNNT NGNGGCAAAT GN 452

SEQ ID NO:3421

SEQUENCE LENGTH:450

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04029

## SEQUENCE DESCRIPTION:

5 GATCAAACT AACCTTTCAG CGTATTCTCA GCTATGACAC AGTGGTGCAA ACAACTGGAG 60  
 ACTCGTGGCA CATACCATAT GATGAAGACT TGGTAGAAAG ATGTTCCCTGT GAAGTACCAA 120  
 CCAAATGGCT TTGCCTCCAC CAAAAGACAT AGAGATTCTT ACCTCTATGC TAAGTTTGTG 180  
 TTTGGGTACC CTCTAGGTTG GCATCAGAGG CTCTTGAGCT GGTGTTTGTG TAGGGCATTG 240  
 CCTCTGTCCT GAAGATAAAA GGATTNTATT AACAGCATTG ACATTGATTT TTTAATGAAA 300  
 10 TGAGATATAT CTTTTCATAA CCAGCTGCGT TTTTTCCTCC TAACATTTGT TTTTGGAGGG 360  
 CTTATCAAGA GTTGGAGACC TTAGTGTAGA GCAAAACCTG CATTTCTCCT ACTGGGCCAG 420  
 CTATTCCACT TAGGCTTGGG TGAATAANAN 450

SEQ ID NO:3422

SEQUENCE LENGTH:444

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04030

## SEQUENCE DESCRIPTION:

20 GATCCCAAGT ATTAGGAGCT ATTTCTTAAA TAGTTTAAAT TTGCCTTTGA AAAAAGTTCC 60  
 ATTACTTAAA AGTATTAATT TAAGCAAAAT CATGGAACAC ATTGACTAAA AAATACCTTT 120  
 TATTTTTACT CAACTTGTTA AAGGGGCAGA TAAAGACTTT GGCAAAATTG ATTAAGTGCA 180  
 CAAAATAATG TTATCCAAAC TGAGTAATTT ATTGCTGGTC TGNGGCTTGC CTGTTTACA 240  
 25 CTTAAGTAGA ATTTACGTTG TTTCCACAAA TGGCAGATAT CACCATTTAA AGGNATTTAA 300  
 TAGTGACCTA TTCAATAAGG CANTCATCTG GGGTAGCAAA CTTTNTTTA AATCTNACAT 360  
 AACCTCAGGC TTTATAANAA NGCCACCATA ATTGGAAAAT TGGGGNTCCT CCCCTCTAAA 420  
 NGCCTTAAGG GATTCAAAGG CTCN 444

SEQ ID NO:3423

SEQUENCE LENGTH:439

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04031

## SEQUENCE DESCRIPTION:

30 GATCTTGTGA AAATGCTGTT AGTATCCAAC CTTAAAATAT ATTAGTATAT GGGTTTTTAT 60  
 TAAAAGAATT ACTTTGAATT TNCTATTTAA TTCATATGTA AATAAAGGAA CATTTCATTT 120  
 CACTTAAAAA AATTATATCA GTTATTAGGC TGGGTGCAGT GGCTCATGCC TGTAATCCCA 180  
 40 GCACCTTTGGG AGGCCAAGGC GGGTGGATTA CCAGAGTTCG GGAGTTTGAG ACCAGCTTGA 240  
 CCAACATGGA GAAACCCCGT CTCTACTAAA ATTACANAAT TNGCCAGGTG TGGTGGCGCA 300  
 TGCCTGTAAT CCTGGGCTAC TCAGGAGGCT TGAGGCAGGN GAATNGGNTT GAAAACCCCN 360  
 GGGGGNNA GGTTCGCGTT GAGCTGAGNN TTGCGCCATT NNACTTCCNN CCTGGGCAAG 420  
 45 GNNGGGNGNA ACCTNTNNN 439

SEQ ID NO:3424

SEQUENCE LENGTH:437

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04032

## SEQUENCE DESCRIPTION:

GATCTAAGAA ATCATGTGCA TATATCTTTC AGATTCTAT TTTGGGAAAN TGAAGGTTTC 60  
 TACAACATAT TGTTCAGTG TTCAAATAAA CTGAAGGACT CAACATTACA TTTGAACTAT 120  
 ATCCTTCCTA GTGGGTTAGT GTGAAAAAGN GNTTGGCTGA TTCCTAAAC TCTGCCAGCC 180  
 CTGCAGTAAT CTCCAGGGNC NNGTTATTGT TCAGACATTC CNTGGTGATT CCTGGGAAGG 240  
 AAGCTTGGCT GCTCAGTTTC TGAGTCTGGG GTGAGATAAT GTTCTGGGAA GGGACATCTG 300  
 TTCTTTGGTG TAATCTCTCA TGGTGAAATC TGCTCTGTAC ATCAGACAAT TGCATTGCTA 360  
 CCAAGTTTCA TACCAAATAT TTGAAAGGTT GGTATTGAAT CTAAANCCAA ATATTAGTTT 420  
 TTNTTAAACT CATGGGN 437

SEQ ID NO:3425

SEQUENCE LENGTH:424

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04033

## SEQUENCE DESCRIPTION:

GATCCAAACC TTACACCTGA GTCTGTTAAG AGCGCCCTGC TACAGGAGGC CACAGACTGC 60  
 CTGATTCTNN NGGACCGCTG TTCTCAAGGA CGGGTAAAGG GTCTCCTGGC CAAAATTCCC 120  
 CAAAGCTGTG AAGACAGAAA AGTGGTGAAC TATATCAGAA AAGTGCAGCA GGTTTCTGAA 180  
 GGCGCACCCCT ACAATGGAAC TTAAGACTTG TATTACTTTC CCAAGAGGAA AGGATTTTTT 240  
 TCCCATCCCN NNTTGTATGA ATGGAGTTAT TTANGAAAA ANGATATTTT TACACGAAAC 300  
 TTTGTAAGTG AAAGCTGCTT TTTCCTTCCT TTCCTTTCCT TTTACCTCCA TAAGGAATAG 360  
 GGAANGTAGG ACCAAGANAN AATTGAACTC CTTCCCATT TCTAAATAAA GGTTTTGGGG 420  
 GAAA 424

SEQ ID NO:3426

SEQUENCE LENGTH:422

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04034

## SEQUENCE DESCRIPTION:

GATCTCNGAG CTACAATACT CACTANATAT ANTTTTCCAA TCAAAATATN CTATTCTATA 60  
 TTCTAAGGGT TAATATGTGA TTATAGTGTG CACTTGCCAC CATTTTTTTA AATCAATGGA 120  
 CTTGAAAAGT ATTAATTTAG ATGGATGCGC AGATATACCC TCAGTTCAGT CATAGATTGG 180  
 AGTTTGCATA TAATANNNCN CCGGTATGTN GACACTATTC TAAATAGTTC TATTATGACT 240  
 GAAATTTAAT TAAATAAAN NGGTTGTAAT ATGNGATGTG TATGTGTATA TACNGTATGT 300  
 GTACTTTTTA AAATAGGGTG TATGTCCCAA CCCTTTTTTA TACAGGTNTG AATTTAAAAA 360  
 TACCATGGTT ATATACATAT ACCTNGNNTT NGTCCTAAAA TAAAGGNTTT TNATGCACGC 420  
 NN 422

SEQ ID NO:3427

SEQUENCE LENGTH:408

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04035

## SEQUENCE DESCRIPTION:

5 GATCTTTCCA CCTCAGCCTC CTGAGTGGCT GGGACTACAG GTGCATGCCA CCAAGCCTGG 60  
 CTAACCTTTT GTAGAGATAG GGTTTTNCCA TGCTGCCAG GCTGGCTTAG AATTCCTGAA 120  
 TTCAAGTGAT TTGTCTGCCT CAGGCTCCCA AAGTGCTGGG ATTACAGGCA TGAGCCACAC 180  
 TGCACCCAGT CCATGCTACC CTTTTTATAT GAAACACCTA TTAACACGGT ACAACAACAC 240  
 TTCAAAACAT ATTATTTGAA TTTNGGCNTC TGATTTTTTA GTCANCAATC CATTANGGCA 300  
 AANACCTNGT TTTCCAAACT CAGATGTTCT CCAACTTACA CTAATGTNTG GTTTTTTTGG 360  
 10 ACTTNGGTGN GGGGAAAAAN TTAACCNNGT TTTNNTTTN TTATCAAA 408

SEQ ID NO:3428

SEQUENCE LENGTH:378

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS04036

## SEQUENCE DESCRIPTION:

20 GATCTTAGCT TCTTTAATCA GACTTTGTGA CTAAAAAGTT TGGGGGTTTT CTTTGAAAGT 60  
 TTCCAGCCCT ATTCAGAAAG CAACTCTTGG CTGTGTGCAT TTTTCAACTC CAAGCAGCCC 120  
 AGGGGTAAGT AAACAAAGTA TGGATGAAGG TCAGATTTTN TTGTCANNNT CTGAGAAACC 180  
 TGGCAGCCTG CTGTTAACAA CACAGGCCAG TATTGGGTTT TATTGAATTT GGTATGTGAC 240  
 CAAGGTCGGC CTAAAGGATG GCGCAGGTCC TGGGCAGGAA AGAATTTTTC CTTTATCACA 300  
 25 TAACTGTAAT ATTTGGTTGC TCAGCATAAG TNATGGAAGC AACCCTTAA TTTCTAATAA 360  
 ANTTGTGTTA ACCTCAAA 378

SEQ ID NO:3429

SEQUENCE LENGTH:376

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS04037

## SEQUENCE DESCRIPTION:

35 GATCACAACA CCAGTACCAG CACGAAGAGC CTCCTCCCGA AAGAGTCTCG ACTGGACACC 60  
 TTCTGGGACT AGCAGTGAAT CGGGACACAA ACCACCCACC CCATTGGGAG AAAAACCAG 120  
 ACGCCAGGAA AAGAAGAAAC AACAAAGGCA GGAGAACAGC CACTTTCAGA CTTGAAAATG 180  
 ACAAAACCCT CAGTTGAGCC TGAGCCCCCG GCGCGGGGGC TGCTACACTA CAGGACACCC 240  
 AGCATCGGCT TTGACTGCAG ACTGTTACC CACACGAGCC CTGTGCTTTT GGTGTAAATA 300  
 40 ATGTACAATT TGTGGATGTC ATTGAATCTA GAGGACTTTC CCCTTTTAT ATTTGTATTA 360  
 ACTTTAACTT ATTAAA 376

SEQ ID NO:3430

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS04039

## SEQUENCE DESCRIPTION:

50 GATCAAGCTT GTGACTTGA CCGTTTTTAT ATTACTTTTG TAAGTATTCT TGTCCACATT 60  
 CTACTTCAGC TTTGGATGTG GTTACCGAGT ATCTGTAACC CTTGAATTTC TAGACAGTAT 120

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TGCCACCTCT GGCCAAATAT GCACTTTCCC TAGAAAGCCA TATTCCAGCA GTGAAACTTG 180  
 TGCTATAGTG TATACCACCT GTACATACNN NGTATAGGCC ATCTGTAAAT ATCCCAGNGA 240  
 NCAATCACTA TTCTTAAGCA CTTTGAAAAT ATNNCTATGT AANTNATTGT AAACCTTTTTC 300  
 AATGGTTGGG ACAATGGCAA TAGGACAAAA CGGGTTACTA AGGTGNAATT GNCCAAAAAA 360  
 TTTTTTAN 368

SEQ ID NO:3431

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04040

SEQUENCE DESCRIPTION:

GATCAATCTC AATTCCTTTT CATGCCCTCC TGCATTGCTG CTGCGTGGGT ATTTGTCTCC 60  
 TTAGCCATCA GGTACAGTTT ACACTACAAT GTAAGCTATA GGTGGAGCAT CAGCAGTGAG 120  
 TGAGGCCATT CTTTCATCCTT AGGATGTGGC AATGAAATNN TGGTGCAAGT TCCTTTCTCT 180  
 TTTGTGAATC TTTCCCCCA TTTCTGTTT ACATGTAACC CAACAAAATG CAATTTCTAG 240  
 NGCCTTCTGT CCAATCAGTT CTTTCCTCTG AGTGAGACGT ACTTGGCTAC AGATTTCTGC 300  
 CTGTGTTTGC GACATTNNTC CCATTCACAC AGNTATTAN GGGGCTAATN AANNGGANAA 360  
 ATAAGGCTTA CAAA 374

SEQ ID NO:3432

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04041

SEQUENCE DESCRIPTION:

GATCCTGGAG AACCTAAGAC TCCAAAAGCG TGGTACTGGA GGAGTGGACA CTGCTGCCAC 60  
 AGGCGGTGTC TTTAATATTN CTAATTTGGA CCGACTAGGC AAATCANAGG TGGAGCTGGT 120  
 GCAACTGGTC ATCGATGGAG TAAACTATTT GATTGATTGT NAACGGCGTC TGGAGAGAGG 180  
 CCAGGATATC CGCATCCCCA CACCTGTCAT CCACACCAGG CATTAACTCC CCATCGNCCA 240  
 GCTGATGACT CAAGATTCCA AGGAGTTCTG CTCATTCTAA TGGTGGGCCG TTCTACTTGN 300  
 TCTGGACCTG NCCTNGNATC CCCNTNGNCC TTNNTTCCT TAGTTAAAGA CTTNGTTAGC 360  
 TGATGNAAA 369

SEQ ID NO:3433

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04042

SEQUENCE DESCRIPTION:

GATCGTGGGG TTGTTGGCAG AGGGCAACCC TGGGCCCCAC ACCGTGTGGA CAGGCAGACA 60  
 CCAGATTGTC CAGGAGCAGG AGCTGCTGGG ACTGCGCTGG CCCCAGGACCT AGTGGGCCTT 120  
 CTCCTGGCTG CTGAGATGTC GTCTGTGACT GGCCTGGCTG GAGGGGGAGT GTTGACAACC 180  
 CAAAGCTGTT CTCAGTCTG GGGAGGGAGA GGCAGGGTCC CCAATGTCCG AGCTGNATCT 240  
 GGACGCTGCT CTAAAGGAC CTCCTGGGGN AGGGGAAGCG GTAGGNTCTG GACTGGGNAA 300



GATGCTGTAT GACCTCCCTG AAGNACCCGT GACTTCCCCA TGNTTTACCC TTTTGTGN 358

SEQ ID NO:3434

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04044

SEQUENCE DESCRIPTION:

GATCTAGAAA GCAACTTGGA AGTGTAAGA GTCACCTTCA TTTTCTGTAA CTCAATCAAG 60  
 ACTGGTGGGT CCATGGCCCT GTGTTAGTTC ATGCATTCAG TTGAGTCCCA AATGAAAGTT 120  
 TCATCTCCCG AAATGCAGTT CCTTAGATGC CCATCTGGAC GTGATGCCGC GCCTGCCATG 180  
 TAAGAAGGTG CAATCCTAGA TAACACAGCT AGCCAGATAG AAGACACTTT TTTCTCCAAA 240  
 ATGATGCCTT GGGGTGGGGA GTGGTAGGGG GAAGAGCTCC CACCCTAAGG GGCACACACT 300  
 GAGTTGCTTA TGCCACTTCC TTGTTCAAAA TAAAGTAACT GCCTTAATCT TAAA 354

SEQ ID NO:3435

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04045

SEQUENCE DESCRIPTION:

GATCATTAAT GAGGAGCTGA TGGCCTCCCT GGACCAGCCA ACACAGACAN TGGTGATGCA 60  
 CCGCACTGAG CCCACTGCCC AGCAGAACCT GGCTCTGCAG CTGGCCGAGA AGCTGGGCAG 120  
 CCTGGTGGAG AACAACGAAC GGNTGTTTGA CCACAAGCAG GGCACCTACG GGGGCTACTT 180  
 CCGAGACCAG AAGGACGGCT ACCGCAAAAA CGAGGGCTAC ATGCGCCGCG GTGGCTACCG 240  
 NCAGCAGCAG TNTCAGACGG CCTACTGAGC TCTCCACTCT GTTCCCGCC TGGGCCATCC 300  
 AACCTTGAAG TCCTAAACCA CACCTCAGTC ACTAAAGGTC TGTTTAAAGT TAAA 354

SEQ ID NO:3436

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04046

SEQUENCE DESCRIPTION:

GATCTAATTT ATTTATTTAT TGCCTGGCCG GTGACTCGGG GGAGGAGGCG ACCCTGTCAT 60  
 CTGTCCCACC TGCTGCTGCC CCTTGGAGCA GCCTGCACCT NCTCTCCTCC CATCCGGCAA 120  
 CAGTNTGAAA GTACGTGGAG GACGGGACCG GAAGACGAGA GAGGGCTGGA CATCCTGCCC 180  
 ACCGTNTCCC AGCCAGGGCA GGNGAGGGGA CCATGGCCCG NANGTCAAGG GGCCCCGATG 240  
 TGCACAGCTG CCACAGGGAG GGAGNTCTTG GGGAGATGGG CANTCAGGTG GCCCGTCCTT 300  
 GGTNGAGTGC ACANANTTGC GCGNACANAT CGGGGTTTTT CCTGGNTTTN 350

SEQ ID NO:3437

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04047

SEQUENCE DESCRIPTION:

5 GATCTTGAAT CTCTTTCTTT GTTCTGTTTG TTTAGTTAGT ATCATCTGGT AAAATAGTTA 60  
 AAAACAACA AAAAATCTG TATCTGTTT TAGCATGTGC TGCATTGACT CTATTAATCA 120  
 CATTTCAAAT TCACCCTACA TTCCTCTCCT CTTCAGTAGC CTCTCTGAAG GTGTCCTGGC 180  
 CAGCCCTGGA GAAGCACTGG TGTCTGCAGC ACCCCTCAGT TCCTGTGCCT CAGCCCACAG 240  
 GCCACANTGA TAATGGTCTG TTTAGCACTT CTGTATTAT TGTAAGAATG NTTATAATGA 300  
 10 AGATACACAC TATANCTACA AGAAATTATA AATGTTTTTC ACATCAAA 348

SEQ ID NO:3438

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04048

SEQUENCE DESCRIPTION:

20 GATCTGAGCC ACCCTCCCCG CACAGCCCTG CACCCCGCCC CTAGGGTTGG CAGNCTCANT 60  
 TGGCCCTGG CAGAGGAACA AGGACACAGA CATTCCCTCA GTGTGGGGGG CAGGGGACAC 120  
 AGGGAGAGGA TGGTTGTCCC TGGGGAGGGC CCTCTGGCCC CAGGCAACCT TAGCCCTCA 180  
 GAACAGGGAG TCCAGGACC CAGGGAGAGT NTGGGGACAG GACAGCCTGT TTCTTNTAGC 240  
 TTCCTGGGGT GGGAGGCACA GGGGCAAAGC ANTACCCAG GGAAANTGGG AGGTGGTGCT 300  
 25 GGTGCTCTCT CCAGGNCCAC CATGCTGGGA GAGGCGGCCA GAGCTTN 347

SEQ ID NO:3439

SEQUENCE LENGTH:346

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04049

SEQUENCE DESCRIPTION:

35 GATCTTCCCT GGNGGCCTTC GGCTGCNTGC NTGCCTGAGG TCCCNCTGC CAGTCCCGGG 60  
 CCCTGGAGAG CAGATGCTGT CTTGTNATGT ACAGGAGGAC CTTTAAAAA AATCAAGTTT 120  
 CTATTTTTTN CTGGTAGTCC GCATACCCAT ACCCTCTGTT TTTNAAAGGC AAAGGCCAAT 180  
 NAGTCCCAT TTGTAGCATG GCACCAGGGT CTTAGGCCTA GTCCTCTCAT TCCTCCCACC 240  
 CTCCGAGATG GTCAGTGTGT CATGGGAAGC CCACCCCAAG CTCTGCCAGT GCTCTCTGGG 300  
 40 CCTGGNTCCN AGTCAGTGGT GGCCACGATG CGGTACAGGG CATCCN 346

SEQ ID NO:3440

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04050

SEQUENCE DESCRIPTION:

50 GATCCATGTG ATTATTAAAA TGAAGTAGC TGAGAGCTCT AATTTNCCTG TCTTGAAACT 60  
 GTATAAGANC TCATGTGATT AAGTTCACAG TTTATTGTTT GTNTGTTTAG TATTTNAGAA 120  
 ATATACCAGC ACTACTAATT AACTAATGTC TNTNATTTAT NATATTATGA TAAAGTAAAA 180  
 NTTTCACTTG CATTAAAGTCT AAAGTGAAGG GGTAATTACT GGGNGGNGAN TGAGCAGCTT 240

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TGACTTTGAC AGGCGGTTTG TGCAGGAAAG CACAGTGCCG TGTGTTTAC AGCTTTTCTA 300  
GAGCAGCTGT GCGNCCAGGG TAGAGGAGTG TNGAAATTCA TTN 343

5 SEQ ID NO:3441  
SEQUENCE LENGTH:340  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS04051  
SEQUENCE DESCRIPTION:  
GATCTGCTCA GAAAGGAAGA GGCAGGCGCC AGGGGGAACC CCCTTCGTGT TTTGTAACCC 60  
TCCCTTTNAG GTGAAGCCCT TTTCTTGCT AAAACCGCA ATTCTCCGGT TAGAAATNTT 120  
ACTTGGTGTT TTTTGGTTTT GTGAAACGGC CGTCCCAAAG CTGGCTGGAT TCCTAGAAGA 180  
15 GTCTGTGTTG AAGGCATCTT TCAAGCCCTC GCTCTGGTTC TNAGGGCAGC ATTTTCCAGG 240  
CGGGTTTGTG TTGCATTTCT TGGAGCCTCT CCGNGNAGCA ACCAGACGGG AGATTTTAAT 300  
TTTAAGCTGT TCATGCTGGG NCTGACAGCC TGCAGGGTTN 340

20 SEQ ID NO:3442  
SEQUENCE LENGTH:339  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04052

25 SEQUENCE DESCRIPTION:  
GATCCTTGGG CTGGCCTAGA ACCAGTATCT GTAGTGGATA TAAGCCAACA ATACAGCAAT 60  
ACTCAAACAT TCACAGGCAA AAAAGGAAGA TACTTTTNTT AACATTTCTG AAATTCAACT 120  
GGAAGCTTCA TGTGTCAGGA ACATCTTGGA CAAAACCTTA NGTTGTGTTG ATATAAATTT 180  
30 ACCCAAAGAT GATGNCTTTG ATTGGNTAAT TAGTAAGGTC TTTTGTGTAT TTTNCATCGT 240  
ATCAGGTATT GTTGATATTA GAGAAAAANG TAGGATAACT TGCAACATTT AGCTCTGGAA 300  
GTACCTACCA CATTTTNGAG ATTTACCGTT TCCATATTN 339

35 SEQ ID NO:3443  
SEQUENCE LENGTH:339  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04053

40 SEQUENCE DESCRIPTION:  
GATCTGCCGT TNATGTTGCT TTCTCCTTTG TCCTCTTGGA CTTGAGGGCA TTGTGAAAAG 60  
CTTTGCTGTG ATTTAAAAAT GCCAGCAATT TTAATCTAGC AGTGTGAAG CTGGGAATTT 120  
TTTGGCGCAA TCCATGTAGC AGTGACCCAG GCTTGGGAGC CAGAAACAAG TGTGACCTGG 180  
45 GATTTNATTT AACACAACG TTGCCAAAGA GTTGGCTTTG TTTATTTGGT TTTGGCGGGG 240  
AGAGGAGTGG TATTTNATGC TTTCTGTGGA CANTGTAACC CTAAACACAN CANGTATTTT 300  
AANTGCCACC TACATAANTA AACCATANGC NTATTGAAA 339

50 SEQ ID NO:3444  
SEQUENCE LENGTH:339  
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS04054

SEQUENCE DESCRIPTION:

5 GATCTACATA AAAACTGCTA CATGNCAAAA ACCACACCTA AAGAAATTTT AAGAATTTGG 60  
CACAGTTACT CACTTTGTGT AATCTGAAAT CTAGCTGCTG AATACGCTGA AGTAAATCCT 120  
TGTTCACTGA AGTCTTTCAA TTGAGCTGGT TGAATACTTT GAAAAATGCT CAGTTCTAAC 180  
TAATGAAATG GATTTCCCAG TAGGGGTTTC TGCATATCAC CTGTATAGTA GTTATATGCA 240  
10 TATGTTTCTG TGCATGTTCT CTACACAATT GTAAGGTGNC ACTGTATTTA ACTGTTGCAC 300  
TTGNCAACCT TTCAATAAAG CATATAAATG TTGGTTAAA 339

SEQ ID NO:3445

SEQUENCE LENGTH:334

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04055

SEQUENCE DESCRIPTION:

20 GATCAGCCTC TTCCTCTATA AACAATGACC AATTAGACGT TTCCGTAATT CCATGTATTA 60  
TGTATAGTAC ACTCTATAAA TGTAATGTA ATGCTTGTCT AAAAAGTGCA ATTTATTGTA 120  
CATTGTCCCA ACAAATGTTT ACTTTTATAA TCGTTATGAA CTTGAATTGG ATTAGTATCT 180  
TGTTTTTATG TGTGAATGAA GCCTTGTAAT ATAAACAAAT GCAACTGAGA AGGTAACAAG 240  
25 GTGACTGTTT TTGTGAGCCA GTGATGTTTT CAATGCTTTG TGTTGCCCTT TTGGCCCCAT 300  
TAAGCAGTAA TAAACATTG TTCTGAAGTC CAAA 334

SEQ ID NO:3446

SEQUENCE LENGTH:334

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04056

SEQUENCE DESCRIPTION:

35 GATCCAAGAA GCGGGTCCCT GAGACGGGGG GTGGCTGCCC TCCCAGACC ACCCCGGCAG 60  
CCTGAGCAGN TCCAAAGCAC TGGCTTGGGG TCCGAGACCT TCAATGTAAA GCAGGCGGAA 120  
TGGGGGGACA GGACAATTTC TCCCCTCCA GGGGCTCCAG GACTCTCCCT GGGGGGCCA 180  
CCTCTTGCCC CCTAACCTCT TTCCCCTTT TCTGCCCCG TGGGGAGGAG CCCCTTGAC 240  
40 CTGCTCCGTG CCCAACACAT GCCCTCTCTG TACATCTTTT GGTAAATNAT GAGAAATAAA 300  
GGAAGTGGAC GCAAAGTGGA TCGGCAGCA GAAA 334

SEQ ID NO:3447

SEQUENCE LENGTH:332

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04057

SEQUENCE DESCRIPTION:

50 GATCCAATCT CAGTGTCTAA CTCATCATCC CAGATTATTC TGAAGTGGA ACCACCCTCC 60  
GACCCCAATG GCAACATCAC CCACTACCTG GTTTTCTGGG AGAGGCAGGC GGAAGACAGT 120  
GAGCTGTTTC AGCTGGATTA TTGCCTCAAA GGGCGAGTCC AGTCATCAGC TCCGCTGTAA 180

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GCTGTTGGCC CTGCATTCAA GTAACCAGAA CCACCCGTGA GAGCTGCCAC CAGGTANTGT 240  
CACTCGAAGC TTCCTTTTTT TTTTTTTTNA ATTCCGGAAA GTTTAANTCT GTANTCCCAG 300  
GGNCCATTT AAANANGGTT TTTTTTGT AN 332

SEQ ID NO:3448  
SEQUENCE LENGTH:332  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04058

SEQUENCE DESCRIPTION:  
GATCCAAAAA AAGCTNGAAG CCTACATTTC CCAGAGCCCC TTTCAGCTTG AATTCCAAAT 60  
GTGACTTAGC TTCCTCTATG CAGATGTACC TACTTGAAAC TGGGAAGGCC AAATNAGATA 120  
GAGGNAATNT TTCTGCCAAC AAACAGCCAC AGAGCATTTT ATTTTCTAG AAGAGCAATA 180  
ACAGAGACCC CAGGGTGTGG TGTGGCAGGA CGAGGAGCAT CCATTTTGCT GGNGGGGATT 240  
GTGGCTAAAA TAATGNGGCT CTGGAGCCAG CAATNGGCAG CATCTTCATG ACTTTCCAGN 300  
TTCCAGGCTG TAAGCAGAGA TAGCATCTCT TN 332

SEQ ID NO:3449  
SEQUENCE LENGTH:326  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04059

SEQUENCE DESCRIPTION:  
GATCCACTAT ATGCCTCAGC ACATGGAACC TTAATGACCA AAGTGAAGAG CAGATTATTC 60  
ATACGGTGTA ATAAGCATCT GGAATGGACC CATCCGTGTA CTTCAATCAA ATGTGTAAAT 120  
GTCATATTCA TTCAGATTTA TAAAGCTAGT AGTGTATAGT CAGAAACAGA ATCAAAGTTA 180  
GATATACATT TTTAAATATT TACTGCATAT GAGGCTTTCT GTTAATTTT TAATGTGAAT 240  
AATTTATATA TTGCACATTC TAGGGAATAA TATTGATTGT ATGNCTACTG TGCTGCATTA 300  
AGAAAATAAA ATTCCTATAT NCCAAA 326

SEQ ID NO:3450  
SEQUENCE LENGTH:329  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04060

SEQUENCE DESCRIPTION:  
GATCAGAAAA ACTGAAGATG GAAGTTTGG CCGGTGCTCA TTAGACATGA GTCCTCACTC 60  
TGTNTCCTGA GCCCGTTTCA TTCTTCCAAC CTCCCTGCCC CCACACACTT ATCCCAGACA 120  
CAACACCATG TGGTCTGGAG GTCCCAGCCC CCACCCTAAA AAGGTTATCC CNGAGAACTC 180  
CACCAGACTT GGGAGCCCAA GTGCAGTGCC TGGNGCTGCT CCCATCTGCC GGCCCCNTTC 240  
TTTCCTNGCA ATTGGTTTGN ACTCACTGGG CTGTGCTCTN CCCTGTTTAC CCGATGNNG 300  
GGAAATAAAG GCCCTTTTGC CTCCTGAAA 329

SEQ ID NO:3451  
SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04061

SEQUENCE DESCRIPTION:

5 GATCTGGCGC TTCTACTTTG AGGGCTTCTT TGACCTCATT GCTGTGGTAN GCCGGCGTAG 60  
 TCCAGACCAT CCTATACTGT GACTTCTTCT ACTTGACAT TACAAAAGTA CTCAAGGGAA 120  
 AGAAGCTCAG TTGCCAGCA TAAGTGCCAA AGGCCATCAC CAGCATCTGT CCTTCAGGGT 180  
 10 GCTCGGACAG ANTTNTTACC ACAGCAANGG CATAAGGTGC TTTATACGGA AANTCAGNAA 240  
 CTTAACTCTT TTGTTGCAGN TAGTCATCAG TGGCTCTGTA AAAACGGAGG GGGAAAGNGN 300  
 CNGGAGGTTT CTGTTTAATG CATCN 325

SEQ ID NO:3452

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04062

SEQUENCE DESCRIPTION:

20 GATCTGATTT TATGTTTCGTA ACTTTCTGTA AAGAAAGACA CAAGGACTTT TCAAAGACAG 60  
 TTTATATCTT TCCAAGGCAG GAAGCTTTGC ATTTGCAATC TTAGTGTTGT GTCCCTTTCT 120  
 GATTTTCAAA TACATCACAC CTGCCTTCCT GTTTTGGGAG CAAAGATGTA ATTTCAATTC 180  
 25 CCCTTGCTAC CGTCCTTATT TAAATNATTT CCATTCTAAG AGATTTTNGT NATTTNNNTA 240  
 AATGTAATCT GAGCACTTNN TNGTATTCTA AAAGATAGAT GATATCAGAT AAATATGTTG 300  
 TACATTTTGA TTTAAATTAT TTTN 324

SEQ ID NO:3453

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04063

SEQUENCE DESCRIPTION:

35 GATCTGGAAG ACAGACGTAC AGCTTGGAGG GCAGGGGGAC TCTAAGGCAA GGAGATTTAC 60  
 AGTTGGGAAG GAGGCAGTGG CAGAGGGGTG AGGGACAGGG GCCCTTAAGT CCAGCGAGGA 120  
 AAGCTCNNTG TGGGCCCCTG CTACGCTCCG TTTGGGGTGA CCTGGAACGC CTCTTCTCCC 180  
 AGCTCCCTCC AGCCATCAGC AGCCTCTTGT CAAGCTTCTG CCTCGCCCCA GTCTATCCCC 240  
 40 AACCCTCAAT CAAGACCACC TTTCTTCACG GTCATATTT ATTCTTTGTT CCTTTTCTT 300  
 TTTGTAAGAA ACATTCACAA AAACCAGTGC AAAACCAAA 339

SEQ ID NO:3454

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04064

SEQUENCE DESCRIPTION:

50 GATCTCAATG CTGTCTGGGG ACCCTGAAGA GTTTNTNAC CTGTTTCAGTC TCATCTAACC 60  
 TTCCAATGTN TGATGTTTCT GCCAAATTCC TGCCTGATTC TGGGTCCGTC CTGACCTCCA 120

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5 AAGGTCAGNT TGGTGCTTGA GGTCTCCNTG CTCTTGGTGG CAGTGGTAGC AGCAACAGCA 180  
GCAGCAGCAG CAGCAGCAGC AGCAGAGACC TNTCCACTTT CCCTTAGCCC TNTGNTGGGT 240  
AGAGGGAACT TAAGGGACTT CCTCCAGNNG CNTTTAATNT GGAATGGGT AAGAAGGTTG 300  
NGCTCCNCTG TTNGTTN 317

10 SEQ ID NO:3455  
SEQUENCE LENGTH:315  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04065  
SEQUENCE DESCRIPTION:  
15 GATCCTCAAA AAACCCAAAA ACACCATTCT CTAATAGTCA TGACAAATGG CTTCAGTATG 60  
GCTTGTTTT NATTTNCCAG ATGGCTTTN CTCTTATTT TNGAAGCCCC AGTCTTTGAT 120  
TTTACAGGTA ACTTTCAAAA CATCATGATG CTGCCAAATG TACTTTTGTA AACTTAAACA 180  
TTATGATTCC TGTATTATTT CAGTGAGAGC TACAGTGTGA TATTNCAGAG TCTATTAAAT 240  
AAAAATGTGA GTTGAATTA CACCATCTGT GCCAATTACA AAGCAATTAA AGGATTTATN 300  
20 TNTNATGAAA AAAAN 315

25 SEQ ID NO:3456  
SEQUENCE LENGTH:312  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04066  
SEQUENCE DESCRIPTION:  
30 GATCTGAGGC TGTGTCTCTG CCTTGTTTT AGAGGACTTC AGCGTCCAAG ACTGGGGCCC 60  
ACCNTTNTCA CCAGCACTAA ATGCACTAAC AAGGACTCCA GACCTGCAGC CCCAGACCCG 120  
CCGTAGTATA AGCCTAACAA GCAACANGTA GCACCTTAGT CTTTGTTCCA GGAGAGCTGA 180  
GCAAGCTGGT GAAACCACTC TCCTTCCTTT AAACANCGTT TCAACCANCC TTTNCNTGGA 240  
GCCAACNTGT AAAAAGTGGG TTGATTGCTG ACAGNATGGT CTTCTTCCC TGGATTTNAG 300  
35 ACATACCAGT TN 312

40 SEQ ID NO:3457  
SEQUENCE LENGTH:309  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04067  
SEQUENCE DESCRIPTION:  
45 GATCTTTCCG GGGCCTACAG GCGTGTAAGA CAGCTTGGTC TGGTCTGTGC AGAAGTGGGG 60  
AGTGATGGGC AGGTTCGGCA GCCTAACATT GTTCAGGCGC ATGGCCCTG CGGTGTGTAC 120  
ACGAACTCGG CTTCTTTTGT CCTAGGTACG CCAAGGGCAG GTTCTGGAG ACTCCCTTGT 180  
GCCC GGGATG GCAAGGGCAC CGGGCTGGCG TTTCCACATC TGTCTTCATT AGCAGANNAG 240  
TGATGATGGA TTTTATTTC CTCACACTCC AGTTTGTAAT AAAATGCCAA ATTCTGTCAG 300  
50 CTATCCAAA 309

55 SEQ ID NO:3458

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04068

SEQUENCE DESCRIPTION:

GATCAGCACC ATTTGTGGTA TGTTCCGTGA TGAGCGTTTA GTGAGCCTNN TGGCTGCAGA 60  
 GCACTATGAA ATCATGGTAC GTAGTCCCCG GCACCTGTCTG TTATTCCCTAT ATCCTCCTGC 120  
 AACTGTGGTT TGAAACTGCG CATTCTCTAG TAGTATATAT CGTGCCTGTC TTCAAAAACA 180  
 TTTCCCTTNN GTATACTCAT NCCCCCAGG CATTGGGGTA GTGTCAGTCG GACTGCACAG 240  
 GGAACACGGT TTCCAGTGGC TTTGGCCCCT ACTCGGGAAA CGTCTGCCTG TTCTCGATNG 300  
 TGATGGGGN 309

SEQ ID NO:3459

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04069

SEQUENCE DESCRIPTION:

GATCTAGCTG GTCACGACGA TGTTTTACC AAGGTCACAG GAGCATTGCG TCGCTGATGG 60  
 GGTGGAAGTT TGGTTTGGTT CTTGTTTCAG CCAATATGT AGAGAACATT TGAAACAGTC 120  
 TGCACCTTTN ATACGGTATT GCATTTCCAA AGCCACCAAT CCATTTTNTG GATTAAATGT 180  
 GTCTGTGGCT TAATAATCAT AGTAACAACA ATAATACCTT TTTNTCCATT TTGCTTGCAG 240  
 GAAACATACC TTAAGTTTTT TTTGTTTTGT TTTTGTITTT TTGTTTTTNG TTTTCCTTTA 300  
 TGANGAAA 308

SEQ ID NO:3460

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04070

SEQUENCE DESCRIPTION:

GATCAAGCAG AGAAANTAAT TAATTCATG GGAATAATG AACTAGTGAG GATAATATTT 60  
 NCATAATTNT TNATTTGAAA TTTTGCTGAT TCTTTAAATG TCTTGTTTCC CAGATTTCTAG 120  
 GAAACTTTTT TCCTTTTAAG CTATCCACAG CTTACAGCAA TTTGATAAAA TATACTTTTG 180  
 TGNACAAAAA TTGAGACATT TACATTTCTT CCTATGTGG TCGCTCCAGN NCTTGGGAAA 240  
 CTATTCATGG AGTATTTNTA TTGTATGGTA ATATAGTTAT TGCACAAGTT CANTAAAANT 300  
 CTGCTCTNTG TATAGCANGG NNNGGGTTGG GGGGGCGGGN GGNNGGGGGG N 351

SEQ ID NO:3461

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04071

SEQUENCE DESCRIPTION:

GATCAGATAG TTTCTGAGG CTAAAATGCC CCAACATGTA AAAGACTGCN ACAAGGGTTA 60



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ATGAGCCAGG AACTGCGGAT GGTAACCTAC ATCTCTATAA TTACCATAGG ATATATATGA 120  
GTACCATAGG ATTCTTTTGC ATAAGTGTAG AAAGTACAGA CAACACCCTC CCGTGTGTTGC 180  
TATTAGAGTT TTTANTGTTG ATTGGAAAAT GGGAGATTCA CTGTGTGCCA TTCTTGGTAT 240  
ACGTTGANGA AATTACATCA CTAGTACACA CNGNGGNNNT TCCACATTCA CACGCCCCAG 300  
CTCTN 305

SEQ ID NO:3462

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04072

SEQUENCE DESCRIPTION:

GATCAAGCTA CAGATATGGG ATACAGCAGG CCAGGAGCGA TTTCACACCA TCACAACCTC 60  
CTACTACAGA GGC GCAATGG GTATCATGCT AGTATATGAC ATCACCAATG GTAAAAAGTTT 120  
TGAAAACATC AGCAAAATGGC TTAGAAACAT AGATGAGCAT GCCAATGAAG ATGTGGAAAG 180  
AATGTTACTA GGAAACAAGT GTGATATGGA CGACAANNGT GTTGTACCTA AAGGAAAAGG 240  
TGANCAGATT GCNNGGGAGC ATGGTATTAG GTTTTTTGAG ACTAGTGCAA ANGCNGGTAT 300  
AAN 303

SEQ ID NO:3463

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04073

SEQUENCE DESCRIPTION:

GATCCGGTCA TACATCCACA TCAGGCCTGG CCAGCTGGAT GTTCTTAAAN AGTTCACAA 60  
GCAGATTACT GCACGGGCAA CAAAGGATGG GACTTTTGTG ATTTCAAAGA CATGATGTAT 120  
GGGGATTAGA AAGAACTCAA GACACTCCTG CTTGATACAG AACAAAAAGA GCTTAACAGG 180  
ACCAACAGGG CTTAAGCCCA GACTTGACGT AACAGAAATG TGCCAATAGG TAATAGGTAA 240  
TTTTNCTTTC TCTGACTTGT TTTGTTTTCT TGAATAACA CTGTTGTGTG GCTAGAAAGG 300  
AAA 303

SEQ ID NO:3464

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04074

SEQUENCE DESCRIPTION:

GATCTACTTT CACATTCTCA AGTTTTTNTC ATCTGCATTA GAGGTGCCCA GTAGGTTCCC 60  
AGGTTCCAGC GTGCCCCTCC CTCAGACACA CGGACACAAT CAGCCGAGAA GTTCCTGGTC 120  
TGAATCACGA GAATGTGGAG GGGTGGGGGG TGTCAGTGGA AAGGCATAAG GCTGAGCTGA 180  
GACCAGTTGC TGGTGAACT GGGCCAATCT GGGGAGGGGA ACATCCTTGC CAGGGAGTTT 240  
CTGAGGGTCT GCTTTGTTTA CCTTCGTGC GGTGGATTCT TTTTAACTCC GTCTACCTGG 300  
CGTTTTGTGA GAAATGTCAG ATAGGAAAAT AAAAACCATT TGAGTAAA 348

SEQ ID NO:3465

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04075

SEQUENCE DESCRIPTION:

GATCTGACCT GGTGAGATTA TTTCTNATGA CCTCATCAAA AAATAAACAN TTCCCAATGT 60  
TCCAGGTGAG GGCTTTGAAA GGCCTTCCAA ACAGCTCCGT CGCCCCTAGC AACTCCACCA 120  
TTGGGCACTG CCATGCAGAG ACGTGGCTTG GCCCAGAATG GCCTGTGCCA TAGCAACTGG 180  
AGGCGATGGG GCAATGACAG ATACANCAGA ACANTGCTTT TGAGGCANGC TTCTTCCCTN 240  
GNGGGTNGGT TGTNATGGCC NTGGCTTTTT NAGTTGGGNG NCATTANAT TAAGGTTN 299

SEQ ID NO:3466

SEQUENCE LENGTH:415

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04076

SEQUENCE DESCRIPTION:

GATCTACGTN ATCTCAGGGC AGTTCCTACA GATGAAGCAA GAGCTTTTNC AGAAAAGAAT 60  
GGTTTGTNAT TCATTGAAAC TTCGGCCCTA GACTCTACAA ATGTAGAAGC TGCTTTTNAG 120  
ACAATTTTAA CAGAGATTTA CCGCATTGTT TCTCAGAAGC AAATGTCAGA CAGACGCGAA 180  
AATGACATGT CTCCAAGCAA CAATGTGGTT CCTATTCTATG TTCCACCAAC CACTGAAAAC 240  
ANGCCAAAGG TGCAGTGCTG TCAGAACATC TAAGGCATT NTNTTCTCCC CTAGAAGGCT 300  
GTGTATAGTC CATTTCCAG GTNTGNGGAT TTAAATATAT TNGTAATNCT NNGTGTCACT 360  
TTTGGTGT TTATNACTTCA TACTTATGGN TTTTCCATG NCCTAAGNCT TTTN 415

SEQ ID NO:3467

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04077

SEQUENCE DESCRIPTION:

GATCCACCTT CTTCCTTAGG TCCCCTCCTC CATCAGCAAA GGAGCACTTC TCTAATCATG 60  
CCCTCCCGAA GACTGGCTGG GAGAAGGTTT AAAACAAAA AATCCAGGAG TAAGAGCCTT 120  
AGGTCAGTTT GAAATTGGAG ACAAACTGTC TGGCAAAGGG TGCGAGAGGG AGCTTGTGCT 180  
CAGGAGTCCA GCCGTCCAGC CTCGGGGTGT AGGTTTCTGA GGTGTGCCAT TGGGGCCTCA 240  
GNCTTCTCTG GTGACAGAGG CTCAGCTGTG GCCACCAACA CACAACCACA CACAN 295

SEQ ID NO:3468

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04078

SEQUENCE DESCRIPTION:

GATCAAAGCA CTGGGCTTGT CCAGGCNCAT AATAAATGCT CCATTGAANG TACTATTCTN 60

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GTTTTCCACT GCTGTGGAAA CCTCCTTGCT ACTATAGCGT CTTATGTATG GTTTAAAGGA 120  
 AATTTATCAG GTGAGAGAGA TGAGCAACGT TGTCTTTNCT CTCAAAGCTG TAATGTGGGT 180  
 TTNGTTTTAC TGTTTATTTG TTTGTNGTTG TATCCTTTTC TCCTNGTNAN TTGCCCTTCA 240  
 GAATGCACTT GGGAAAGGCT GGTTCCTTAG NNNCCTGGTT TGTGTCTNTT NN 292

SEQ ID NO:3469

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04079

SEQUENCE DESCRIPTION:

GATCTCTTAA GAGATGATGG ACTTATGTAT GTTACAAGAC TTCGAAATGT TGGAGTCCAA 60  
 GTNGTTTCATG AACATATTGA GGATGGAATT CATGGAGCTT TATCATTTCAT GACTTCACCA 120  
 TTTTATTTAC GTCTAGGTCT TAGGATAAGA GATATGTATG TAAGTNGGCT GGATAAGANT 180  
 TTATAAATAT GTGATGTGTA TGTATAGCCC TTACATAGTG GATTGTAATT NGTGATATTT 240  
 TGTGGTTTTG GAGCAAAGAN CAATGTCATT TGAGTTATCT AAATCTACAT N 291

SEQ ID NO:3470

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04080

SEQUENCE DESCRIPTION:

GATCTTTTGA TTCCTCTTGG GCTGAAGCAG ACCAAGTTCC CCCCAGGCAC CCCAGTTGTG 60  
 GGGGAGCCTG TATTTTTTTT AACAAATCC CCATTCCCCA CCTGGTCCTC CCNCTTCCCA 120  
 TGCTGCCAAC TTCTAACCGC AATAGTGA CTGTGCTTGT NTGTTTAGTT CTGTGTATAA 180  
 ATGGAATGTT GTGGAGATGA CCCCTCCCTG TGCCGGCTGG TTCCTCTCCC TTTTCCCTG 240  
 GTCACGGCTA CTCATGGAAG CAGGACCAGT AAAGGGACCT TCGATTAAAA 290

SEQ ID NO:3471

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04081

SEQUENCE DESCRIPTION:

GATCCAAAGT CCTGTGGTTA ACGCCTTCAT TTATAGATGA GGCAGCTGAG GCCTGGGGAT 60  
 GTGAACAACC TGCTCACAGT CCTCATTTAC TGGATTTGAC TTCAGCCAGG TGAAGTGGAA 120  
 TGCCTTGGGG CGTGAAGGG CATTAGGAGT GTTTCATTG ATATGTGAAT GCTCATAAAA 180  
 AAATGTCAAG GAATGAAGAA CAGCANCTCT CAGTGGTGCC TGCATTTATA ATTATTTATG 240  
 TGAAAGTCAA ATTCATGTAC AGTAAATTTG TTATAAGAAT ATTCAAA 287

SEQ ID NO:3472

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04082

SEQUENCE DESCRIPTION:

5 GATCCAAAGT GCAAGGNTTT GATTATAAAC ATAATTTCTT AGACTGAAAG TTTTGGAAA 60  
 AGATGCAGGG TCTGAGTCAG GCCTTCTGGT TATATTGTGC AGTTTCAAAA GAACTATTTA 120  
 ANACTCTTGA AAACATCATGT AAATAAAAAAT CATAGGGTGA AAATTGTATT TGTTAAAAATA 180  
 CCTTAATAAT TAAAAATGAC CTGATTTCTT GGAAAATTTT ATTATTCAAA AGGTGGAGGC 240  
 ATTGTAAAAA GGAAATAGTG ATGTAAATAA ACATGTTCTC TTTCAAA 287

10

SEQ ID NO:3473

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS04083

SEQUENCE DESCRIPTION:

20 GATCTGTTTG TCACTGACAG ACTGTAGTAG TGTCTGTGTG CTGACTGATA GATAGACTAT 60  
 AGTAAAATTT GGGTGTGGCC TGACTAACGG TCTAGGGTCT GTAAGCTGAC AGTCTGCCTG 120  
 CTTTCTGATT GTATCCATTG AAGTGTATGT ACATTATGGT AATNCTCTGT CTATTAAATG 180  
 TGTCTAACAA AGGAAGGAAT TAAGCACTCC ACATGTTTTT TTTATAGGGG AGTTCCTGTAC 240  
 ACTATGATTT TAAATAGATA TTTCTTATAT AANGGAAA 278

25

SEQ ID NO:3474

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04084

30

SEQUENCE DESCRIPTION:

35 GATCCCAACA CTGAAGGGGT AGAAGGCCAG GGGGGCATGG AGAGTGACGC TCCATTATAG 60  
 TGAAGAGCCA AACATATGTN AACTGTTTGC TGTGTGGAGG TGTTAGTTCT GCTGCCTACC 120  
 ATCTTCATCT CTAGCACCTC CCCTGCCAAG AGTCAACCAC TAAGCAATCC CACCCAAGCC 180  
 TGGATGCTTC TAGAGGGGCC CACTCCCAGC TGGGAGAGTN TAGGGGATAT GCTCACACCA 240  
 CATTAGCAGC AACCAATAAA AATGCTGGAA ACAAGAAA 278

40

SEQ ID NO:3475

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04086

SEQUENCE DESCRIPTION:

45 GATCTTAACT GTGTCATTTG AAACCCTGTG CGTTTGAAGT GGTGGAGACA GGACCTTTAT 60  
 CATATTCTGA GCTTTAAATA TATAAACNGG TAAATCATTG CATTTAATAA GACATAGCCC 120  
 AAGTCCCAGA ACGCGTTTTG AGAGTAACCA GAAACAGAGG TTATTTGTTC TGCTTTCTTT 180  
 TATCACTGCT ATTGGATGGG ATATCCCAAA CAAGTGATG TCGCCCCAA TTCTATTTTC 240  
 CACTATTCAA TGATTAAAT AATTACAAAA ACGCAA 277

50

SEQ ID NO:3476

55

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04087

SEQUENCE DESCRIPTION:

GATCTTTCCA AATACCCAAA TGTCCCTGCA AGCCCGTTAA ATAATTCCTT ATGCTACCT 60  
TAATAACATA CAATGACCAC ATAGTGTGAG AACTTCCAAC AAGCCTCAA GTCCCTTGAG 120  
ACTCCCCAAT ACCTAATAAG GCATGCGAAA TGTTCCTCATG AACTACCCCA CAACACGCCT 180  
AAAACCTCAA ACACCCAAAA ATATNTCCTC CAATGTCCTG AAACATGAAC CCAAAAAGAG 240  
ACCCACAATA AACTCGTGAC TTGTCCCNCT AAA 273

SEQ ID NO:3477

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04088

SEQUENCE DESCRIPTION:

GATCCTCTCN ACCCTCCTCT AGCCATCCCT TGGGGAAGGG TGGGGAGAAN TATAGGATAG 60  
ACACTGGACA TGGCCCATG GAGCACNNGG GCCCCACTGG ACAACACTGA TTCCTGGAGA 120  
GGTGGCTGCN CCCCAGCTT CTNTCTCCCT GTNACACACT GGACCCCACT GGCTGAGAAT 180  
CTGGGGGTGA GGNGGACAAG AAGGAGAGGA AAATNTTTC TTGTGCCTGC TCCTGTACTN 240  
GTCTCAGCT TGGGGNTTCT TCCTCTCCA TN 272

SEQ ID NO:3478

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04089

SEQUENCE DESCRIPTION:

GATCTTGATA TTNGCCTCT TTGAAGAGAC AGCCCTGGCT GCTTTCCTNN CCTACTGCCC 60  
TGGAATGGGT GTTNTCTTA GGATGTATCC CCTCAAACCT ACCTGGTGGT TCTTGCCTT 120  
CCCCTACTCT CTTCTCATCT TCGTATATNA CGAAGCAGAA AACTCATCAT CAGGCGACGC 180  
CCTGGCGGCT GGTGGAGAG GGAAACCTAC TATNAGCCCC CCGTCCTGCA CGCCGTGGAG 240  
CATCAGGCCA CACTCTGTC ATCCGACACN 270

SEQ ID NO:3479

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04090

SEQUENCE DESCRIPTION:

GATCACCAAC AGGGAAAGAC ATCCTGGTTC TTTTGATGTG GTGCATGTGA AGGATGCCAA 60  
TGGCAACAGC TTGCCACGA GGCTTTCCAA CATTTTGTG ATTGGCAATG GCAATAAACC 120  
TTGGATTTC CTGCCCAGGG GAAAGGGCAT TCGACTTACT GTTGCTGAAG AGAGAGATAA 180  
GAGGCTGGCC ACCAAACAGA GCAGTGGCTA AATTGCAGTA GCAGCATATC TTTTTTCTT 240

TGCACAANTA AACAGTGAAT TCTCAAA

267

SEQ ID NO:3480

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04091

SEQUENCE DESCRIPTION:

GATCCCTGGA GTGCCTTGGT GTTTCAGCC CCTGCAGGAA GCAGAATGCA NCTTNTGAGG 60  
CACCTCCAGC TGCCCCCGGC CGGGGGATGC GAGGCTCGGA GCACCCTTGC CCGGCTGTGA 120  
TTGCTGCCAG GCACTGTTCA TCTCAGCTTT TCTGTCCCTT TGCTCCCGGC AAGCGCTTCT 180  
GCTGAAAGTT CATATCTGGA GCCTGATGTC TTAACGAATA AAGGTCCCAT GCTCCACCCG 240  
AGGACAGTTC TTCGTGCCTG AAA 263

SEQ ID NO:3481

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04092

SEQUENCE DESCRIPTION:

GATCGGGAAC AAATGNAATC TGTGGATGCA TCAAGCTATC GTCAGTCAAA CCCCTTTAAA 60  
ATGTTGCTTT GGCTTTGTAA ATTTAAATAT GTAAGTGCTA TATAAGTCAG GAGCAGCTGT 120  
CTTTTAAAA TGTCTCGGCT AGCTAGACCA CAGATATCTT CTAGACATAT TGAACACATT 180  
TAAGATTGTA GGGATATAAG GGAAAAATNAT ATGAATGTGT ATTTTACTC AAAATAAAAG 240  
TAACTGTTTA CGTTAAA 257

SEQ ID NO:3482

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04093

SEQUENCE DESCRIPTION:

GATCTACATT TTGTACATAT TTATATAAAA TTTACCTTTA AGTATTTACT TTAAAAAATT 60  
TAATGGCTTA ACTCGAACTT GAAGACACAT ACTTCAACTG TCCTTATTGT CCATTAANCT 120  
GATAATTTTN ATTTTCCTNG CTTTATAGA TTTNNCTATA TAGGAATCAA GATTTANGAA 180  
ATTTTGCATT AAAANTAGTG TACCAATGCT TCATATACGT TAGTTATTTG CTATTATGTA 240  
GGGAAGAGGA TTGTN 255

SEQ ID NO:3483

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04094

SEQUENCE DESCRIPTION:

GATCTGAAAT NAGAAATATC CAACATTGCA CGAGTATCTT TTTTTATNCC TCCACAGACT 60

# EP 0 679 716 A1

CCGCCAGAGA CACCTAGTCC TGATGAAACG TCTGCTCCTT GTCCTAATAT TCATATCAAC 120  
AGCACCATTCT CTGGCATTCA CATTTTAAAA ATTATGTGGA AGTGGATAGG AGAACTGCAG 180  
CTGTCAATAG CCTAGGGCTG AATTTTGTG AGNTAANTAA NATAAATCAT TCATCCTTTT 240  
TTTTNGNTTT ATAAA 255

SEQ ID NO:3484  
SEQUENCE LENGTH:253  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04095

SEQUENCE DESCRIPTION:  
GATCTAGGTG GTTTGTAATT GTGCATTACT GACTGCATAT GTTTGTGTAT GTGTAAATGT 60  
GGGCTCCCTG TTAAGTGGGG CTCATGGATA CGAGGCCTGA GGAAGTGTGG CTTGCTAGTC 120  
TGTTACGTTA ACATGCTTTT CTAAAAATTGC TTCACGTGTT AATTCATTTA CTCCTGCATT 180  
CATTGACTGT TTTTGTCTT TTCCATTAC TTTGTACTTA TTTTTCAT TAAATTTTGC 240  
ATTTATTTTG AAA 253

SEQ ID NO:3485  
SEQUENCE LENGTH:251  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04096

SEQUENCE DESCRIPTION:  
GATCCTAGTT CCTTCCTTCC CGAGTGATAC CCATGAACTG CCAGTAGAGG CTGCTATCGT 60  
TCCATGTGTA AGGAATGAAC TGGTTCAAGG CGCGTCCTAC CCAGTCATTT TCTTTACCTT 120  
ATACTAATTC TTCCTGAATA ATGTCTTCAG TTTCTTGAGG AGACTCCTAG TTTTGGTTTT 180  
CAAATTACTT GGAGGGCTGC CTAGGAATCT ATCTCCCTCT GAAATAAAGT TTCCTCATCT 240  
TCCACNTAA A 251

SEQ ID NO:3486  
SEQUENCE LENGTH:249  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04097

SEQUENCE DESCRIPTION:  
GATCATACGG CCTTCCAGGA GACGCTGGGA TGTAAGATAC TCTTGGAGGN TGGCTCTGAA 60  
CTCGGGTGTC TGAATCACAG GGCAAGGGTA GCGTGCGGCT GTGGCTAACA GCAGAGTCAC 120  
TTCCCTGGCC TAGCTTGGGG ACCTGGGGAG GAGGAGGTAG CTCTGGACAC CAGGGTTCTT 180  
CCCATTGTGG GAGAGTNAGT TTTTAGGGG GAGACCTGTC CCCCAGATTA AAGAACTGGG 240  
AGCCCTAAA 249

SEQ ID NO:3487  
SEQUENCE LENGTH:248  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS04098

SEQUENCE DESCRIPTION:

GATCAAAGAA GAGAGTAAAG CTATGTCTTC AATTTAATTT CAATACCTGA TTTGTACTTT 60  
 CCTTGAAAGC TTTACTTTAA AATACCTTAC TTATAGGCCT GGTGTCATGC TATAAGTATG 120  
 TACATACAGT TTCACTTCAA AAATAAAAAA AAANTCCCTA AAANCTCTCT ATACTCTCTA 180  
 TAACANTNCT TTATCANGAN CTCTGGNCAA TGGTATTATT TNGGANANTC ATGGTGATGT 240  
 ATTTNTNN 248

SEQ ID NO:3488

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04099

SEQUENCE DESCRIPTION:

GATCTGTGTT GTAGAACATG AGGGTGTAAAG CCTTCAGCCT GGCAAGTTAC ATGTAGAAAG 60  
 CCCACACTTG TGAAGGTTTT GTTTTACAAA TCACTTGATT TAACACACTC AGGTAGAATA 120  
 TTTTAATTTT TACTGTTTTA TACCCAGAAG TTATTCTAC ATTGTNCTAC AGCAAGAATA 180  
 TTCATAAAAG TATCCCTTTC AAATGCCTTT GAGAAGANTA GANGAAAAAA AGTTTGTATA 240  
 TATTN 245

SEQ ID NO:3489

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04100

SEQUENCE DESCRIPTION:

GATCCTGATN ATATTTGGCA GCTGTCCTCC AGTCTTAAAA GGTTTGATGA CAAATACACC 60  
 TTGAAGCTGA CCTTCATCAG TGGGAGAACA AAGCAGCAGC GGGGAAGCCGA GTTCACAAAG 120  
 TCCATTGCTA AGTTTTTTTG ACCACAGTGG GACACTGGTC ATGGATGCAT ATGNGCCTGA 180  
 AATATCCAGG CTCCATGACA GTCTTGCCAT AGAAAGANAA ATAAAGTAGC CACTTCTANA 240  
 AGTAAA 246

SEQ ID NO:3490

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04101

SEQUENCE DESCRIPTION:

GATCCTGGGT ACTGAAAGNC TTAGGGAAGC TGGCCTGAGA GGGGAAGCGG CCCTAAGGGA 60  
 GTATCTAAGA AAAAAAGCGA CCCATTGAGA GACTGTCCCT GAAACCTAGT ACTGCCCCC 120  
 ATGAGGAAGG AACAGCAATG GTGTCAGTAT CCAGGCTTTG TACAGAGTGC TTTTCTGTTT 180  
 AGTTTTTACT TTTTTGTTT TGTTTTTTA AAGATGAAAT AAAGACCCAG GGGGAGAAA 239

SEQ ID NO:3491

SEQUENCE LENGTH:239



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04102

SEQUENCE DESCRIPTION:

GATCTGGGGA AAGGAGAGAC CATGGTGTGA ATGTAGAGAT GCCACCTANC TCTCTCTAAG 60  
GCAGGCCCTGT GGATGAAGGA GGAGGGTCAG GGCTGGCCTT CCTCTGTNCA TCANTCTGCT 120  
AGGTTGGGGG CCCCGNCCN NCCATACCTA CGCCTAGGGA GCCCGTCCTC CAGTATTCCG 180  
TCTGTAGCAG GAGCTAGGGC TGCTGCCTCA GCTCCAAGAC AAGAATGAAC CTGGCTGTN 239

SEQ ID NO:3492

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04103

SEQUENCE DESCRIPTION:

GATCTGTGTT TCCTCCCCAG TCATCTTTCT TGTTCAGAG AGGTGGGGCT GGATGTCTCC 60  
ATCTCTGTCT CAACTTTATG TGCACTGAGC TGCAACTTCT TACTTCCCTA CTGAAAATAA 120  
GAATCTGAAT ATAAATTTGT TTTCTCAAAT ATTTGCTATG AGAGGTTGAT GGATTAATTA 180  
AATAAGTCAA TTCCTGGAAT TTGAAAGAGC AAATAAGAC CTGAGAACCT TCCAGAATCT 240  
GAAA 244

SEQ ID NO:3493

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04104

SEQUENCE DESCRIPTION:

GATCCATAAA AGATTGTATT TTTATTACTA TTAAACAAG TGATTAAATT TAGTCTGCAC 60  
ANNNAGCAAG GGTTCACATG CATTCTTTTA TACTGCTGGA TTTTGTGTG CATCATTTAA 120  
AACATTTTGT ATGTTTCTNC TTATCTGTGT ATACAGTATG TTCTTGAATG ATGTTTCAAT 180  
GTCAGGAGNN CTGTGAGAAA TAAACTATGT GGATACTGTC TGTTTATATT ATAAA 235

SEQ ID NO:3494

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04105

SEQUENCE DESCRIPTION:

GATCGACTGT AAATAGAGGA CTTCTGGAAC ATTCAAATA TTCTGGGGTT GAGGGAAATT 60  
GCTGCTGTCT ACAAATGCC AAGGGTGGAC AGGCGCTGTG GCTCACGCCT GTAATCCCAG 120  
CACTTTGGGA GNCTGAGGTA GGAGGATTGA TTGAGGCCAA GAGTTAAAGA CCAGCCTGGT 180  
CAATATAGCA AGACCACGTC TCTAAATAAA AATTANTAGG CCGGCCAGGC AAA 233

SEQ ID NO:3495

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04106

SEQUENCE DESCRIPTION:

GATCATGGAG ACCTGGCTGG TAGCTGTAAC AGAGATGGTG GAGTCCAAGG AAACAGCCTG 60  
 TCTCTGGTGA ATGGNACTTT CTTTGGTGGA CACTTGGCAC CAGCTCTGAG AGCCCTTCCC 120  
 CTGTGTCCTG CCACCATGTG GGTCANATGT ACTCTCTGTC ACATGAGGAG AGTGCTAGTT 180  
 CATGTGTNCT CCATTCTTGT GAGCATCCTA ATNNNTCNNT TCCATTTTNA TGACAGGANG 240  
 AAA 243

SEQ ID NO:3496

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04107

SEQUENCE DESCRIPTION:

GATCCAGAAC TGAGGTCAC TGGTTCTAGA ACNGNNACAT TTACCTCGAG GCTCTTCCAT 60  
 CCCCAACTG TGCCCTGCCT TCAGCTTTGG TGAAAGGGAG GGCCCTCAT GTGTGCTGTG 120  
 CTGTGTCTGC ACCGCTTGGT TTGCAGTTGA GAGGGGAGGG CAGGAGGGGT GTGATTGGAG 180  
 TGTGTCCGGA GATGAGATGA AAAAAATACA TCTATATTTA AGAATCCCAA A 231

SEQ ID NO:3497

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04108

SEQUENCE DESCRIPTION:

GATCTGCAGC CAGGCCTTTC TGAAGNGTT ATTCTGNTAA AAATGGTCTN AGTTNTCTGA 60  
 AAAGCCAGCT CTTGAACCTC TTCACAACAG TATCAACACT GGCTTCTCCC GGTTTATNTT 120  
 ATGCGTGCGA GAAGTCAGTG GTAACNTCTG CAGGGCTTAA TACATTAGTG GTAACCTGGT 180  
 TAAAAACAA AGACTGTAAG CCTGTGTGTG CCACTGNNNG CTTCAACNGN N 231

SEQ ID NO:3498

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04109

SEQUENCE DESCRIPTION:

GATCCCAGTT TGCAGCAAAC CCCACACCCC AGCTCACACA GCAAAAACAA TGGACAGGCC 60  
 CAGAGGGTGA AGCAAACAGT GTCCCTTCTG GCTGTNTTGG AGCCTCCCCA GTAACCACCT 120  
 ATTTATTTNA CCTCTTTCCC AAACCTGGAG CATTTATGCC TAGGCTTGTN AAGAATCTNT 180  
 TCAGTCCCTC TCCTTCTCAA TAAAAGCATC TTCAAGCTTG TAAA 224

SEQ ID NO:3499

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04110

SEQUENCE DESCRIPTION:

GATCGGGAAC AAGCACGTTG TACCCTTGGC TGGACATGGC CAAGACACAA GGCATTCCAC 60  
GGCGGCAAGC TGACCGCACA GCAGTCTGGC TTGATTTTCA GCCGTCATCA TTGGGTTCTG 120  
TTTTGACAGC TCTGCTGCCC ATAGGGACTG CGACTGGGNC CAGGTCAACC ACGCCAGGGG 180  
GGTGTACCA GCCTTTTCTT TTTTNCCTTC TTTTNTTTT TTCCCCCTA AAGTTGTNNN 240  
AAAGCNAANC CNTGGGAATA ATGGTTTNTT TGGANTNAAA CCCANNATTT CAGN 294

SEQ ID NO:3500

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04111

SEQUENCE DESCRIPTION:

GATCCAAGTT TGATAACATT GGCATGAATG CCATGGCTAA CAAAGATAAT GCAAGTNTCA 60  
AACAGCTTAG ATGGGAGGCT GAACGTGATG ACTGGCTACA CAACAGAGAT GCAAAAANGTA 120  
TCATCAGGAA AAGGAAACAT TTTAAAANGA AGAGGNTTAA AACCACTCAA AAANCTAAAA 180  
NCCAAGGGAA ATGAGTTATT ANTGTAANTN ATAGNTTAA N 221

SEQ ID NO:3501

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04112

SEQUENCE DESCRIPTION:

GATCTAATTG TATTAGTATT GTGAATAATC ATGTGAAATG TTTTGAGACA GAGTACTATA 60  
TTTGTGAATA TAATNNTATG GTTTTTTCA CTTAGAACCT TTCTGTGTGG AAAACTAAGA 120  
AAATTGCTTT CTGCTGTATA ATCTGGCATT CATTGTAGAT TAAAGCTTAT TTNCTGTGA 180  
ATAAAACGNN NNCAATAAAA TACTATTCTT TAAAATTAAA 220

SEQ ID NO:3502

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04113

SEQUENCE DESCRIPTION:

GATCTGGACA CCCTGTCTCC TGAGGAGCGC CGGGCCAGGC TGCGGAAGTN TGAGGCTCAG 60  
CTCCAGTCGA GGAAGGAGTA CGAGCAGGAG CTCAGTGATG ACTTGCATGT GGAGCGCTAC 120  
CGACAGTTCT GGACCAGGAC CAAGAAGTGA CCGTGGCTCC AGCCACCCCG GGACATTGCT 180  
AAGATGGGAG GGCTGTTCTT AAATNACTCG TTCTGAAGC TGCAA 226

SEQ ID NO:3503

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04114

SEQUENCE DESCRIPTION:

GATCATGCCG AAAAAGTGGC GGAAAAGCTA GAAGCTCTCT CGGTGAAGAN GANNCCAAGG 60  
AGGATGCTGA GGAGAAGCAA TAAATCGTCT TATTNATTT NCTTTTCCTC TCTTTCCTTT 120  
CCTTTTTTNA AAAAATTTTA CCCTGCCCTT CTTTTTCGGT TTGTTTTTAT TCTTTCATTT 180  
TTACAAGGGA CGTTATATAA AGAACTGAAC TCAAA 215

SEQ ID NO:3504

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04115

SEQUENCE DESCRIPTION:

GATCTNTTCT TAATGTACAT AGTGCTAACA TGAAGACCTT TTTNTGCACT ATATGCAAAC 60  
AGGGTAACTA ACTAAAACAA AGCCACTTTC AATCTTCAAT CCTTGAAGGT ATATCTAGGT 120  
TTATNACAGT AATTGTNTTT ACATTTNATG GTGCCTAGTA TTGACAAAAT GTTATTTCCC 180  
TACATTAAAC ATGACTCCAT AGACCTTTTC AAA 213

SEQ ID NO:3505

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04116

SEQUENCE DESCRIPTION:

GATCTAATGT AAAATCCAGA ACTTGGACTC CATCGTTAAA ATTATTTATG TGTAACATTC 60  
AAATGTGTGC ATTAAATATG CTTCCACAGT AAAATCTGAA AAACTGATTT GTGATTGAAA 120  
GCTGCCTTTC TATTTACTTG AGTCTTGAC ATACATACTT TTTTATGAGC TATGAAATAA 180  
AACATTTNAA NCTGAATTNN TTAACNTGA AA 212

SEQ ID NO:3506

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04117

SEQUENCE DESCRIPTION:

GATCAGAGAT GCTGTTATC AGTCCCAACA AGATGGCCTA GAAATCGCAT TCTCACCTCG 60  
CCTTGCTGCT GCTTTAATTC CAAGTTCTAT TTCTTCCCTT ATAGTTTCT ATGGGAATGA 120  
GGCGGATACA GGAAACACCC TATCTCCTCT GTATTTTGT AGTGGAATTT CTATTTAAGG 180  
GGCTCATTA AGCATAGTAT TTATACACAA A 211

SEQ ID NO:3507

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04118

SEQUENCE DESCRIPTION:

GATCGAGATN CAAAGCCACA TNCTCTCTCA CCAAGNTAAA CTATTANAT TAATTGTTAG 60  
CGGTGTTATG CTGCTTTCTT CTTTGACAAG GCCATGACTA AGAAGGCTCT AAGTAAAGGA 120  
AGAATCATTT ATTCCATAGT CAGCTAACTG GTAGCAAAGC CTTCTNTTCC AAGACACCAA 180  
GGGAGAGGGG AGGACATAAA TTATGCAAA 209

SEQ ID NO:3508

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04119

SEQUENCE DESCRIPTION:

GATCCCCTCT TNAGTCCNCT GCCCCTTCCA AGGACACTAA TGAGCCTGGG AGGGTGGCAG 60  
GGAGGAGGGG ACAGCTTCAC CCTTGGAAGT CCTGGGGTTT TTCCTCTTNC GCCCCTTGTG 120  
GTTTCTGTTT TGTAATTAA GAAGAGCTAT TCATCACTGT AATTATTATT ATTTTCTACA 180  
ATAAATGGGA CCTGTGCACA GGAGGAAA 208

SEQ ID NO:3509

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04120

SEQUENCE DESCRIPTION:

GATCCAAGCA TATAAAAAGC CTNTATATTT TTNAAAAACA CATCTTAACT CCACGCTTTA 60  
CGATATTATA AAAGTTGAAT GGTCCTCTT GGTAAGGATA TTTGCTTACA AGTGCTAGGA 120  
AATAACTNNC TGATAGCTGC GTTAACATAC TTNGTTTTGC CTAGAGAGGG GCAATAAAAA 180  
TGAACCAAAG GATATTCCA GAAAGGATTA AGAAAGCTGT TTAAGANGGC CATGACTCTT 240  
TAGGTGTGTA TGTGTACCTT TCAGCATCCT AGGAATTTN ATACTAAAAG CAAAATGTTT 300  
TTCCCAGTTA GTCTTCTTCA GN 322

SEQ ID NO:3510

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04121

SEQUENCE DESCRIPTION:

GATCCGNCCA CCTNGGCCTC CCAAAGTGCT GGGATTACAG GTGTGAGCCA CCGTGCCCGG 60  
CCTCTTTTAA TTTATNCCTA AAATATTACC TTGAGGCCAA ATNCTGCGCT TAAGGAGAAT 120  
GTGCACCAAG TGCTGGGGTG GGGGCTGGTT ATAAACGAGG CCACAAATNA TGCTTGTA 180  
TAAATTGTGT GGTTCAAATC TGAAA 205

SEQ ID NO:3511

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04122

SEQUENCE DESCRIPTION:

GATCCCTCAC TTTATTTATA TTCCCACTAT AACCAGTAAG TTCATTTCAT AGGCCCTATC 60  
ATGCATTAAT CATTGNATGN NAGNAGTTAA TGAAAACTTT TCCTGTTACA ACGCCCATTTG 120  
CCGGCAATGA ACGTACCAAA ACCGCCAAGG AAGTCATTGT TATTGCACAA TACATGAGGA 180  
CCTGGAGCTT TTCAAAAAGC TTAAA 205

SEQ ID NO:3512

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04123

SEQUENCE DESCRIPTION:

GATCTAAAAC GGCTATTTAA TATGTTACAA GGCCTTGAG TATGGTTGCA TGTCCAAATA 60  
TAAATGTTTT TAAATTAACCT CTAACATTTG GTTATAAAAG TTTANCCATA ATAATAGAAT 120  
TTTTAAACA CGNTGTNTG GTTTAATCTT AGCATATTTT TCCAATAAT AAAGCTCAGT 180  
ATTCGTCTGN GTTCTCAGNG GAAA 204

SEQ ID NO:3513

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04125

SEQUENCE DESCRIPTION:

GATCTCTCTC ATTCATTTCA ATGTATTTTT ACTTTAAGAT GAACCAAAAT TATTAGACTT 60  
ATTTAAGATG TACAGGCATC AGAAAAAGA AGCACATAAT GCTTTTGGTG CGATGGCACT 120  
CACTGTGAAC ATGTGTACCC ACATATTANT ATGCAATATT GTTTCCAATC CTTNCTAATA 180  
CAGTTTTTTA TAATGTTGAA A 201

SEQ ID NO:3514

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04126

SEQUENCE DESCRIPTION:

GATCCAATTT ACATCCACAT TTTAGGTNCA ACAGCAAGAA GTTCAGAGAG AGATTTCCTCA 60  
ACCAGACATT GGGTCACTCA CTGGTCACCT TGCCAGTNCA TTTTATTAGA AGGGAATCTG 120  
TTGTAGCAAA TGGGAATAAA CCTGGGTTTC TATAGACCCA GAACTGAAAA AATAAACATC 180  
GTGCTGTTTT TAATTNGAAA 200

SEQ ID NO:3515

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04127

SEQUENCE DESCRIPTION:

5 GATCTTAGTT TTCTTTTGTT TATTTCCCAG CTCATTTTTT TCTTCTGGTC AGTTTTTTTA 60  
AGGGGGGGTG TTGTGGTTTT TTGTTTTTGT TTTGCTTCTG AGAAAGCATT TGCCTTTCTT 120  
CCTCTCCCAA CATAACAATC GTGGTAACAG AATGCGACTG CTNGATTAC CGATGTATTT 180  
AATGTAAGTA AAAAAAGGAA AAAAAGAAA 209

SEQ ID NO:3516

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS04128  
SEQUENCE DESCRIPTION:  
GATCCATTCC CTGCAACTNA AGATTCTAAG GAACTGGGTT TCTCAGTATA CAATGGGAAT 60  
GGTTGGNAGG AGGTAAAGAG TAGAAGACAG TATCAAGANT CCAGAGCCCA GCACCTGTAG 120  
20 TCCTAACTAT NCANATTCTT TGAGCCCAGG AGTTTGAGTC CAGCCTGGAC AACATATTGA 180  
GACCCCATC TCTCTAAA 198

SEQ ID NO:3517

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS04129  
SEQUENCE DESCRIPTION:  
30 GATCATGAAT AGGAGCCCAT GCTAGAAGTA CATTCTCTCA GATTTGAACC AGTGAAATAT 60  
GATGTATTTT TGAGCTAAAA CTCAACTATA GAAGACATTA AAAGAAATCG TATTCTTGCC 120  
AAGTAACCAC CACTTCTGCC TTAGATAATA TGATTATAAG GNAATCAAAT AAATGTTGCC 180  
TTAACTTCAA A 191

SEQ ID NO:3518

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS04130  
SEQUENCE DESCRIPTION:  
GATCCAGGCA GCCAAGAACT TGATGAATGC TGTGGTGCAG ACAGTGAAGN CATCCTACGT 60  
CGCCTCTACC AAATACCAAA AGTCACAGGG TATGGNTTCC CTCAACCTTC CTGCTGTGTC 120  
45 ATGGAAGATG AAGGCACCAG NGNNAAAGCC ATTGGTGAAG AGAGAGAAAC AGGATGAGAC 180  
ACAGACCAAG N 191

SEQ ID NO:3519

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04131

SEQUENCE DESCRIPTION:

GATCTCCCC AAAGATTCCA GGCGGTGCAA CCCTGCNTGT TCGAGGTGGA GCTGCTCAAA 60  
 ATAGAGCGAC GAACTGAGCT GTAACCAGAC TGGGGAGGGG CAGGGGGAGA GGCCCCATC 120  
 AGGGACCAGA CTGTTCCAGA AAAAAACAA AAAACANAAA CAAACAAAA AACACTTAA 180  
 AGCCAAA 187

SEQ ID NO:3520

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04132

SEQUENCE DESCRIPTION:

GATCGAGACT CTNCCAGAAA AAAAAACAAA AAAAAAAAAA ATCCGTTTCT AAGGACGGCG 60  
 GGGATTTCGGT TCGAGCCCGT GGCTGCTCTG TTTTGTTTTG CTTTCTTGGT ATATAATCCT 120  
 ANAAATAAAA GGGTAATATA AATATTTNAG AAGAGGGAAA TTGCTGAAGA GTAGTAAGGG 180  
 CAAA 184

SEQ ID NO:3521

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04133

SEQUENCE DESCRIPTION:

GATCAGATGA CCATTGAGGA CTTGAATGAA GCTTTCCAG AAACCAAATT AGACAAGAAA 60  
 AAGTATCCCT ATTGGCCTCA CCAACCAATT GAGAATTTAT AAAATTGAGT CCAGGAGGAA 120  
 GCTCTGGCCC TTGTATTACA CATTCTGGAC ATTAAAAATA ATAATTATAC AGTTAAA 177

SEQ ID NO:3522

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04134

SEQUENCE DESCRIPTION:

GATCCCATCC GAAGCTCAGG GTATGGAGAG CGGGGAGCTC CNCCAAAGAT TCCAGGCGGT 60  
 GCANCCTGGT GTTCGAGGTG GAGCTGCTCA AAATAGAGCG ACGAACTGAG CTGTAACCAG 120  
 ACTGGGGAGG GGCAGGGGGA GAGGCCCCCA TCAGGGACCA GACTGTTCCA AAAAAAANC 180  
 AAAAAACAAA ANCAAACAAA AAAACACTTA AAAGCCCAAA 220

SEQ ID NO:3523

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04135

SEQUENCE DESCRIPTION:



GATCCTACCT AAGGGGCACA ACTAGTAAGG GAGTAGAGCT GAGATTGGCT CCAGAGTTCT 60  
 TGTTTTTCAGC CACCATTTTA TGCTGCCTCT CCAGTNATTT TTTTCCCAT TTTCTTCAGT 120  
 NTTTCTATAG CAGAGATTTG ATAATAAAAA GAAAATCCTA AACAAATGAGA AA 172

SEQ ID NO:3524  
 SEQUENCE LENGTH:169  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04136

SEQUENCE DESCRIPTION:  
 GATCGCACTG CGCAGGGGTG CCACGGAGCT CACCCACGAG GACTACATGG AAGGCATCCT 60  
 GGAGGTGCAG GCCAAGAAGA AAGCCAACCT ACAATACTAC GCCTAGGGCA CACAGGCCAG 120  
 CCCAGTNTC ACGGCTGAAG TGCGCAATAA AAGATGGTTT AGGGTCAAA 169

SEQ ID NO:3525  
 SEQUENCE LENGTH:169  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04137

SEQUENCE DESCRIPTION:  
 GATCTCAGGC ATCGGATTAT TTCTCCTGTA AATATTTCAG AATGTATCTN TCCAAGATGA 60  
 GAGCTCATTA AAAGACAATT ACAAAGCTTA TCACATCCAA AAGANTTATC AATAATTTN 120  
 AAATATTATT AANCGTGTA TAAATNTNCA AAGTNCCACT TGCCTTAA 169

SEQ ID NO:3526  
 SEQUENCE LENGTH:165  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04139

SEQUENCE DESCRIPTION:  
 GATCAAAAANG AGTNAANCTA TCCAAAAAAA ATTTGTATAT TTGGGAAAAA TGGATTTTTA 60  
 CATAGCTTTT GTATGCAGAT ATAAACTGT AATTATGAAT ATAGTGGGCG TAGATAAACT 120  
 CATAAGCTTA AATTCTAAAA ANGAAAAAGC TTATACCANG ATAAA 165

SEQ ID NO:3527  
 SEQUENCE LENGTH:165  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04140

SEQUENCE DESCRIPTION:  
 GATCAGCCGA TGACAGAGAT TGTAAGCCGT GTGTCGAAGC GAAAGTTGGA GCCGCCACGT 60  
 GCGGGCNCCTG GTGCTTNANC TGTGCTGTAA CGACGAGAGC GGCGAGGATG TCGAGNTTCC 120  
 CTATGTCCGA NACACCATCC GCTGACCCCG TNTGNTCCTN TAGGN 165

SEQ ID NO:3528

# EP 0 679 716 A1

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04141

SEQUENCE DESCRIPTION:

GATCCATTG AAAGTNATT TGACATAAGG AGTAAGGTTA CTACTGATTC CTACTCAGGA 60

GGCTAAANTG GGAGGACCAC TTAAGTATGG NAGGTCGAGG CTATAGTGAG CCATTACTGA 120

GCCACTGCAC TACAATCTGG GCGACANAGC AAGACTCTGT CTAAA 165

SEQ ID NO:3529

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04142

SEQUENCE DESCRIPTION:

GATCCTGTGT TTGCAACTGG GGAGACAGAA ACTGTGGTTG ATAGCCAGTC ACTGCCTTAA 60

GAACATTGA TGCAAGATGG CCAGCACTGA ACTTTTGAGA TATGACGGTG TACTTACTGC 120

CTTGTAGCAA AATAAAGATG TGCCCTTATT TTACCTACAA A 161

SEQ ID NO:3530

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04143

SEQUENCE DESCRIPTION:

GATCAGTCAT CCACCAGGAA CGAAGATTTC CTGAAGAAGA CCTGGTCCCT CTGGAGGTTG 60

CGGTGGCTGA AGGATGCATC ATGTGCTCCT ACCCTGCTCT ACCGCTTTNT TGGGTCACAG 120

AGGCCAAATG TGAGAGCATT GAATAAATAT CTTAAGCTAA A 161

SEQ ID NO:3531

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04144

SEQUENCE DESCRIPTION:

GATCTCGTGA AGCCCGCAAG GACCGAACAC CCCACCCCG ATTTAGACCT GCGGGTGCTG 60

CCCCACGTCC CCCACCAAAG CCCATGTAAG GAGCTGAGTT CTAAAGACT GAAGACAGGC 120

TATTCTCTGG AGAAAAATAA AATGGAAATT GTACTTAA 159

SEQ ID NO:3532

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04145

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCCTTACA GTAGAGGTGA CCCCTGTAAT ACCATCTGCT GCCGTGAGGA CCTGAACTCA 60  
 CCTAACCCAA GTCCTGGAGG TTNNNNGAC ACAAAGGTGG CAGATATCTA CCTAGCATCT 120  
 CAGTACACAT CCTATGCCAT AAGTGGTCCC ACAGTACAAG GTGGCCTCCC TGTTTTTCGC 180  
 TGGGACCGTT TCAACAAAAC TCTACATCAG GGCATGCCAG AGGTCTACAA CTTTGATTTT 240  
 ATTACCATGA AACCAATTTT GAAACTTGAT ATAAAATGNA GGAGGGGAGAT GACGGACTAG 300  
 AAGACTGTAA ATAAGATACC AAAGGCACTA TTTTAGCTAT GTTTTCCCA TCAGAATTAT 360  
 GCAATAAATT TNTTAATTTT GTCAAA 386

SEQ ID NO:3533  
 SEQUENCE LENGTH:391  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04146

SEQUENCE DESCRIPTION:  
 GATCAGATTA AACCATTGAA GTTGAAGTT CATNAGGCTA AGCCTGTNCC AGAAAATCAC 60  
 CCACAGTGGG ATACAGCAAT AGAGGGGGAT GAAGACCAGG AGGACAGTGA GGGCTTTGAA 120  
 GATAGCTTTN AGGAAGAAGA GGAGGAAGAA GAAGATGATG ACTAAGCAGT ACTCTGAATG 180  
 GNCCACAGTG TTTGCACATA TTNCAATTT TTTNCTGTTT TGGAAGTGTA TCATAAACCA 240  
 GAAACAGTAC AGAACTGATG TTGNGGGNGG TGTNGTTTTT TTACTCTAGA NATGGGTGCA 300  
 TAATATNACT AGGCAGTGGC GGTGCCTTGG TNCANCCTGN AAAATGTAA GGCTTTNTTG 360  
 AAACCTTTCC AGTNGGGGNT GGTCCNTTNA N 391

SEQ ID NO:3534  
 SEQUENCE LENGTH:157  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04147

SEQUENCE DESCRIPTION:  
 GATCCGCCCG ACTCGGCCTC CCAAAATGCT GGGATTACAG GCGTGAGCAT TCAAGTCTGG 60  
 CGAGAGAGAT TGTTTCTAGA TGAGGGTGGG GCGGGGTGTC CTTAGCCCAA AGCTTGTGCC 120  
 AGTCTCTATC GGAAATAAAT GCCCCCCAAA CCTCAAA 157

SEQ ID NO:3535  
 SEQUENCE LENGTH:154  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04148

SEQUENCE DESCRIPTION:  
 GATCTACAGC AAAACACAGC GGGAGAGGTT CGCCTGGGCT CTCGCCATGG CAGGAGAAGA 60  
 CTTTGAATTC TAACGACGAG CCGTGTGAA ACTTCTTTT TATGTGTGTG TGTTTTTTTC 120  
 ACTATTAAAG CAGTACTGGG GAATTTTGTA CAAA 154

SEQ ID NO:3536  
 SEQUENCE LENGTH:151  
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04149

SEQUENCE DESCRIPTION:

5 GATCTAGGCA ATGATTTAGA GGAAACCTCN TCACAAAAAC CCCAGAGGAA GAATATGACC 60  
TGTGTTTCAA ATTTTGCCTT TCTGAACTAT TTAAAATTAT GTGTATGTTT TTGCTTTGTA 120  
TTTTAAAAGT AAAGCTGCTG TCCTCAAGAA A 151

SEQ ID NO:3537

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04150

SEQUENCE DESCRIPTION:

10 GATCTATGAA AGCGGGGAGA GGGAACCTGA ATATTAATTA TGAGCACAAA TTTGAAGGAA 60  
AGAAAACAAA GAACCATTAT CTAATCAAGC TTTGAAAGTC CTGCATGTTT GCCTTTTATT 120  
TTAGTGTTGA CGCCAACATA GACTGTCTAA GGTATTTTTT TCCCCAAACA CTTGAATCTT 180  
20 GGTGTTGGT ATGTAATCCA CTCTCTAGAG TCCAGTGTAC TTTAGACTTC ATCTGAGTCC 240  
AATATATGTA CCACACTACT GTTTTATTAA TGTAAAAACC TTGTAAATGA ATTCAGATG 300  
GGTGATTAA GTGAGTCACA AGTCACAAAA CTTTGCTATT CATAGTTTAT CTNGN 355

SEQ ID NO:3538

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04151

SEQUENCE DESCRIPTION:

25 GATCTCTGCT TCCTGTACCT TGACATGCAA AAGGCTCTCC TAATACTCCA CATTCAAAC 60  
GAAGAGGAAA ATTGAAATCT CTAATGAAGC TGCTGTGTGT ATTTATGANT ATTAATGAAT 120  
AAAACTGCT TGGATGGTTT ACCTTAAA 148

SEQ ID NO:3539

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04152

SEQUENCE DESCRIPTION:

35 GATCAACAAC TNGNTACTCT CGGGAAGACT CCTCTACTCA CAGCTGAAGA AAATGAGCAC 60  
ACCTTCACA CTGTTATTAC CTATCCTGAA GATGTGATAC ACTGAATGGA AATAANTAGA 120  
45 TGTAATAAAA ATTNAGTTCT CATTTAAA 148

SEQ ID NO:3540

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04153

## SEQUENCE DESCRIPTION:

GATCAGAGTA AACAAAAGGA ATCTCAAAGG AAATTTGAAG AAGAACTGT AAAATCCAAA 60  
 GTGACTGTTG ATACTGGAGT AATTCCTGCC TCTGAAGAGA AAGCAGAGAC TCCCACAGCT 120  
 GCAGAAGATG ACAATGAAGG AGACAAA 147

SEQ ID NO:3541

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04154

## SEQUENCE DESCRIPTION:

GATCGTGGCG CATGGCTTG GGATTAACT ACCCTTGAG AGGACCCTTG TCCCAAACCC 60  
 TTCTTGTTCT CTCCTCCAAA AGTAGCTTCC TCCAACCCGC AGCCTCTCTG CACACTAATA 120  
 AAACATGTGG CTTGGAAAGG TTCAAA 146

SEQ ID NO:3542

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04155

## SEQUENCE DESCRIPTION:

GATCTTTAAG GACAAGTTTA TCCAGCATCC AAAAACTTT GGACTAATTG CATCATACTT 60  
 GGAGAGGAAG AGTGTTCCTG ATTGTTTTT GTATTACTAT TTAACCAAGA AAAATNAGAA 120  
 TTATAAAGCC CTCGTCAGAA GGGN 144

SEQ ID NO:3543

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04156

## SEQUENCE DESCRIPTION:

GATCTGGGTT TTNATATCTT TATCTTCATT CAGTGAAGCA AGCCAAAAGC NCACATTTGT 60  
 ATGCNTTAGG TCTTCTTAAA ATGGTATCTG TAAACATGTG TCCAATATAA AANCTATTTT 120  
 NAATAAAANG TTACATGAAA 140

SEQ ID NO:3544

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04157

## SEQUENCE DESCRIPTION:

GATCAGCAAT GAAGAACTGG NCGGACAAAA TTNAACGTTN ATGTAATGGN ATTCCAGATG 60  
 TAGGCATTCC CCCAGGTCT TTTCATGTGC AGATTGCAGT TCTNATTCAT TTGAATAAAA 120  
 AGGAACCTGG AAANCAAA 138

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SEQ ID NO:3545

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS04158

SEQUENCE DESCRIPTION:

10 GATCTAAATG GGCCAGGTG TTTACCCTTA TNTNGTTTTC TGCTAAATNA TGGAGGTTTG 60  
GGGAGTTCCT TCTCCACTTG TTTGTGGAGG CCTGGGGAGT TTTTNAGAC CCCCAGTAAA 120  
ACTNGTTTAA TCCTAAA 137

SEQ ID NO:3546

SEQUENCE LENGTH:136

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04159

SEQUENCE DESCRIPTION:

20 GATCCCTGTA GAGGTGGTAT TAAAGATGGT CACTGAGATT AAGAAGATTC CTGGTATTTC 60  
TCGAATTATG TATGACTTAA CATCAAAGCC CCCAGGAAGT ACTGAGTGGG AGTAATAAAC 120  
TTCTTGTTC ATTTAA 136

SEQ ID NO:3547

25 SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04160

30 SEQUENCE DESCRIPTION:

GATCCTAAAA TNNTCTACTT TTGTNGCCTT ATCAGTNCTT TGCAATCTGC CTGTGGTTAT 60  
CAGCACTTAA AGCACAATTT TGAAGGGGAA AAAAATGATA ATCACCTTAG TCCCAAAGAA 120  
ATAATTTGTC ANNCN 135

35 SEQ ID NO:3548

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS04161

SEQUENCE DESCRIPTION:

GATCTGGACT GGCTGGGAGT GGGGAGGGCG TGGAGACAGT CTACGGAAAG CGCTANAGGA 60  
CCCCCGAGAG GGTGCAGTGG AGCCCTGAGC ATTGTAATAT GCGGCCAGC CTATAACAG 120  
45 CCTCCGTGCT TAAA 134

SEQ ID NO:3549

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

CLONE:HUMGS04162

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## SEQUENCE DESCRIPTION:

GATCCTTTGC TGTAACCTNG GAGAGACCAG TCCCAAACAG AGGGGAATTT TAAGCCCTTC 60  
 TCATCACCCA ATTGGATGTT TTTGCTTATA GCAAATTCCT GCAAAATAAA TAAATAAATA 120  
 TTTGCAAAAC TAAA 134

SEQ ID NO:3550

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04163

## SEQUENCE DESCRIPTION:

GATCTATGGG AAGATACTTA TTTTCTGAG GTCCTTATGT CCTGTCATAT AATTAAAGAC 60  
 TCAAGAGAAT TTATGTGAAA TGCTTTCTGT ATGCCCAAAT CTCTAGATTA AAATTATATA 120  
 GCTGCTCCTG AAA 133

SEQ ID NO:3551

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04164

## SEQUENCE DESCRIPTION:

GATCTCAGTT CCNTAAAAA TGATAAAAAT TTTTCATGTA TATTACATAT CTACCTACCA 60  
 GAAATCCTTT TTACAATTTT ATATACAATC ATTTTAAGAC CTTTTTGAAA TAAATAATGC 120  
 AAATGAACTA AA 132

SEQ ID NO:3552

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04165

## SEQUENCE DESCRIPTION:

GATCACGGGG TGGNAGGNAA CCGNGGCGTC CCTGCNTGGG GCCCATGGGT GANACACTCC 60  
 AGTACTGAGA CCTAGAGTCC AGATGCTTGT AGGAGCCAAG TCGTGTTCTA AGTATTTATT 120  
 TAAAACAAAA GAATCACGTT TTCCCATTTG TAAA 154

SEQ ID NO:3553

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04166

## SEQUENCE DESCRIPTION:

GATCCTTAAT TGTAGCCTTT GAAGGATGCC CTGTGTAGAT TATTCAGTGC CACAAATTGA 60  
 AAGCTTCCAT GTTTAATNTT ATCCTCTTGC TATATAAATA AAGCAAATAT ATTTAGGCCA 120  
 GGGTCTCACT GAGGGGGAGC TGTCTGTCA TCTTTTAGAG TAAACTATTC TATAAACATA 180  
 TGCAAACAGC CCTAAATAAA TCTAAAGTCT AAA 213

SEQ ID NO:3554

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04167

SEQUENCE DESCRIPTION:

GATCCCAAGG GCCCAGATAA CGCCCCAAC TTCTTGGGGT TCACACGCGT CCTGAGACAT 60  
CTGGGAACTG CCTCTGCCTG GNCCAAAGCT ATTCCATTAA AACTTTATTG CTGTNCTTAC 120  
TCAAA 125

SEQ ID NO:3555

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04169

SEQUENCE DESCRIPTION:

GATCTGTGTA CAATTTTNGT CACTANGACT TTCCTCCAAG AACTAAGCCA ACTTGATGTN 60  
NCAAAGCACA GCTGTATATA ATGGTGATGT CATAATAAAG TTGTTTTATC TTTTAAGTAA 120  
AAGTAAA 127

SEQ ID NO:3556

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04170

SEQUENCE DESCRIPTION:

GATCAAGGAC TCTGGATAAT TGGCATAACA TCCTGGAATA GCTGAAACAG AGATATTATT 60  
CTCTGCTGTC CTCTGTTGTC TTTGTCTTTT CACGTCTTAA TAAAAGTGCT GGTGACAAGA 120  
GTGAAA 126

SEQ ID NO:3557

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04171

SEQUENCE DESCRIPTION:

GATCAGAGCC ATACCCCTCT TCACCAATGG GAAGTCAAGA CACCTATGGG TAAAAGTTCT 60  
CTCTGATGCA TGAAACTCA GAGTGATAAA GTAATTTTAA AATAAAAATT TGGAGAAAGC 120  
AAA 123

SEQ ID NO:3558

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



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CLONE:HUMGS04172

SEQUENCE DESCRIPTION:

GATCTAAAAG TTTTCACACA TAAATTTTCAT TAATTTGAAA GATTATTTTT AACTGCATA 60  
GGTCCACTTG CCTCTAAATA AAATNAACCT AAAATAAAAA CAACTATAC TTTGTGAGAA 120  
A 121

SEQ ID NO:3559

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04173

SEQUENCE DESCRIPTION:

GATCTCCCC AACCCACAA AATGCTTAAA AGATAACTTA GCTCTTNTT CAGGGCTCAG 60  
TCCTTTGGAT GTAATCCGAC TAGGCCAGTN AACCTAAATA ATAAATATCC TCCTCAACAA 120  
A 121

SEQ ID NO:3560

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04174

SEQUENCE DESCRIPTION:

GATCCTGAGT TTTCTGGGAC AATTCAGCT TTAATCAATA CATTTTGTTA AATGTGCCAT 60  
AAAATGAGAC TTTTACGCC TTTATAAGGC CTTAGATGTA AATAAACTCA CCCAAACAAA 120

SEQ ID NO:3561

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04175

SEQUENCE DESCRIPTION:

GATCATTGTA TTCAGAGATT GTAAATGAAA AAATATAGAA ACTATTTAGT TTTGGTAGAT 60  
TTTTTTCTG ACAATGTGAC CAGACTGAAT TTCCTCATAA AGAAAAAATG GCGTGCAAA 119

SEQ ID NO:3562

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04176

SEQUENCE DESCRIPTION:

GATCCAGCA TTTTCATCG ACTTGTAATT GTTCTGCTA CCTGACAATC ATCGCCTTGA 60  
GTACTGGGAC AACCTTTGAT TACTCATTAT ATCCTCAATA AATATTTGTT GAACTAAA 118

SEQ ID NO:3563

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04177

SEQUENCE DESCRIPTION:

GATCCTGGCT AGANTGNTAA TTAAAAGTAT TTAATTTGAA GCACCATTN ANTGTTCGTA 60  
CTAGTAGAAA ATGATGTGAA TTTCTTTTCT GTTCGGCTCC TATTTTCCTC ATCATTN 118

SEQ ID NO:3564

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04179

SEQUENCE DESCRIPTION:

GATCATAGTC GGGCATACTT ATCTATATCC NTAACCTCTA TATCTTTAAA TAAATGTGAG 60  
NACTGTTCTC ATGGAGANGA AA 82

SEQ ID NO:3565

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04180

SEQUENCE DESCRIPTION:

GATCTAAAGC NTTTTGTGCA GATTATTTAA TATNATGACT TCATGCTTTA TTATGCCTTA 60  
TNATGGCTGA CGTATTACTG TGGTGAAACA AAATATCTTT AAAAGTTAAA ACATCCAGAT 120  
ATATAAGCAA TTTTNCCTA AGGATAAAGT ACCTTTAAGC ATGAGTGTAT CACAGCTTTC 180  
ATTAGGNAAA CTTTTCATTA CATACTTGTT TAAN 214

SEQ ID NO:3566

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04181

SEQUENCE DESCRIPTION:

GATCCCNAA TGTGTATGAA TGACTGAGGC TTTGTAAATT AAGGGACGTT TGTTTGAATA 60  
AAGTTATTTG ATGGGGTCAA AGAAGCCATA TGTGATTGA AA 102

SEQ ID NO:3567

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04182

SEQUENCE DESCRIPTION:

GATCCTCTCC TTAGTCTTAG CTCATGGGGC TCTTTATAAA GGAGTTGGGG GGTAGAGGCA 60  
GNAAAATNGG AACCAGAGCTG AANGCAGAGG CTGAGTTAGG N 101

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SEQ ID NO:3568

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04183

SEQUENCE DESCRIPTION:

GATCTGCAGT GCTTCACTGG AAATAATTTC TTCATTGCAG ATACTTTTAA GGTGGCATT 60  
NATTCATTTC CTGTGCTTTA AATAAACAAA TGTACCAA 99

SEQ ID NO:3569

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04184

SEQUENCE DESCRIPTION:

GATCACCTG GGCACATGTT GTCAGGACCT CCTGGGGTTG TGTCATGGAT GCGTGCCTC 60  
AACCTTAGCA AAATAAACTT TCTAAATTAC TGAGAAA 97

SEQ ID NO:3570

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04186

SEQUENCE DESCRIPTION:

GATCTTCAGT GTGTCTGCAT AAGCTAACTT AAGATGAATT TAAGTACANN TTTCTGAAAT 60  
ATTTCTATTG AAATAAATTA CTAAAATTA NNAAT 95

SEQ ID NO:3571

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04187

SEQUENCE DESCRIPTION:

GATCTTTGTG AATTCTATGA ATGTATTAAG TTATCATATG TACTCCCCAA AATAGGTACA 60  
TCTATTATGT ATCAATAAAA AANTTTAAAA CAAA 94

SEQ ID NO:3572

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04188

SEQUENCE DESCRIPTION:

GATCCCTTGA GCCGAGGAGG TTGAGGCTGC AGTGAGCTAT GGTCACACCA CTGCACTCCA 60  
GCNTTGGTTA TNATGCAAGA CCCTGTTTAC AAA 93

EP 0 679 716 A1

SEQ ID NO:3573

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04189

SEQUENCE DESCRIPTION:

GATCGCACAC CTTTGCAACA GATGTGTTCT GATTCTCTGA ACCTACAAAA TAGTTATACA 60  
TAGTGGAATA AAGAAGGTAA ACCATCAAA 89

SEQ ID NO:3574

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04190

SEQUENCE DESCRIPTION:

GATCAGTGTC TCTAGTCCTA CCCAGTTTTA AAGTTCATGG TAAGATTGGA CCTCATCTCC 60  
CTCAAATAAA TNTATTGGTG ATTTTNGAAA 90

SEQ ID NO:3575

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04191

SEQUENCE DESCRIPTION:

GATCCGCCAG GTGCGGGCGC TACTGCAGGC ACAGCAGGCC TAGGTCTCTC CACACCTGCC 60  
CCCTAATAAA GTGGGCGCGA GAGGAAA 87

SEQ ID NO:3576

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04192

SEQUENCE DESCRIPTION:

GATCCACCCA CACCTAAGTC ACAGAATTC TAAGTTCCCC AACTACTCTC ACACCCNTTT 60  
AAAGATAAAG TATGTTGTAA CCAGAAA 87

SEQ ID NO:3577

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04193

SEQUENCE DESCRIPTION:

GATCAAACCTG AATGAAACCC CCACACACAC ACACATGCAT ACACACACAC ACACAGCCAC 60  
ACACACAGAA AATATACTGT AAA 83

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SEQ ID NO:3578  
SEQUENCE LENGTH:83  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04194  
SEQUENCE DESCRIPTION:  
GATCCCTATT CTGCGTGTAT GTGTTTGCAC ATGAGTGTTC GTAGACCATA GACCATTAAA 60  
AAATACGGAA TTCAAAAGTT AAA 83

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20  
SEQ ID NO:3579  
SEQUENCE LENGTH:84  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04195  
SEQUENCE DESCRIPTION:  
GATCTATGAA TGTTTTNTT AAAATTACA AAGCTTTGTA AATTAGATT TNTTTAATAA 60  
AATGCCATTT GTGCAAGNTT TAAA 84

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SEQ ID NO:3580  
SEQUENCE LENGTH:112  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04196  
SEQUENCE DESCRIPTION:  
GATCACATAA AGGCAAGAGG ATACTTCATG AATAATACAT TTNAATGCAA ATAAACAGAT 60  
GGTTCCTTC TACTAGCTAT NNCCCTGTCT TNNTATACAC TGAGTAGATT AN 112

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SEQ ID NO:3581  
SEQUENCE LENGTH:74  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04197  
SEQUENCE DESCRIPTION:  
GATCTATGTC TGTTGGTGGC AATGTGAGGG TGATACTCTC TCACTCTAAT AAACCTGGCA 60  
CTTCTCCGAG TAAA 74

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SEQ ID NO:3582  
SEQUENCE LENGTH:74  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04198  
SEQUENCE DESCRIPTION:  
GATCCTGTAT GTGTGTTGAG ATTTAGAGGT TTCATTTATN TTGTCTGCTA ANAAATTGTT 60  
ACTCTAATAA TAAA 74

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EP 0 679 716 A1

SEQ ID NO:3583

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04199

SEQUENCE DESCRIPTION:

GATCACTGTA TAGACTGTTA AATTTGATTT CTTATTACCN ATTGTAAAT AAACGTGTG 60  
AGACAGACAA A 71

SEQ ID NO:3584

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04200

SEQUENCE DESCRIPTION:

GATCTATTTTCTCTACT TTGGANATGA TTGCATAATA AATAAAATTT TACTGTTTTT 60  
TTAAAAGGAA A 71

SEQ ID NO:3585

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04201

SEQUENCE DESCRIPTION:

GATCTAAAGA TGTTTAGGGA AGAGCTCGAC TAAAGAACAA TGAAATAAAT GGTCCAAGGG 60  
GAAGTCAAA 69

SEQ ID NO:3586

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04202

SEQUENCE DESCRIPTION:

GATCAAAAAT GTAAGTCTAT TGGTAGAGAT TAAGTAAAGT ATTTATTGCT ACATCATAGT 60  
TGAAA 65

SEQ ID NO:3587

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04203

SEQUENCE DESCRIPTION:

GATCTGTGTT GCATTTCAA ATAACTGGT GTGTGCTCTG CCTGGATTG AAA 53

SEQ ID NO:3588

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04204

SEQUENCE DESCRIPTION:

GATCTCAGCC CAGGACGNCA AGCAAGCAGG TCTTGTGAGC AAGATTGTC CTGTTGAGAC 60

ACTGGTGGAA GAAGCCATCC AGTGTGCAGA AAAANTTGCC AGCAATTCT AAAAATTTGT 120

AGTAGNCGAT GGNCNAAGNA TCAGTGGATN CAN 153

SEQ ID NO:3589

SEQUENCE LENGTH:29

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04205

SEQUENCE DESCRIPTION:

GATCCAAATA AAGGTAGCTG CTGACCAAA 29

SEQ ID NO:3590

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04206

SEQUENCE DESCRIPTION:

GATCTCTCTA CAAGAGCCCC TGCCCCTCTG TTGGAGGCAC AGTTTGTAGAA TAAGGAGGAG 60

GAGN 64

SEQ ID NO:3591

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04207

SEQUENCE DESCRIPTION:

GATCCTTTGC GTGACAGTCT TGTATGGAAA ACAGATGCTG ACAGAATTGT AGACTACCAT 60

NCCN 64

SEQ ID NO:3592

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04210

SEQUENCE DESCRIPTION:

GATCTCGCCT TGTTTCTTAC AAGCAAACCA GGGTCCCTTC TTGGCACGTA ACATGTACGT 60

ATN 63

SEQ ID NO:3593

SEQUENCE LENGTH:63  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04211  
 SEQUENCE DESCRIPTION:  
 GATCTTTGCG AATTACAATG CATATATGTC TATTTATTCA ATATCTGTCA TATAATANCT 60  
 ATN 63

SEQ ID NO:3594  
 SEQUENCE LENGTH:58  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04213  
 SEQUENCE DESCRIPTION:  
 GATCTTAAGA AAACCTCATA CTGTATGAAT AAGAAAATAA AATATTTAAA ACTTGAAA 58

SEQ ID NO:3595  
 SEQUENCE LENGTH:64  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04214  
 SEQUENCE DESCRIPTION:  
 GATCGCCAAG TTCAAAGCTG TGCACATGTG GACACTCAAT AAATGTTCAT TGGTGAAAAA 60  
 CAAA 64

SEQ ID NO:3596  
 SEQUENCE LENGTH:56  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04215  
 SEQUENCE DESCRIPTION:  
 GATCCAAAAA GAGTCGACCN GCATTNTTTA TATTAAAAAT AAAGTCAAGA TTAAAA 56

SEQ ID NO:3597  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04216  
 SEQUENCE DESCRIPTION:  
 GATCTTTGTT AATGTCTTGA TTCTGTTCGC AAAGCACAGA CTAGTGCTTA AA 52

SEQ ID NO:3598  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear



CLONE:HUMGS04218

SEQUENCE DESCRIPTION:

GATCGCACCA CTGAGCTCCA GCCTGGGCAG CTGNATGAGA CTNCATCTCA AA

52

SEQ ID NO:3599

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04219

SEQUENCE DESCRIPTION:

GATCTGGAGG GACACACAGG AGACACCTGG CATAACCAAA AAATGATTAA A

51

SEQ ID NO:3600

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04220

SEQUENCE DESCRIPTION:

GATCGAAAAC ATATAGANAA AATAAAATGT GTGGTTGCAC CTGTACTGAA A

51

SEQ ID NO:3601

SEQUENCE LENGTH:466

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04247

SEQUENCE DESCRIPTION:

GATCTAGAGG AGGATTTGCA GGAAGAGCTC GTGGAAGAGG TGGTGACCAN CAGAGTGGTT 60  
 ATGGGAAGNT ATCCAGGCGA GGTGGTCATC AAAATAGCTA CAAACCATAC TAAATNATTC 120  
 CATTTGCAAC TTATCCCCAA CAGGTGGTGA AGCAGTATTT TCCAATTTGA AGATTCATTT 180  
 GANGGTGGCT CCTGCCACTG CTTAATAGCA GTTCAAATA AATTTTTTGT ATCAAGTCCC 240  
 TGAATGGAAG TATGACGTTG GGTCCCTCTG ANGTTTAATT CTGAGTTCTC ATTAAAAGAA 300  
 ATTTGCTTTC ATTGTTTTAT TTCTTAATTG CTATGCTTCA GANTCATTTG TGTTTTATGC 360  
 CCTTTCCCC AGTATTGTAG AGCANGTCTT GTGTAAAGC CCAGTGTGAC AGTGTCATGA 420  
 TGTAGTAGTG NCTACTGGTT NTTTAATAAA NCCNTNTTGT ATGAAA 466

SEQ ID NO:3602

SEQUENCE LENGTH:429

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04248

SEQUENCE DESCRIPTION:

GATCTATAAA TCAAGAAAAT CCATTGTCAT AACCATTTTT AAAAGTCAAT AATTAAGACA 60  
 TCCTTAATTA AAAAGTTTCA AATCTAGACA CTAATGTGT GTGAATGTAC AAAGAAAACA 120  
 AACCATTGCT TATGCTGTTA TATACTAGAG AAATTTTGT TTGCTTGCTG TTTTAACTTG 180  
 ACAGATGAAG GACTTTAGTT GAACTTCATA TTGTAAGAAC TGTTAATAAA AGTTGTCAAG 240

TAAAAAGCGC TATATCTAAA AAGACTTTAT GAACAGTTAT TCTATCAACT TTAAAGGGT 300  
TTAAACCTG CCCAGAAATT ACCTTGGTAT CTGAAGTTTC CCTCTGTCTC CTCCTCTAA 360  
TTNAGGCTTG TTATTGTCA TGCACCAGCA TTTGGGGGNT AATAANAATT TCTTNGGTTT 420  
TNGTGGAAA 429

SEQ ID NO:3603

SEQUENCE LENGTH:419

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04249

SEQUENCE DESCRIPTION:

GATCTGTTGT TTGTTTTTAA GGTGGTGTTC TGTAACTTC CAGCAGGATG CAGAATCTAA 60  
CTGGTAAACC TATAAATTGG TCAAATTTNA CCCATGTTGT TTCTTTGAAA ACAATGTATA 120  
TNCTCTAATA TTTGGATATA GGGTATATGA NCATTAATGC AACTTAATTG TATTTCCAAG 180  
TACAGTACAT ATGTNCAGAT TTCTTTTCT AACCTTATT AGTGATAGAG GTGTGGTAAA 240  
CNCTTCCATT ATGTTTATGT ATTANCACTG TAATTTTGTC ATTTTNATAT ATTTNGATGT 300  
TATGTAAC TAATGATACA GGATTAGGTA TTTCTTCTG TATTCCTTT TATGTGGAGA 360  
TGATATTTT ACATAGCAA GTATTGTAAT GCATTAATAA TAAATGGTCA ACCATTAAA 419

SEQ ID NO:3604

SEQUENCE LENGTH:419

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04250

SEQUENCE DESCRIPTION:

GATCTGCTAG TTCCAGGCCT CTAAGACAGG AACGTATGTG CCATAAGTGN GTCTACTTCA 60  
CAGACTCAAT GAGGCAGAAA TTATTGTAGT TTTCTCCTAT TTCTTCTGCA CCCAATTTT 120  
TNCTTGATT TCAAAGGCCA GGCCATGTAC ACTAACGTCC TTGAAATTTG CAGTTCTGTA 180  
TGCTTCTATT CCAATCATT CATTACCAAT AAAAACGGAA TACCACCCTT TCCATTTTAT 240  
AGNCTCATC CCCTATTTCT GTCAGACAGT TATATGACAG GGTGGNCNGN GGGCCTCTTA 300  
GTTTCATCAA AGTCTNNCT GNAGTGCTAG NCTTTCAGAC TCTTATCACT GGAAATCNTT 360  
AAGGGTTGAG GGGGNTTAN TTTCCAGNA CTTGTGNAGG GNTTCAACTG TCAAACTN 419

SEQ ID NO:3605

SEQUENCE LENGTH:404

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04252

SEQUENCE DESCRIPTION:

GATCCGACAC AGAGAACAGG AGGNACTAGA GGCGACANAN AGNAGGGCTT TAAGCCAAAC 60  
TACATGGAAA ATGGTGATAA AAGAAAATNT GGCTGAAGTT ACCCGAAGTT CAGCTTGCGAG 120  
TGTAATTCAG AAGAGTTAAG ACCAGAAGTA CTGGAATCAT ACTTCCTTT AGTCTTGCCA 180  
CTTGCTTAGT GAGGCTTTTC CGAACCTGGA AGGAGACGTC TAGAAATCCC AACTTTGCTG 240  
TGTAAGGACC ATTAGCTGCA AGTCAGTGA AGTCTATAGA AAANAGTGTG AATTCCATAG 300  
TGGTCTTGAC TTCTTAGCAA GGATTTGGA TAAGTCTAAA ACTTCAGACT TAAAGCTTTG 360

AAGCATGTGA ACTGCATGAN ATATTAANCA TTTCGAACTT CAAA

404

SEQ ID NO:3606

SEQUENCE LENGTH:403

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04253

SEQUENCE DESCRIPTION:

GATCCATGAA TTAACAGAGG CATATATTTA AAATGAAATT TAATGAGCAC TTAGTGACTT 60  
 CATTTGTTCA AGAATATTTG ATTCCTATT GTGTGCATGG GAGGTTTACA AAAGACAGAC 120  
 TGTCCTATG CTTGTNCAGC TTACAATCTA TTAACTATT AGAGGCCCTG TGAGATGTAG 180  
 GCAGTTATTT ACAGATGAGA AACTAACAC AGCAGTGGCA ATGCTGGGAA TGGCCAACAG 240  
 GCTTGGAATT CAACTAGTT TAGCACCAA GCCAGTNCTA TTAAGACCTG AAGTTCAACA 300  
 GTGGATTCTT TACCCAAATA GTTTTTAAAG TATGCTCTAA GGNCCAATGT TTTAATGAA 360  
 ATCTTGGNTT NCAAGTNGG NNTAAAAGG TTCTGAGCAT AAA 403

SEQ ID NO:3607

SEQUENCE LENGTH:396

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04256

SEQUENCE DESCRIPTION:

GATCTTACTT CGTTGACCCA TATTTTCCC CTGACCAAGT TACCTGTAAA CTGGAATTTG 60  
 CAAGGGGATG CTGTGATGAT AACCCCTTTC TATTGCTGTA ATGTTTATAT AACCTGGGAA 120  
 ACTGAGAGAA GGGGATGTGT AAATAAAAGC TTAAACATTT TAGTAATGTG TTAATATGTC 180  
 ACTCTCTCTT ACCCTGTTTC CCTTTTTTGC CAGATGATGA TTTTTTTATT TTTATTTTGT 240  
 ACTTTACTGG ATGACTGTGA AGCGNTGAGT ATTGGGTTGG GGTAGGTGTG TTGATTTTGA 300  
 GAGTGCATGT TAAGACCTGA AGGGGAACTA CTTGAGGATG ACTTAAGAAG CATCCCATGC 360  
 AAATATCTTG TTTTGGCCNG AATAAAATAT TTCAAA 396

SEQ ID NO:3608

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04257

SEQUENCE DESCRIPTION:

GATCTGCCCG CCTTGGCCTC CCAAAGTGCT GGGATTACAG ACATGAGCCA CCACGCTTGG 60  
 CCGGGATAGT ATATTTTAT AGCACTTCCC CTACTGATTG CTGCCTTCTC TGTGGCTACA 120  
 AGGGACCCAC AGAATTACAG GGAAGTTACA GGGNNGCAGG TTTCATCTCA ATATTGGGAG 180  
 AGATTTCAAA CAATCACACC NNNNNNCGA AGGAGTGGGC TGTCAC TAGG AATTTTATT 240  
 CCCAGTCCGT CAGGAATTTT GTAGAAGGGC TTCATGTGCT GGTACCAATA GGACAGGAAG 300  
 ATTTAATCA GCTTACTAT CTATGTTTTT TTATGGAAAC TGTGTGTATG TATACATACA 360  
 TTTTCAAAA AGNANAAATT AAATGATTAT AG 392

SEQ ID NO:3609

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04258

SEQUENCE DESCRIPTION:

GATCCGCCCC CCTCCGCCTC CCAAATTGCN GGGATTACAG NCCTNAGCCA TNCCCACCCG 60  
 GCCAATAAAA ATTTTAAAGT AGCTAAATTT GACTCTCATG CAAATAAGAT AAAATGAACA 120  
 TATGTTAAAT ATTTTAACTT AATGAGAGAA ATAGTAAGAT GTTACCAGTT ACTTGATGAT 180  
 GGAGGAAAGG ACGAAAAGCC AAGGAATACA TGGAAATGCAG CTCTAGGTGC TGAAAAAGGC 240  
 ANGGAAAGGT TCTACGTTAG NGCTTCCAGA GGGAGCTCAG CCCTGTCANC ANCNTNGTTT 300  
 CAGCTCAGTC ATATCGNTGT TTAGACTTTC TGGTCCCCAG NGCTGGGCGG GGGATATATT 360  
 TCCTGCTGTT TTAAGNCNCC NNATTTTGTG GN 392

SEQ ID NO:3610

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04259

SEQUENCE DESCRIPTION:

GATCCTAAGG GGTTCAGGGG GACCCTACCC CCACCTCAGG TTGGGCTTCC NTGGCCACTC 60  
 ATGCTCCACA CCAAAGCAGG ACACGCCATT TTCCACTGAC CACCCTCTAC CCTGAGGAAA 120  
 GGGAGACTTT CCTCCGATGT TTATTTAGCT GTTGCAAACA TCTTCACCCT AATAGTCCCT 180  
 CCTCCAATTC CAGCCACTTG TNAGGCTCTC CTCTTGACCA CTGTGTTATG GGATAAGGGG 240  
 AGGGGGTGGG CATATTCTGG AGAGGAGCAG AGGTCCAAGG ACCCAGGAAT TTGGCATGGA 300  
 ACAGGTGGTA GGAGAGCCCC AGGGAGACGC CCAGGAGCTG GCTGAANGCA CTTTTGTACA 360  
 TGTAATGTAT TATATGGGGT CTGGGGCTCC N 391

SEQ ID NO:3611

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04261

SEQUENCE DESCRIPTION:

GATCCGACCG CGTGNTGCCG CTCTGCTCTC TCATACGCGT GTATGTTTGG TTCCATGTCA 60  
 CAGCCCCCTA GGAGCCAGTN ATGCTCGGCC TTGCGCCCGT NCCACCTCCC AGGCCACCCT 120  
 TCCTGGGCTT CTGGGCCACC TGCCCTCGGG GGGCCCCCTGC NAGGGTGCCT GGNGTTCCCA 180  
 CGTGTCCCGG GGCTTTTCCA GGAAGCCCGA GCCCAGGACC TGTTGGCAGA GTTGCCAGGG 240  
 TTACATTTTT NAAGCACCTG CTCCTTTTNT TGCAGTGTAT TTTCTACAAC CAGATTGTAT 300  
 TAATATTTTT AACTTTGCCC TTTTAAAAA TATACCTAAT ACAATATATT TAATTNTGAA 360  
 TTAAACTCTT AACTTTTCT TCCAAA 386

SEQ ID NO:3612

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04264

SEQUENCE DESCRIPTION:

5 GATCCCTTTG GGGCATGAAG TGTGACAAGT GTGGGCTCCT GAAAGGANTG TNCCAGAGAA 60  
 ACCAGCTAAA TCATGACACC TTCAATTTGC CATCATGACG CAGACCTGTA TACATTAGGN 120  
 TAAATCTGAA TTTCCACTGC TTTGGAGAGT CCCACCCACT AAGCACTGNG CATNNAAACA 180  
 GGTTCCCTTTG CTCAGATGAA GGAAGTAGGG GGTGGGGCTT TCCTTGTGTG ATGCCTCCTT 240  
 AGGCACACAG GCAATGTCTC AAGTACTTTG ACCTTAGGGT AGAAGGCAAA GCTGCCAGTA 300  
 10 AATGTCTCAG CATTGCTGCT AATTTTGGTC CTGCTAGTTT CTGGATTGTA CAAATAAATG 360  
 TGTGTAGAT GGAAA 375

SEQ ID NO:3613

SEQUENCE LENGTH:372

15 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS04265

SEQUENCE DESCRIPTION:

20 GATCCTAGAC CAGCATGCCA GTGTGCCAAG GCCACAGGGA AAGCGAGTGG TTGGTAAAAA 60  
 TCCGTGAGGT CGGCAATATG TTGTTTTTCT GGAACCTACT TATGGTAACC TTTTATTTAT 120  
 TTNCTAATAT AATGGGGGAG TTTCGTAAGT AGGTGTAAAG GGATTTATAT GGGGACGTAG 180  
 NCCGCNNTCC CNNGTGTGT AGGTTTCTCT TTTTCAGGCT TATACTCATG AATCTTGTCT 240  
 25 GAAGCTTTTG AGGGCAGACT GCCAAGTCCT GGAGAAATAG TAGATGGCAA GTTTGTGGGT 300  
 TTTTTTTTTT NACACGAATT TGNGGAAAAC CATTAANTCA TTCAAATAA TAANCTNTTT 360  
 TTATTNGGGA AA 372

SEQ ID NO:3614

SEQUENCE LENGTH:372

30 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS04266

SEQUENCE DESCRIPTION:

35 GATCTAAATA TATATTTTGT ATATTATAAT ATTTTAGGAA TAGCTTAATT AAGANCTCAC 60  
 AGACTTTGAC AAAGTGGTAA CTAGACTTTT AATTACTAGA TTCTTCAAAT TAGGCTTAAT 120  
 GCCTGCTAGC ATGCCAATCC AATCCCATGA CTGATGTTAT TATACACTAT GGCAAATACA 180  
 AAGTTGTAGT ATTATGGTTC TTGATGGTGT GATTTACTTA TGTAATTAT GTACAAATTT 240  
 40 AAGTTCAATG AAACACTGAT TTAATGTACT GAAAGGTAAA TAGTACCATA GTGAATTATT 300  
 TCCTGTCTTG CCTTAGGTTT ATTTTATNA TCTTCAATAT TAGANTAAAT GCTAAATTAT 360  
 TTTCATTTTA AA 372

SEQ ID NO:3615

SEQUENCE LENGTH:370

45 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS04267

SEQUENCE DESCRIPTION:

50 GATCTGAACT CCTTATACAT AAGAAGGTGT GTATATTAAT CCAATTATGG ACTTAAATA 60

55

EP 0 679 716 A1

TTTTAAAAGT ATAAATACCC TTATTTGCTG CAAAGACCAG TGTGTAGGCA TTTGCTTTTT 120  
 AGCAATATTT TTAAGTGCTC CATTTTAATG CCGAGGAATA AGTCTTTTGG CAACACAAAC 180  
 TGGTCAATAA TAGGTAATGC AGGTATGTTT AGGTAAAGCC AACAATGTTT TGCATTTTAA 240  
 TGCTTATTTT CTGTCAACAC TAATGAAGTC AACATTGCCT GAATGTCTGA ATAATGAAAC 300  
 ACATCCCNCT TTAAGATAT GTAAGTAAA AAGAAATAAA AAANAAATTA AAAGGTAGGT 360  
 TTTTTTAAA 370

SEQ ID NO:3616  
 SEQUENCE LENGTH:370  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04268

SEQUENCE DESCRIPTION:  
 GATCCCATTA TATAGTATGT ATAGCTGAAA TCTGTAATTC AATCACTTTT TCTCTTTTAT 60  
 CCTCTAACCA AAAAATTGTT TAATTTTGCA TCCCAAATGT TTTAATCTT TGTATATTTT 120  
 TNAAAAATCC NTTTCTCCTC AGCANTGCCT TTTTNGTGGT TGTAATAGA CTTACTTGCA 180  
 CTTTGAAGAT GAGTTACTCC TTGTCATCTT ACAAATATGT GATATGGTAA TTTNCATAAC 240  
 AGATGTCAGT TTTGANCCAA GAATTGGTGA TTTGTTTATA AGAAAAAAC TGGCTTCATT 300  
 NCTGTGNAAT TGCTCTTGG NAAATTNCTN NTTNACACGT GTAAGCCAAC CTGAGGTACC 360  
 GTGATGGGTN 370

SEQ ID NO:3617  
 SEQUENCE LENGTH:368  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04269

SEQUENCE DESCRIPTION:  
 GATCCCTGCT CAAGCAGCAC AGAGGAAGGG GCAAGACGTG GCCTGTAGGC ACTGTNTCAG 60  
 CCTGCAGAGA AGAAAGTNAG GCCGGGAGCN TGAGCCTGGG CTGGAGCNTT CTCCCTCCC 120  
 CANTTGGACT AGGGGCAGTN TTAATTTTNA AAAGGTGTGG GTCCCTGTTT CCTCTTCCAG 180  
 GGGTCCAAGG GAACAGGAGA GGTCACGGG CCTGTTTTTT CCCTCCTGAC CCTGCATCTC 240  
 CCACCCCGTG TATCATAGGG AACTTTCACC TTAATATCTT TCTAAGCAAA GTGTGAATAG 300  
 GATTTTNACT CCCTTTGTAC NNCNGNCTGA GGAAACGCAA ATAANAAGGG CAACATGTTT 360  
 CTNTTAAA 368

SEQ ID NO:3618  
 SEQUENCE LENGTH:364  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04270

SEQUENCE DESCRIPTION:  
 GATCGGCCCA GCTCCTGAAC TNTGANGAGG CCATTCATAT GGCATTCCTG GAACAAAACA 60  
 CTGCACAGGT ACCAGCCTCT CCACTCCTGA CCGGGTTGGT GCTGAACAGT CAGGGATTGT 120  
 NCTTGAAC TA GACTTCTGAT GCTTCTTGCA ATCTTCTTTC ATCTTTCCCT GAAATACACA 180  
 AAATAAACAA NTACAATAAC AAATAGTAAT TAANTGACTT TCAGGATAAC ATCTAGTTGT 240

TCAGACTTCA CCCTTCACAG GTGTGTGTGT ATGTGTGTTT ATGTCTGTAT ATTGANGCAN 300  
 TTTGAATTTA TTTTACTGTA TATNTNCTGA GTAAANGACT GANATGNNCT NCTTGGGTCA 360  
 GAAA 364

5

SEQ ID NO:3619  
 SEQUENCE LENGTH:363  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04271

10

SEQUENCE DESCRIPTION:  
 GATCTGAAGC CTTCCATAAA TNAGAGGCCA TTCATATGGC ATTCCTGGAA CAAAACACTG 60  
 CACAGGTACC AGCCTCTCCA CTCCTGACCG GGTGGTGCT GAACAGTCAG GGATTGTTCT 120  
 TGAAC TAGAC TTCTGATGCT TCTTGCAATC TTCTTTCATC TTTCCCTGAA ATACACAAAA 180  
 TAAACAAATA CAATAACAAA TAGTAATTAA ATGACTTTCA GGATAACATC TAGTTGTTCA 240  
 GACTTCACCC TTCACAGGTG TGTGTGTATG TGTGTTTATG TCTGTATATT GANGCAATTT 300  
 GANTTTATTT ACTGGTATAT GTTTCTGAGT AAAAGNCTGA AATGNNCTNC TTGGNNCNGG 360  
 AAA 363

20

SEQ ID NO:3620  
 SEQUENCE LENGTH:361  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04272

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SEQUENCE DESCRIPTION:  
 GATCCAGGAT GTACTTGGAT GAGGAGGCCT GGCTTATCTA GGAAGTCGTG TCTGGGGTGC 60  
 TTATTGCTGC TCCATACAGC TGTACGTCAG CCCCTTGGCC TTCTCTGTAG GTTCTTGGCA 120  
 GCAANNNGC AGCTTTCACT CAGTGACACA AGTAATTACT GAGTCCTAAT TTGATAGCCA 180  
 CCAACTGTAC CTGGGTAGGC AAAGTCAGAT TTTNGAGGAC CTTTTCCTG ATTTGAAGTT 240  
 TTAATTACCT TATTTTCTNT TATGCTTNC CTCTGTCTTG TAATCNTNCT CTTCTAAAA 300  
 ANCCCTCCCTA TAAATTCAAT TAATTGGGT TAATTTTAGG ATAAACCCAT TTANTTCNAA 360  
 A 361

35

SEQ ID NO:3621  
 SEQUENCE LENGTH:359  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04273

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SEQUENCE DESCRIPTION:  
 GATCCAGATN CTTTCGGATG TCAGGGATAT TCACATTGAC ATGTCTNNNN AGTGTTCAG 60  
 GAGATTTTAG TTTGAATAGT ACAATTTTTT CTTCTTACAA CAAAACCTTAG AACGGCTTCT 120  
 AACTTATTTT TTCATGGCCA AGAACTACC CTAACCTATC TCGATAAATA TTTAGTTCTG 180  
 TCTTATTTCT AATGTGTAAA ACAGGTTTTA AAAATAATAT ATAGATTTTG CATTTATAAA 240  
 AAAAGATTTA ATTTATAGAA CCAAACTNGA ACATATGTTT AATTTAGCCT AATCAGAAGG 300  
 TTACAGAAAA AGTTGCTGTA AAGATAGAAT AAAGGGTATT GTACTGGTCT GTTTTTAAA 359

50

55

SEQ ID NO:3622

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04274

SEQUENCE DESCRIPTION:

GATCTACAGC AGCTGCATCG AGGACTCCCA CAGAGGTGCT ATAGGGCTGC GCATTGCACT 60  
GGCCATCTCA GCTATAGCCG TCTTCCTGGT CTTGGTGTCT GNCTGTATCC TTCGATTGG 120  
CACCAGGTCT CTCTGCAACT CCATCATCTC CTTGAACACT ACAATNAGCT GTNCTGAAGC 180  
CCAGAAAATT CCATGGACAC CCCCTGGAAC TGCTCTGCAG TTTTACTCCA ACCTACACAA 240  
TGNTGAAACC TTTTCTTGGG TGAATTTGGT ATTGTGGTGT GTGGTCTTGG TGCTCCAGGT 300  
CGTGCACTGG AAGTCTGAAG CCACCCCATC CCGGCCTCTG GAGAGGGGTG ACCCTN 356

SEQ ID NO:3623

SEQUENCE LENGTH:420

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04275

SEQUENCE DESCRIPTION:

GATCCCCCT GNCAGACACC AAAGCTGTGA ACAGAAAGAC TGCCTGGCCA GCAAACCTTG 60  
GGACATCAGC CTNGCCCAGC CTGAAAGCAT CCGNAGTGAC CTAGAGAGTT CTGATGCACA 120  
GTCAGACGAT GTGCCAGACA TCACCTCANA TGAGTGTGGC TCCCCCGCT CCCATACTGC 180  
AGCCTGCCCC TCGACCCCCA GAGCCCAAGG TGCACCGAGC CCAAGTGCCC ATATGAACCT 240  
CTCTGCCCTA GCCGAGGGAC AAAGTGTCTT GAAGCCAGAA GGTGGAGAAG CCAGAGTATG 300  
AAGTGGAATG AATGCTCCTG TTCTGAGANG AACTTTGTAA CTGCATCTTT TGGAATTTTT 360  
TTTTTTTTTT GCCCAGGGGN NAGGGTTTNT GGTTTTTAAT TTANAGGNCN TTTGGGCAAN 420

SEQ ID NO:3624

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04276

SEQUENCE DESCRIPTION:

GATCAGAATT AAAGTAGTAC TATGAAATGT CCTTTTGAAT GTNAGGTCAA GAAATCCATG 60  
TACAGAGTCG TGCACTTCAT TGGCTGTAAAC TGTCAAACCT GCCTTGATT AGAAGTTAAA 120  
TCCCATCGTA AATACATCAC GAGGCCAGCT GTGTGATTTC TGAGACCTAG ATGAGAGTCC 180  
NATTACTTCA AGCNTTGATT CAGTAAATNT TAAGCAGCAG AAGNCTTCGG ATGGGTTGAA 240  
AATCAATNTT ACAAGGTTTT AACTCATAAA CCCATNNGGG NTTTTTTTTT TCCTCTGCAA 300  
NNGGTTNCTA AGGCTANTCC NTGGTAACAC TNTGGGAAAN AAATNTGGAG GN 352

SEQ ID NO:3625

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04278



## SEQUENCE DESCRIPTION:

GATCTCCAGT NGGCCTTTGC AGGCCCGGCC TCCTGCCTCT NGAAGGCCTA NCACGGGCCC 60  
 GGCTCGGCC TCGGCCTCAC AGCAGACTCT CCACGCCAG CTAGCTCTTG CCTCACTGCG 120  
 GCCTCCCCAG TCCAAAGCTC CTGCCTTNG GCCACTTCGG CAGGTCCAGC TCCTGCCTGC 180  
 CAGTGGCCTC TTTAGGCCCA GCTCATTCCT CACGTCGGCC ATTCCAGGCC CCGTTTTTCC 240  
 CTTCCGGCAG CCTCTTGGCC TCTAATTGT TTATNTTTTG TGTATAAATC CCAAAATATT 300  
 GAATTTTGA ATATTTCCAC CGGGGGNGTA AATATTTTGA TAGGTAAA 348

SEQ ID NO:3626

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04279

## SEQUENCE DESCRIPTION:

GATCTTTATT AAGACAGTGG AAAGTATACT ATTAAGTCAT CATAGTCTTT TGGAGACTTG 60  
 TCAANACAG CAATNAGAAA ATAAGACCTA GCATACCGTG GAGAACCATT AAAAATTTNA 120  
 NANGAAACAA CAAGTATTAT GTCAACTTAC TTCAAAGCG AGTTTTGGGA TTNATGCAG 180  
 TAAAGATTCC CTGTTTTATG ATTGTCCCTT GAAAGTCAA TGGGGGCCTG TCCATTGTCC 240  
 TCTATTAANC TTNCAGAACT GTCACCAACA AATTTGAGTT GCCTTGTCTA GGGTTCTGGG 300  
 TAGTGAAGAT ATTNATNAT ATAATNAAAT AACTGTAG TACTTAN 347

SEQ ID NO:3627

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04280

## SEQUENCE DESCRIPTION:

GATCAGAGGA GGAGTGTGAG TGTCTCATA CTCACAGCAA AAGGAGGGAA TTCAGGAGAG 60  
 GATTGAAGAA GCGGTTCTG TTTTAAGGC ATTTGCAATC ATTGCTGGAG AGACAGAACC 120  
 AACAGATGGG GAACAATGGC CAGGGACTCC AGGCCTGATT TAAGCCAATG CCGCCCTGTG 180  
 GTCTTTACCC ACGAATGGTG TGGAAAATNA GAGCAGGGAA GAGGATTTAC TCACTGGCTG 240  
 TGGAGTTAGG TCAGAAGGGG GNTGGAAAGA TGGAAACGTA TGGNTTTGGG GACATTTCTT 300  
 AATCTNTAGG CTTCACCTC CTAACTGAA ATTAAGGCC N 341

SEQ ID NO:3628

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04281

## SEQUENCE DESCRIPTION:

GATCGACCTG TCATGTTTTT AAGGTTATCC AGGCTGTATA TCTCTGGAAN AGAAGGGAAT 60  
 GGCAAAGAGT GGGAGTCTGA GTCAAGTTTG GTTTTGNITT NNNAAGAGAC AAGGTCTCTG 120  
 TAATCCAGGC TGCAGTACAC TGGCATGNCC ATGGCTCACT ATAGACTTGG GCTCAGCCAA 180  
 TCTTCTGCC TCAGCTCCT GAGTAGCTGG GNTTGGTTTT CCCCAGGGCC ATATGTCAGC 240  
 TTATTACCC TACTCACTG GTGTNTCCA GNCTGCCAGC CATGCTGTTT ATCCAGTATC 300

TTCTNNATGG GGATTACCTA TTAAGGGGAC TAACACAAAA N

341

SEQ ID NO:3629

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04282

SEQUENCE DESCRIPTION:

5 GATCATGGAA CCCCTCTTCC GGCAGTTGGC CAAATGTGTC TCCAGCCCAT ACTTCCAGGT 60  
 GGCAGAGCGA GCTCTCTATT ACTGGAATAA TGAATACATC ATGAGTTTAA TCAGTGACAA 120  
 CGCAGCGAAG ATTCTGCCCN NNCATGTTTC CTTCTTGTA CCGCAACTCA AAGACCCATT 180  
 10 GGAACAAGAC AATACATGGC TTGATATACA ACGCCCTGAA GCTCTTCATG GAGATGAACC 240  
 15 AAAAGCTATT TGATGACTGT ACACAACAGT TCAANGCAGA GAAACTAAAA GAGTTGCTAN 300  
 AANTGNAAGA NCGGGNNGAN GCATGGGTTA AATTAGAAAN 340

SEQ ID NO:3630

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04284

SEQUENCE DESCRIPTION:

25 GATCTGCCAC ATGTNTGAGG GTTGCAGAGC CCGCTGTGGA GGTAAGATTG GAAACACATG 60  
 NAGCAGAGGG AAGACATTGA AGAAAACATC TCTNCTGGAA TATTTGGAAA AGAACACTCT 120  
 TCTGGACCTG GTTGAAGCAG GAAAGATGGA GGCAAAGTAG TGAAATAATC CAGAATTTCA 180  
 ATGCTTTTNA ATGTNCTTAG TGATACTGAC CTGTGATAAT ATAATTCCCA GGGAGGACTG 240  
 30 GGAACCTTAT CTCTTGAGAT ATTTGCATAA TTTATTTAAT TTAAGCCTCA TTCTCCTTTT 300  
 GTNCATTTTG GTAATAAACT GGATTTGAAT TGTGAACAN 339

SEQ ID NO:3631

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04285

SEQUENCE DESCRIPTION:

40 GATCCAGCCA GTATAGAACT AGCTCTGTAG GGGTGAGGAG GACTNTGCTA TGTATCATCC 60  
 TNGATTGTNT TCCTTCAAGG AGCATTGCAC TTGCCTTCCC AGACCTTCCA CCTTAGGTTT 120  
 TGCTGCAAAA AGCACCAGTG CTGAAGATGC TGCAAGACCA AATCATAGCT CATAAAATCA 180  
 GGTCTTGAGA TAGTTACCCA TAAAGAGGAA TCCTTTGAGT GTATGCCATT GGTGAGCCGA 240  
 45 TGAGCATGGA CCATAGAAGG GCTCAATGTA GANTGAAACT ACCCGTGTGT AAAAAGAAGN 300  
 TTGGNTTAAA ATGGCTACTT TGGATGGGNA CCAGTGTCTN 339

SEQ ID NO:3632

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS04286

SEQUENCE DESCRIPTION:

5 GATCAGAGGG GAAACAAACG CCAAGGGGGT GGGAAATGGGT CGGCATCTGG AGTCTGAGAC 60  
 AGCTGCCCTC CTGCGTCAAG GGCTGGGGGC CTCAGCTTCC ATCCTGTGCC AGCCTCCATG 120  
 TGGACAGCTC AGCTTATTGT CCACCACCTG GAAATNCCTC GAAGCTTCAT NNGTCCAGGT 180  
 CAAGAGAATC CTGTTCCCAG ACCTCTGCCC AGCCAGGCCT TCCCAGCTCA GGGCTGACTC 240  
 CTGCACCAAG TGACGCACTT TTNATAACTG GTCTACCAAT GNCTCCCTT CAAGTGAGAA 300  
 10 CTACCCITTA CATTTAGGAG TGTGGCCCCG CAGTAAA 337

SEQ ID NO:3633

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS04287

SEQUENCE DESCRIPTION:

20 GATCCCTGTA TGCNGCCAAG GATGGGACTT CCAGCTAATG AATTTGTACA TGCAGCCAAA 60  
 TTTACAGGAA TTTTTTTAAA AGGCAGAAAA ACTTGAAATA CCAACATTCT GGCAAAAAAN 120  
 ANTCAATTTT ATGANGAGTA AGTGGAACCT GGGNTGCAGG ANCAAAAGAG GGAAATGTTG 180  
 GGCAAAACATT TTNNTGGGAG CTCCCTTCGC TGTGTGCAG CAGAAACAGA TTCTNAGTTC 240  
 ATTTTACTC CCACTGTATT ATAGTTTANC AAAANTNGTT TATATCTTGG AAAAAAANCT 300  
 25 TTCTGTTTAA AAAANTTAAN CAAGTGAATG TNGGAAN 337

SEQ ID NO:3634

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS04288

SEQUENCE DESCRIPTION:

35 GATCCCACTG ATTGGCCAGC CGAGCGAGAA CCAGGCTGCT GCATGGCACT GACCGCCGCT 60  
 TCCAGCTTCC TCTNAGCCGC AGGGCCTGCN ACGCGGGCAA GCGTGCTGCC TCTNTNCTGT 120  
 GTCGTTTTGT TGCCAAGGCA GAATGAAAAG TCCTTAACCG TGGACTCTTC CTTTATCCCC 180  
 TCCTTTACCC CACATATGCA ATGACTTTNA ATTTNACTN TTGTAGTTTA ATCCTTTGTA 240  
 TTACANCATG AAATATAGTT GCATATATGG ACACCGACTT GGGAGGACAG GTCCTGATTG 300  
 TCCTTTCTCC AGTGTACATG TTTTACTCAC ANATAANATT NTTTCAGCAA GTAAAGNGGG 360  
 40 ANNGGGTTTT GGTNGNGNGG NGTGNGGTGN 390

SEQ ID NO:3635

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS04289

SEQUENCE DESCRIPTION:

50 GATCTGGCCA TTTGTACAT AATCCAGCAC AGATAAGCTG GGTGGTAATG ATAATAAAAA 60  
 TGGTTTTCTC AAA 73

55

# EP 0 679 716 A1

SEQ ID NO:3636

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04290

SEQUENCE DESCRIPTION:

GATCACCTGG GTTCTTTAT TTATCGACTG TGTCATGACA AGGAACTTA CAAACTGCAA 60  
CGCAGAGAAA CTATTAAAGG TATTCAGAAA CGTGAAGCCA GCAATTGTTT CGCAATTCGG 120  
CATTTTGAAA ACAAATTTGC CGTGGAACT TTAATTTGTN CTTGAACAGT CAAGAAAAAC 180  
ATTATTGAGG AAAATTAATA TCACAGCATA ACCCCACCCT TTACATTTG TGCAGTGATT 240  
ATTTTTTAAA GTCTTCTTC ATGTAAGTAG CAAACAGGGC TTTACTATCT TTNCATCTCA 300  
TTAATTCAAT TAAACCATT ACCTTAAA 328

SEQ ID NO:3637

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04291

SEQUENCE DESCRIPTION:

GATCCTGTGA ACCGTTACTT TGCCTAAATC ACTTGAGACT TGAGTNTTTA ATAACAAAGC 60  
ATCAATATTC ACTAAAGTCA ATCTNTTTTN ANTTTCTGTN ACTTGGCTAG AAGCTCTTGA 120  
CACTAAGGGA TTAGTGTTAA TTTCCCTGG GGGTGTTCCA CTAGGGCATT ACTGTATAAT 180  
GACTTGATGT TGCCACATAG ACTTCAAGAT ATATAATATT TTNAGGATTT TTTGATTGG 240  
CCTATGTTTT ATGCATAGT GTGAACCGTG TAAAGCTGG TTAACCTGTA TATAGATAGC 300  
TTATTGTTGA CTAGTTATAG TGTATTTN 328

SEQ ID NO:3638

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04292

SEQUENCE DESCRIPTION:

GATCCTTTCC CTGGATACAT AACCCTAGTA GATAATGTTA CTGCAAGATG TAATGNCCAA 60  
ATCCAACCTA CTGCAAAATNT TACTATGGAA ATCTCAATGC AAAAGTAGCC TTTGTNATTT 120  
TTTTTTTAAA CCGTCTCCAT AACAGANCAC TTAGAATTAT TAGCCATTTG CTGCAAAGTA 180  
TTGTTTTTAA AATGTCTGGC ATATACACCA CTAACATTTA ANTGCCAAC ATTCGGTCTA 240  
TACGTGAAAA ACCTAGANGA AANGCCCTGT TGGAGTTTGT ATGTAGAGTG CAATANTACA 300  
TCAATAAAGG TATTTTAAAA TGGAAA 326

SEQ ID NO:3639

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04293

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTGTTGT ATGTAATAAG TAACACAGAG TTTTAAAACA AATTAATTAT TTAGCTTTAT 60  
TGAAGTTTGT NTTTTNCCTT CCGAACCTGG AGTATCATAT TATAAACAGC AGTTTCACAC 120  
CAGAATAGCA GTGCCCTTNC TTTTGTACA TACTGATTGG NCCTTTCTTT ACTGTTACGT 180  
GGACACTTTC TATGTTAGTT TTGATGCATA ATTCTTTGAA TCCTTTTATA CAAACTAGAA 240  
TGTATGTGTA AGAATACCTG TCCCTGCAAT GTAGTAACTA CAAACTTATT TTTAAATAAA 300  
TAGAAACTT GTTTTCTAA GCTAAA 326

SEQ ID NO:3640  
SEQUENCE LENGTH:325  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04294

SEQUENCE DESCRIPTION:  
GATCCAAGAG TTAGTGATT TCAAAAGCCT TGGTCTCAGG AGAAGATTAA ACTTTTCATAT 60  
TGGGCAGTGG TTCACTTTAA AACACACACA TACACACACA AAACAATTTT TTAAGAAATC 120  
CTAATAAGTA ACATACCCAA AATGCTCTGT CTTGAGTCAT GAGAACCATC AGTTCTTGAT 180  
ATTGTCTAGA CTTGCATCTA GAGCTACGTT GTAAAATTCT TTAGGCATG TGTTAGATTT 240  
CTGTGTAAAC TTTGTTTAAA TGTAACCTTC ATACTACATT GTCAGTTTTT GTCTTAATAA 300  
AACTATAGAT TTATAATCCC TGAAA 325

SEQ ID NO:3641  
SEQUENCE LENGTH:391  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04295

SEQUENCE DESCRIPTION:  
GATCGGAATT TCCACCAATC AGCGGGAAGC CTCGGCCCTG TAACTGCTAA TGGGAGACAG 60  
CAGCGCCACG CCACAGGCTT TTCCCTGGT TTCGGGAGGG NTGGGGAGCC AGGTGGGGCT 120  
CCCGNCCAGA CCCTTTCCCG AGGTCCGNCC TCTCCGCCTT NTCTNTAAAT TCCTCTTTTG 180  
AGTNCCCTCC CTTCCGGTTG AGAGGCGGGG GTTGGCCCGT AGTTGTACAC TCAGTCACCC 240  
TGAAGTGTGG AGGNGGNGGG NCTCCNTTGT GGAAGTATTT GCGTGGGGAT TTGGTNTGTT 300  
TTATTAAGGG ATTTGAAAAA ATTCAGATGG ACTTNACTAG TATGGACTGT TNGGGTAAAT 360  
ATTNGCTTNC NGGGTTAATA AAATGGACAG N 391

SEQ ID NO:3642  
SEQUENCE LENGTH:324  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04296

SEQUENCE DESCRIPTION:  
GATCCAGTCA ATACATGCAG ACCAGTAAAA TCTGATTTGT GCAGAGTTCT CCATCTGACT 60  
CTCACTTATT TCTGTAGATA TATACATATA TAAATACAAG TATGTNCTTA CGGCACAGTA 120  
TTGCTGACCT TTAGTTCGAG GTTTTGTGCGG TTGTTGTTTA TTTTCTTCCT CTTGCAAGTG 180  
CTATCCATGT GAGTGTGTGA AGTTTCTCTA ATAAGTAAAA CACAGGCCCT TTTCTTGTT 240  
TGTTTTGTGT TAGTTTATTG TAAACAGCCA TTTGTTGTAA ATNATTATTG GCATTAAATT 300

ATAATTTATG ATTTTCAAAG CAAA

324

SEQ ID NO:3643

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04297

SEQUENCE DESCRIPTION:

GATCCAGTCT AGGCCCGTAT GTTGCAATTT GCTGTCATGT CTTCTTAGTC TCCATCNCAT 60  
CTCAGTGGTC TTTTCTTTTC CATGACTGTG ACAGAAATGA TTTGTATCCT TCATATATCT 120  
GCAGTCACAT GAAGTCTATT TGTCCCACTA CTGGTGACGT AAATTTTGGT AACTTGGTTG 180  
AGGGTGGTAC CGTCTAGGTT TCTCCATATT AAGTTGCTAT TTTNCCTTGT GTATTTAATA 240  
AGTATCTTAT AGGGAAATCC TTTGAGACTA TGTAATATC ATATTACATG TATTTNGCCT 300  
GTTTTCATCAT CTTTGAAGA TAN 323

SEQ ID NO:3644

SEQUENCE LENGTH:320

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04298

SEQUENCE DESCRIPTION:

GATCTGGAGC ACAAGGAACT CCCATACATT CCTAGTGGGA ATGCCTAATG TTAGAGTCTG 60  
GAAGACATTT TGGCAATTNC TTAACCAAGC TCTTCTTACC ATAAGATGAA GCAACTCCAC 120  
ACCTTGGTAT TTACCCAAAC GAGTTGAAAG CTTATGCCCA TACAAACACC TGTACAAGAA 180  
TGTCTATAGC AGCTTTATTC ATAATTGCCA AANCTTGAGG GCATCCAAGA TATCACTTAA 240  
TGGGTGGACA GATAAGCTGT GGTACATCTA TACAATGGAA TATTAAGGTG CTAAAAAGAA 300  
ATGAGCTCTG AAGCCACAAA 320

SEQ ID NO:3645

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04299

SEQUENCE DESCRIPTION:

GATCGGGATT AATATTAGTG CATTTTTAAA AACTTAAAA GTTTTACAAN TGTATTTGTG 60  
TATTTCTGT TTTGGTGCCT GTTTTATAGA AGATGATTGA NGAATCACTG AAGATTAATA 120  
TAAAAAAGGA ATTAGAAATG GAAAATGNAT TAGAAATGAG TAATCAAGAA ATAAAAGACA 180  
AATCTGCTCA CAGTGAAAAT CCTTTAGAGA AATACATGAA AATCATCCAG CAGGAGCAAG 240  
ACCAGGAGTC GGCAGATAAG AGCTCAAANN NGATGGTCCA AGAAGGCTCC CTAGTGGACA 300  
CGCTGCAATC TAGTGACAN 319

SEQ ID NO:3646

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04300

SEQUENCE DESCRIPTION:

5 GATCATAGAA GAAGAANCCA GTAATTGANC AAATCCTATT TAATGACATC CTTGTAGCAT 60  
AGATGGTCTA TAATGCTGAC CACAGATTTC TTAGAAATGC TGCTCTCTCT ATTTAACTAA 120  
CATTTTGTNC AGTTTTGCCT CCAGTGGAAG CAGAAAGGGT TTTNCAGCT GTTAAATCCT 180  
AAAANTCAAT ATAATTNATT TATGTAAGAA AAATAACTCA ATCAATATAT TTTTGAACCT 240  
TTTAAGTACT AATTTNNTNT TTATCAAGTA GAAAAAAAT GTATTTGCCC TAAATCCTTA 300  
10 AAATACAAAT GCTATAAA 318

SEQ ID NO:3647

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS04302

SEQUENCE DESCRIPTION:

20 GATCCTGAGG CTTTGGCTGA AATTCTGCTT GAAACTTGTA AATCAATCAC ATATTCTTTA 60  
GAAAATAAGA CCTACTCATC TGTGAGAACA GAAGCTTTAT CTGTGATAGA ATTGCTGCTT 120  
AAAAAACTTG AAGAATCTAA ACAGTGGGAA TGTTTGACAT CTGAATGCAG AGTGCTCCTA 180  
ATTGAGTCTT TAGCTACTAT GGAGCCAGAC AGCAGACCTG AACTGCAGGA GAAAGCAGCG 240  
TTACTGAAGA AAACACTTGA AAATCTGGAA TAANTTAGAN GGGGAAGAAA CAAACAAGTG 300  
25 CCATGTTTCAAT TGGGGGN 317

SEQ ID NO:3648

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS04303

SEQUENCE DESCRIPTION:

35 GATCCTTCTC CTTCCCTGGG ATACAGCACC TCCACCCTGC CAGGCCACCC NTGTAAAGGC 60  
AGCCAATTCA GAGCCACCTC TTATGCCTGC ATCTCCCCA ACAATTCCTG CTGGGAAACC 120  
ACTCCTCGTA TGGTGTCTAT TACACCAGTG GGTTC AAGC TTGAGAAGAA TCAAGTTCTA 180  
CAGGGCTGCT TAAAACACAG GTTGCTGGGT CCTGTNTCTC AGAGTTTTTG ACTCAGTCTT 240  
GGTTGAGAAT TTTCAGTTCT AGAAGCTCCT GGGTAATGCT AATCCTCCTG TTCTAGGGGC 300  
40 CATAGTCATT GTCCATN 317

SEQ ID NO:3649

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS04304

SEQUENCE DESCRIPTION:

50 GATCTACACG CGGCTGGCCA CCATCTACCA CAACTNCCTC CTGGACCGTG AGAAGTCGCT 60  
CTTNTTCTAC CAGAAGGCCA GGACCTTCGC CACAGAGCTC AACGTCCGCA GGGTCAACCT 120  
GCCTCCTCTG CCACTCTGCG GGTGGGCCCC CTGGTTGGCC CCCAGCCACC CTNGCTGAGG 180  
ACAGCATCCA AGGGAGTGGG TTTTGTGCAA GGGCTAGGGG TCTCCTGCCT NTCCTGGTGT 240

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CGNCGGTGGC TCATTTTCTN GCAAATNGAG GCACGAACGC AGGGNCCAAA TAGCAATAAA 300  
TGGGTTTTGT TTTTAAA 317

5 SEQ ID NO:3650  
SEQUENCE LENGTH:317  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS04305  
SEQUENCE DESCRIPTION:  
GATCTATGCA ATTTTAAAC TAGTAATGGG CCAATTAAAA TATATATAAA TATATATNTT 60  
NCAACCAGCA TTTTACTACT TGTTACCTTT CCCATGCTGA ATTATTTTGT TGTGATTTTG 120  
TACAGANTTT TTAATGACTT TTTATAATGT GGATTTCTTA TTTTAAACC ATGCAGCTTC 180  
15 ATCAATTTT ATACATATCA GAAANGNCG ANTTATATCT AATTTATACA AAATAATTTA 240  
ACTAATTTAA ACCAGCAGAA ANGTGCTTAG GAAAGTTATT GTGTTGCCTT AGCACTTCTT 300  
TCCTCTCCAA TTGTAAA 317

20 SEQ ID NO:3651  
SEQUENCE LENGTH:316  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

25 CLONE:HUMGS04306  
SEQUENCE DESCRIPTION:  
GATCTGAATT CTAAAGCGTC TTTTATTGTT TACTTTTAGG ATGAGGAAGT ACAGACAATT 60  
GGTCAGATAG AACTGTGCCT CACTAAGCAA GACCAGCAGC TGCAAACTG CACCGAGCCG 120  
GGGGAGCAGC CGTCCCCCAA GCAGGNNGTC TGGCTGGCAA ATGGGGCCGC CGAGAGCCGG 180  
30 GGTCTGAGAG TCTGTGAAGA TGGCCAGTC TTCTATCCCC CACCTAAAAA GACCAAGCAT 240  
TGATGCCCAA GTTTTGGAAA TATTCTGTTT TAAAAAGCAA GAGAAATTCA CAACTGCAG 300  
CTTTCTAAAA AACAAA 316

35 SEQ ID NO:3652  
SEQUENCE LENGTH:374  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04307

40 SEQUENCE DESCRIPTION:  
GATCCTTGGG TTGTAAAGAG AGTAGAAACC CTAGGNAGCA GTGCTTTTGG GTCCTAGAAC 60  
CTGTTGAGTT TCTAATGAAT ATTTGTAGAA TCTNATAAAA CAGTTTAAAT ACAAGCTTAA 120  
GTGGCTTATG AATCCTGTNA AGCTCATTTA TGGNCTAGTG TAAAACAATG TGAAGCTCTA 180  
45 CTAAGTNCTG TCCTTAATCA TAAATAATAG CCCCTTGNGG NCTAGCCTGT CCTCTGGTCA 240  
CCTTACCAGT TGGGTTGCAC ATTGTGTGGT CGTCCAATTA AACTCAATCT TNCGTGTGNC 300  
AGGNGNTAGT CTNTCCAATC ATGNCATAGN TTTCATCTGG TTTTGNCTG GTGGACGNAC 360  
CTTCGGANTA ANTN 374

50 SEQ ID NO:3653  
SEQUENCE LENGTH:316

55



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04308

SEQUENCE DESCRIPTION:

GATCAGGACC AACCTGGAAA ATGCCAGATT TGGCTATGCT TTTTAANACA TTNATTTGGA 60  
 CAGCTCACCA ACCCCTGAAG GGGCCGTTAA GCCTGGTTAG TTTTNTACCT ACTCCGAGTN 120  
 TCCTCCCCTG CCCCACCAGA TTGCTGCAGG GGC GCGGTGT GCCTGGNAGC CAAATTNTTG 180  
 ACACTTCTTT TTTCTATGC ACTGTTTTTA CACAGCTGTN ATTTTNTTT CAAAATTGCA 240  
 GCAGTCCCAC AAGATGTNTG CATTTGGACA AATAGTACTT AAAAACAAN CAAACAAGCA 300  
 CTCAGCCCAG TTCCTN 316

SEQ ID NO:3654

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04309

SEQUENCE DESCRIPTION:

GATCTAATGC AGAACTTATC AGATATTGTG AAAAATCAGT GTGGGAGGTA TTCAGTCAAA 60  
 AGTCAGAAGG AAATGTATTA TCGTTATAAT TTCAAACCTT AAGAAAGCCT AAATTACCAA 120  
 TTGCATATCA AATTTTTTTG ATAATGTAAG GAAAACTTAA ATCCCCTCCA TATCCTAATT 180  
 GGCATTTATA ATAATATGAC ACTTAACCCT GACAGCTAGA GTCTTACTTT ATGCTAATGC 240  
 TAGATATCTA TTTTNAANTT CCACGTGTGT AAACATGCTA TACTCTTCTG ATATTAANCT 300  
 TACTAAGTAC ATAAA 315

SEQ ID NO:3655

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04310

SEQUENCE DESCRIPTION:

GATCCAAGAA GAACTAGAAA AAAAGTTGTT TGCAGGCTTG CAACCTCTCA NAAATTTTAA 60  
 GGCTAGCTCT TCAACTATGT CTTTNAAAAA GAATATGTCT GCCCACAGCA GCCAGAAGTG 120  
 ACAGCATTCT TGTGAATGTT TACATCCTGC TGCTGATAGG TTCAAGGAAT TCTTTAAACC 180  
 AGATTCTGCT GACATGAGAA GCTCCAGTGA TTTGTTTTTT TGAAGGTCTG TATCAGAGCA 240  
 AGCCTAACAT CTAAATAANG TTTGATTCTG GATTTTCCAG GTGGGAAATA AATAAAGAAA 300  
 ATTTGGCTTG TCAAA 315

SEQ ID NO:3656

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04311

SEQUENCE DESCRIPTION:

GATCCGTGCC CGCNTCCAGG AGAAGTTGTC ACCTCCCTAC AGCTCCCCAC AGGAGTTTGC 60  
 CCAGGATGTG GGCCGCATGT TCAAGCAATT CAACAAGTTA ACTGAGGACA AGGCAGACGT 120

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GCAGTCCATC ATCGGCCTGC AGCGCTTNTT NGAGACGCGC ATGAACGAGG CCTTCGGTGA 180  
 CACCAAGTTC TCTGCTGTGC TGGTGGAGCC CCCGCCGATG AGCCTGNCTG GTGCTGGCCT 240  
 GANTTCCCAG GAGCTGTCTG GTGGCCCTGG TGATGGNCCC TNAGGCTGGG GGCCCCATGG 300  
 TCAGCCCAGN NTGGGTTCTG TTCTNTGGNN CTGTTCANNC NNAANCN 347

SEQ ID NO:3657

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04312

SEQUENCE DESCRIPTION:

GATCATAACT GAACCAGAAT TTGGATTATA GANGTGCACT TCCTAGCTGT TTTTATTTA 60  
 GGTATAGGAA CACACAATGA GAACCTTATG TTTAGAAATG AGCAGTAACA ACAGAGGGTA 120  
 ACTACACTGC AAGACTTAAA TGGTTTGAGC ATGTGACACT ATCCTTTTGT TGGGGGGAGC 180  
 AGGGTATAAN ANTATACATA CAGGAGATTA GTTTAATAGT AAAGTTTTAT ATGTATGTTT 240  
 AACTTCCATG ATATTTATNA TTTNGTAGAG ACATTTGTGA TTGTNTAGAG TTCTNGTNTT 300  
 TTTTCTATTT ATN 313

SEQ ID NO:3658

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04313

SEQUENCE DESCRIPTION:

GATCTTAAAA GTGGAAAGCA GAAAAAATAC TGTTTCCTGA AATTNAAAAG TTTTGGCAGT 60  
 GCCCAGCAGG CCTCAACAT TCTCACAGGC AAGGACTGGA AGCTGAAAGG CAGGCATGCC 120  
 CTAACCCCA GGCACGTCCA TGCCTGGNTC AGAGGCTTAC CACCTGANTC AACAAGGCTC 180  
 CCAGGGCTTC GTGTGTACC TCCCCCTTT GAACAGGAGG TCTTGACAGC TCTGAACTG 240  
 GACCACCGA AGATAGCAGC CTGGCGCTGG ANGCCGGAAG ATTGGAAAGC TCTACAACAG 300  
 TTTGTGN 307

SEQ ID NO:3659

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04314

SEQUENCE DESCRIPTION:

GATCCCCAGA GAGGTGGCCC TGGACCTGGA GTCAGGAGGC GGTGTCCAGA AGAGTCGCTC 60  
 ATCAACCCCG GGTCAAGAG TAAGAAACCA GCTGGTGGCG TGGACTTCGA TGAGACCTGA 120  
 AGGTGCAGCA CAAGCGTGGC CCCCGGGGA GTCCGCCTAT NAGGGGAGAG GCAGTCTTTG 180  
 AGGCCCCCAT CAGAGACCCC CCGCCACCAC CTCCACCTGC CTGTCCTGGG CCAGGACTAA 240  
 CACGGCTCCT CAAATTCCTT CCCTGTCAAA TAAACAGCTC CCTTGGTTGG AGGCTCTNGT 300  
 GGGAAA 306

SEQ ID NO:3660

SEQUENCE LENGTH:371

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04315

SEQUENCE DESCRIPTION:

GATCCCCTGA GCAAGTCAGA AGTTACTCTC ATCAGTCGTT CATGGTCACA ACCTGAGGTA 60  
CTCTGCTGAG TGGGCAAGGC TGAAGAAGAG GCCTGTGGAA TGCAGCATT A CCTGCTGGAC 120  
AGAGCAGGGC AGGCAGTTCT ATGCCTTGGA GCTCCTGACT GCAGGGACTC TGTCCCCACA 180  
CTCAGAAAGA CTCAGCTCAC TCAATGAGAG AATGTGATT ACTTTATAGA ACGTATAATC 240  
AACTTTGTTG AATAATTTGT TCTATTAAGG CTGTCTAAAG TATGTNATGT CTTCATCATA 300  
GTATGAAGTG TTGAAAATTA ATAACGGGCC TAGTTTAGGA AAAAGCTGCT TAAANGNGTG 360  
TGGCCCGTAN N 371

SEQ ID NO:3661

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04316

SEQUENCE DESCRIPTION:

GATCTGTATT GATATTTGAT AGTGAAAATG TTTATTCAAT TTTCCCCAA AATGTATTTG 60  
TTCCTCTTAC TTGTTTATTC AGCTGTGGTG ACTTCAAAAT ACTTTTCCCA GGTGACAAAA 120  
AAAAACTCAG AAAAAATTTT AATCTTAATT GCATTAATAC TATAAATTGA TTTGGAAGGA 180  
TTTAACATTT TATAATATNG GNNTTCCTCT GCAGTAATGT GGCATATTCT TCCNNNGTT 240  
CAAGCATTA AAAAAATCTCT TAGCAAAGCT GCACAGCCTT CTTCATAAGG GTTCTCTATA 300  
TTTN 304

SEQ ID NO:3662

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04317

SEQUENCE DESCRIPTION:

GATCTGCGGT GGGCCAAGAG TATCCAGGGA GAAACCTGTC CCTGGCAGGG CTGGAGCAGG 60  
GACACTCCAG GCCCAGCTGA GGCTTCCTGC TCTGCATGGC AGGGGACATC TCTNACCTGG 120  
TCAGGACCCT GGAGGTGGGA CAGCTGGTGC TAAGGGAATG TNAGCGCATC AGGGTTGGGG 180  
AGAAGCAGTG GGTGGTCCAG GAAACCCCTG AAACAGCTGG CCCTGGGGTC CCCTTTCAAG 240  
TGTTTCCAGT TGTGGCAAGG GGTCAAGGAG ACCTTGCAAT GCAAATCTNT TAGAAAAAAC 300  
AAN 303

SEQ ID NO:3663

SEQUENCE LENGTH:302

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04318

SEQUENCE DESCRIPTION:

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GATCTGAAAG ATTACATTTA GAACATTTAG TACTATTACA CTCTCAGAAA CTGTNGTAAA 60  
 AAGTCACATT TTCAAAACTT CATGCATATT GTATTCTTGT TGGAAATAAG TCCTATAGTT 120  
 TCTTAATTGT CTTTCATGCCG TCCATATTTA ACAAACATTG CAAGTCCTTT TTATATTTGG 180  
 GTAATNATTT GTAATTTAGT GAAGGAGACT AGGGGATGTT TTCTTCCAAA GGAATTTAA 240  
 AATCAATTTT ATGGTATTTT GAAAGTAAAA TACTCCTTAA CGTGTCAATA TTTTAAAAAT 300  
 GN 302

SEQ ID NO:3664  
 SEQUENCE LENGTH:301  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04319

SEQUENCE DESCRIPTION:  
 GATCCTCTCA GAGTGCCAGG CATCCCCCCC GNACCAGCAG AGGCTCATCT TTATNAGGCA 60  
 AGCAGCTGGA AGATGGCCGC ACTCTTTNTG ACTACAACAT CCAGAAAGAG TCGACCCTGC 120  
 ACCTGGTCTT GCGCCTGAGG GGTGGCTGTT AATTNTTCAG TCATGGCATT CGCAGTGCCC 180  
 AGTGATGGCA TTAATCTGCA CTATAGCCAT TTGCCCCAAC TTAAGTTTAG AAATTACANG 240  
 TTTCAGTAAT AGCTGNACCT GTTCAAANTG TTTAATAAAN GGTTCGGGT GCATGGGTAA 300  
 A 301

SEQ ID NO:3665  
 SEQUENCE LENGTH:300  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04320

SEQUENCE DESCRIPTION:  
 GATCTGAAAA ATGAAGTTTG GTATCAAAAA NGTCATGACC CTGTATGTAA AGCAGAAAAAC 60  
 TTCAAATCTG ACTGTTTCCC ATTACCTGCT GAAGTATGTC TCCTGTTTCT TTTCAAAGAG 120  
 GAAGANGAGT TTACAACAGA TGANGCAGAT GAAACTAGGA GCAATGAAAC CCAGAATCCT 180  
 CATAAACCAT CACCTAGCAG GCTGTCAACA GGTGCATCTN CTGATGCTGT CTGGGNTAAT 240  
 GGCATTGATG ATGCTTATTT TTTAGAAAGCT ACTGAAGATG CTGAATTAGC TGAAGCTGCN 300

SEQ ID NO:3666  
 SEQUENCE LENGTH:300  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04321

SEQUENCE DESCRIPTION:  
 GATCACTNAA TGGTCAAGTG GAACAAGCAC TACACGACTA ACCCCTATTG GGGTTTTTAA 60  
 CTTAAGGGAG GCTAATTTTT AATTTAAACT GCTCGAGATA TGAGTTCTGC AAAAGGTGGT 120  
 CCGCATCCTT GGCCCTCTGG ACATTATCAC TAAATTGCTT GTGCCTGTTA ACAAGAATAC 180  
 TGACCAGAAT GCTCTTCATG TAGCTTATAC AGTTGGTTCA CTTTCATGCGG TTCTTGACAT 240  
 GTTTATTTCT ACCCTTAATG CAATGAAATG TTTCATTAAT AAAAAACCAC TTTATATAAA 300

SEQ ID NO:3667

EP 0 679 716 A1

SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04322

SEQUENCE DESCRIPTION:

GATCTTTCTG GCTCCACTCA GTGTCTAAGG CACCCTGCTT CCTTTGCTTG CATCCCACAG 60  
 ACTATTTCCC TCATCCTATT TACTGCAGCA AATCTCTCCT TAGTTGATGA GACTGTGTTT 120  
 ATCTCCCTTT AAAACCCTAC CTATCCTGAA TGGTCTGTCA TTGTCTGCCT TTAAAATCCT 180  
 TCCTCTTTCT TCCTCCTCTA TTCTCTAAAT AATGATGGGG CTAAGTTATA CCCAAAGCTC 240  
 ACTTTACAAA ATATTTCTC AGTACTTTGC AGAAAACACC AAACAAAAAT GCCATTTTAA 300  
 AAAAGGTGTA TTTTTTCTT TAGAATGTAA GCTCCTCANG AGCAGGGACA ATGTTTTCTG 360  
 TATGTTCTAT TGTGCCTAGT AACTGTAAA TGCTCAATAA ATATTGATGA TGGGAAA 417

SEQ ID NO:3668

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04323

SEQUENCE DESCRIPTION:

GATCTCTGAA AGCTCAAATG GATGGAATTT AGTTTGCGGG AAAGAGGCTT TGCTTTGCGC 60  
 ATATCAGGCT TAGGACTGTG GGAGGCTTAA GAAGCAGATG CTTCTTTNAT TGTACTCTTG 120  
 TNCTGCCCTT GTTTTTTGAA GGCTCTGACT TATAACTNCT GTATCAGAAG AAACATTTTG 180  
 ACAGTGTCTT GGTGGGAGAT GAACATCCCT AATTGACATG TGATGACTAT TTCTNATTCC 240  
 ATTCATCTAA GAGTCATTGA AATTTTGTTT TGCTTGTTG TTAGCTTCA AGGTCTTN 298

SEQ ID NO:3669

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04324

SEQUENCE DESCRIPTION:

GATCATCTCT ATATCTAATT TGTATTATNA CTAATCTTAT TCCAACCTATT TNCTTTATNA 60  
 TACTGAAACA GTTTGNCCT TCAGTCTCTG CTTGGGCTAC CTAAAAGGGA AGGGCCCCCT 120  
 ATCCTGTAAT CACATGACTT ACTTCACCTT GTCAATCACT GAGAAGATTC ACCCTCCTTA 180  
 CCCTGCCCCC TTGTCTTGTA TGCAATAAAT ACCAGTGGGC CTAGCCCTCT GGGACCACTA 240  
 CCGGTCCCGG GGTCTTGATG GTAGTGGNCC CANAGCCCAG CTTGCNTNCN CAAA 294

SEQ ID NO:3670

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04325

SEQUENCE DESCRIPTION:

GATCAAGAGG CCACCAAGTTG TACTTCAGCA CCAATGTGTC TTACTTTATA GAAATGTTGT 60  
 TAATGTATTA ATGATGTTAT TAAATACTGT NCAAGAAGAA CAAAGTTTAT GCAGCTACTG 120

TCCAAACTCA AAGTGGCAGC CAGTTGGTTT TGATAGTTG CCTTTTGGAG ATTTCTATTA 180  
CTGCCCTTNN NTNCTNACTG TTTTATTACA AACTTACAAA AATATGTATA ACCCTGTTTT 240  
ATACAANCTN GTTTCGTAAT AAAACTTNTC CCTTTTTTTA AAATGNAANT AAA 293

SEQ ID NO:3671

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04326

SEQUENCE DESCRIPTION:

GATCTATAGT ATTTTAATGT GCATCTACTT TAAATNAGTC ATCTTGGGGT TTNATAATT 60  
CCCTTATGTT CTTGCCCTC TACACTTGAA ATAACAAAAT GCCTTAATTT TATGGATTAG 120  
TTCTCTTATA GTAGACAGGC AGCTATATGC AGCAAAACCA ATAAAGTTAT TTTTCAACTT 180  
TCATAGTTGT AAAATATCTT ATAACAGAAT ACAAACAGC TANGAAAACA TGCCACATT 240  
NATTTTNGCA TTTTCAAATA ATTN GTTTTT GGTGTAAGCA CAGGATAAAA AN 292

SEQ ID NO:3672

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04327

SEQUENCE DESCRIPTION:

GATCAAGGAT GCAACCTCAG GTTGAGAAAG AAACAGGGTT CCCTGGGCCC ATTAGACTGT 60  
TTGCAGGGCA TCACTGCTTC CCCCTGACAC CTCACAACTA GCAAAAATTG TCTTTGTCTT 120  
TGGAAATNAT AGAGGGATTT GGGTATCCAG ATTGTGCAGA TGCAAACTTA GGCTGTCTTG 180  
ATGNNNACTT AGAACCACAG AAATGCTTTT AAAATGCCTG TTTTAAGATG GAATTGTTGT 240  
TTNATAATT TGATTTTAGT GCTAAATAAA TGATTGGCTT TGTACATGAA A 291

SEQ ID NO:3673

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04328

SEQUENCE DESCRIPTION:

GATCTAAAGG CTCTGGNTTT GCCTTCTTTC AGTCTGACAC TGAATAACAA CCTCGACAAG 60  
GTGGGCATAT ACCTGGATTA TGAAGGAGGA CAGTTGTCCT TCTACAATGC TAAAACCATG 120  
ACTCACATTT ACACCTTCAG TAACACTTTC ATGGAGAAAC TTTATCCCTA CTTCTGCCCC 180  
TGCCTTAATG ATGGTGGAGA GAATAAAGAA CCATTGCACA TCTTACATCC ACAGTAATGA 240  
GTCATAATAT TATACAAATT CAGAGTGTTA TTAAGAGGT TTTGAAATAA A 291

SEQ ID NO:3674

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04329

## SEQUENCE DESCRIPTION:

GATCCCAAAA GCTGTTTTNA GGTATAAGGA CAAGGAGAGG AGACAAGTGA CGACAGCCAT 60  
 TCCCCTTTGC AGCTATCTAC TGTAGTGACA GCCATTTCTT GGTGATGGG TTGGAAGTCA 120  
 TCAGAGGTTT GAAGAATTAC ACTGGCCTTT GTTTTCNNG AAATGCCGAC CATGGAGATG 180  
 CTTTAGAGTC TTCTCAAATA GCTTAGATGT TGTAAATGNGG TTAAGCTTTG CTTCAATAAA 240  
 CAGGGGCCCT CAGAAGTTCT CCTTTAAATT TTTCANATAA AAAATTTAAA 290

SEQ ID NO:3675

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04330

## SEQUENCE DESCRIPTION:

GATCTATCCC TGTCTCACTG AAAGCCCTG TGTAGTGTCT GTGTTGTTTT CCCTTGACCC 60  
 TGGNNTTCC TATCCTCCCA AAGACTCAGC TCCCCTGTTA GATNGCTCTG CCTGTCCTTC 120  
 CCCAGTCACC AGGGTGGGGG GGACAGGGNN AGCTGAGTGC ATTCATTTTG TGCTTTTCTT 180  
 GTGGGCTTTC TGCTTAGTCT GAAAGGTGTG TGGCATTCTG GGCAATCCTG TAACTTCAAC 240  
 ATAGATTTT TTTGTGTGTG TGGAAATAAA TCTGCAATTG GAAACAAA 288

SEQ ID NO:3676

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04331

## SEQUENCE DESCRIPTION:

GATCAACCCC TGACCTAATC GGTATGTGA TCTACAGATT ACAGACATTG TATAGAAATG 60  
 CACTGTGAAA ATCCCTATCC TGTGTTGTTT TAATCTAACT ACCGGTGCAT GCAGCCCCCA 120  
 GTCATGTACC CCCTGCTTGC TCAATCAATC ATGACCCTCT CACACACATC CCCTTAGAGT 180  
 TGTGAACCTT TAAAAGGGAC AGGAATTGCT CACTTGGGGA GCTCAGCTCT TGAGACAGGA 240  
 GTCTTGCCAA TGCCCTGGC TGAATAAACC CCTTCCTTCT TTAAA 285

SEQ ID NO:3677

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04332

## SEQUENCE DESCRIPTION:

GATCACAAAA ATGGAACCCC CTGTTTCATG CTTCTACAGT CCAGCCAGCC AATCTGAAGA 60  
 TGTCATTCTT ATAAAAAAGT ATGACCAAAT GGCTATCTNC CACTGTTTAT NTTGGCCTTC 120  
 ACTGACTCTG CTAGGTGGTG CCCTGATTGT TGGCATGGTG AGATTAAAC AACACCTGTC 180  
 CTTACTGTGT GAAAAATATA GCACTGTAGT CAGAGATGAG GTAGGTGGAA AAGTACCTCA 240  
 TATAGAGCAG CATCAGTTCA AACTGTGCAT TATGAGGAGG AGCAN 285

SEQ ID NO:3678

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04333

SEQUENCE DESCRIPTION:

GATCTCTGTG TTTGCAGTCA AAGGGCGGCT CACACATGGT CAAGTATTAT AAATNTCCTG 60  
TGTATCTNAC AATGGAATCT ATTCTACAAT TTTAAGTATA CGCTTTCTGT ATATGGCCAT 120  
TAAGTGAAGC TTAATAATCT TGTNTTNTCT GTCCTCATAG ATATTTTAAT CTGTGGCATC 180  
CTCCTGTAAT CTCAGCATTT TGGGAGGCTG AAGATGAGAG GGTGCTTGA GGCCAGGAGT 240  
TCAAGACAAA CCTAGGCAAC ATAGCAACCC TGTCTCTCCA AA 282

SEQ ID NO:3679

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04334

SEQUENCE DESCRIPTION:

GATCTGAGGT GATATGTTCT GAATGTAAGC ACCGTCAACA TCAGACACCT ACTCATGGAC 60  
ATGTGGTTGC CGGATTTTCT TAAGATGTTT CCAGAAATGA CTGATATTTT ATATTTTATAC 120  
ATTTTAGATG ACAAAGCTTG ATATTTATTG CTGTCGCACA TTTTAAAGTT TTCTTTTGG 180  
GTTGCTCTGT GNCANGGCGT GGTACATGG TGNTAAATCG GTACCTGATA ATGTACCCAA 240  
ATACTATGGC CAGATAATAA ATTGNGGTGC AAACAACAAA 280

SEQ ID NO:3680

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04335

SEQUENCE DESCRIPTION:

GATCACTGTG CAGTGGGACC ACCCTCACTG GCCTTCTGCA GCAGGGTTCT GGGATGTTTT 60  
CAGTGGTCAA AATACTCTGT TTAGAGCAAG GGCTCAGAAC NCNNAATAC TGTCATGGAG 120  
GTGCTGAACA CAGGGNNGGT CTGGTACATA TTGGAAATTA TGAGCAGAAC AAATACTCAA 180  
CTAAATGCAC AAAGTATAAA GTGTAGCCAT GTCTAGACAC CATGTTGTAT CAGAATAATT 240  
TTTGTGCCAA TAAATGACAT CAGAATTTTA AACATAAA 278

SEQ ID NO:3681

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04336

SEQUENCE DESCRIPTION:

GATCANAGAN TNACAACTGT TCATTATAGT GGTGCCTTAG GCAATCTTN CAAAGTAAAT 60  
TCAGGGCCCC ATTGCTACTT ATGCCATATT TGGACATACT TTTTTTCT TCAATTTGT 120  
AAACTTCCTG GAAAGCTGTC TTCACTAAGT ATCCCNAGT CTCTATCTAT GNGGNTAGTA 180  
GTCATGGAAA TAACACATAA AGTAGGCCAG NAGTTNGNTG GAACGTGTTA GAAACTGTTT 240  
TGTGCTTNA TGGATGTCAT ACTTGNCANT ACATGTN 277



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SEQ ID NO:3682

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04337

SEQUENCE DESCRIPTION:

GATCTTTCTT TACTTGATGT GTCCTTCTNT TCGCAGATTG ATAACAGAGC TGTGCTAGAA 60  
CTGAATGCAA GCTTTCCAAA ANTNTTCATA AAAAANAGCT TTAATCAGTG ACTTAATATA 120  
TGTNCTGTAT TAAAATTAAT GTGCTTTGTT GGGGTTTAAT TTTGGNATTG GTTTTGGGTT 180  
TTNTTTTTAG TTGTTTTAAT GGTAAGAATT AAGACATTTT NTAGATTTTA AAGAAAAATA 240  
TGAAATTNTC CATTAAATCA AGTAAAAATG TGAAA 275

SEQ ID NO:3683

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04339

SEQUENCE DESCRIPTION:

GATCTCCGCA GTCTTCAGCG CATTGGCCCG AAGAAGGCC AGCTAATCGT GGGCTGGCGG 60  
GAGCTCCACG GCCCCTTCAG CCAGGTGGAG GACCTGGAAC GCGTGGAGGG CATAACGGGN 120  
ANACAGATGG AGTCCTTCCT GAAGGCAAAC ATCCTGGGTC TCGCCGNCGG CCAGCGCTGT 180  
GGCGNCTCCT GACCGTCGTC TCCTCACTCC GNCTTTTCAA ATTTTGTAT AACCCCGTGT 240  
TGTGTAAATA CAGTTTTTGC TCCGGTAAA 269

SEQ ID NO:3684

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04340

SEQUENCE DESCRIPTION:

GATCAGGCCA GTAGGTGTG AATGCAGGCT GGAGCCCCCG AATGCCCCAN NCACACTGCA 60  
GCATTGACCA GACCATCCGA AACCTGCGTC CCTGGTGATG TTCTCAAGCC TCGGAAGTGG 120  
CAAATGGAAA TAATATGGCC GGTGCGGTT GTAGGAGAGT TGTGACTTAG GCAGGAGTCG 180  
ACCTCCTCAA GTAATGGAAC GATTTCAAAG GCAGGCTGCC CTGACCAAAA ATATCTGCCA 240  
TGAATAAAGG TGCCTGAAAT CCTAAA 266

SEQ ID NO:3685

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04341

SEQUENCE DESCRIPTION:

GATCTACTTT CAGGATTATT TTTGTNTTT GAACGTGACA GTNTGGATGA GGCAAGTNAG 60  
TNTAGATGCT GCGACCCTGC GAGAAGCAAT AGCTAGTGAA CACATTAGCT CCCTACATGG 120

GACGCAGCTC CCTCTGACAT GTGTCTCTGC CCTTAACCAA GACAGAAAGG GGGTAAATGG 180  
AGGATTGGNT TACTGTCTTT GCTGGTTAGT TTTGTGAAAT TTAAAAATG TTCAACTTTT 240  
GANTAACTC CTTTAACTT CTAAA 266

SEQ ID NO:3686  
SEQUENCE LENGTH:270  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04342

SEQUENCE DESCRIPTION:  
GATCTCCTTC AGTNGTCTAC CCACTTCCGT CATTGTCCTC CGCTAGAATA ACAGAGTAGT 60  
TGGTAGTCAT GGCCAGAAGG GGGGTGGGGG CAGTGTGAGG ACTTGGGGTT TCTGTGCTGT 120  
GTGACACAAG GAGATAAGTG ACAATNTTGA AGTCCTAACT TGCATTATTC TAGAAAGTAT 180  
AGTGGTGATT TTTGTGCAA GATTTGAAGT TTAAAAAAG TACCAAGTTC CTGAAATTCA 240  
ATAAAATATT TTTATTAATT TTAATGGAAA 270

SEQ ID NO:3687  
SEQUENCE LENGTH:264  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04343

SEQUENCE DESCRIPTION:  
GATCTCAGCT CACTGCAACC TTCACCTCCC GGGAGCATGC TGCTCTATCT TTTTTNCAG 60  
ATGTTTGAGC TATTCCAGGT TTTTGGGAT TTCTGTTGNT TTGTTTGTG TTTTGCTTTT 120  
CTACATAATT GTTTGGATAA TCTGTGAGT ATCTACGAAG TGCCTTGATA GTAAATATAT 180  
NAACCCTGTG TATCAATNTG GGGTAATTNC ACATNTTTT CTATGTTGAG TTATCAATAA 240  
ATTGATATTG TATATGNCTC TAAA 264

SEQ ID NO:3688  
SEQUENCE LENGTH:262  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04344

SEQUENCE DESCRIPTION:  
GATCCTCAGT GCAAAATGTC TTGTGTANTT NTNTGTGAAT CCATGGGTCT GGCTAGAGGG 60  
CCCAAAGCTT GTAAATATGG GGATAGTCTG GGTCAGACCC ATCTNTCCCT TACCCATCTT 120  
GCTTCCAAGA CCATTTGTAG TGAGCGAGTG GATGCTGTGC TACGTGTGAA ATCTGTCTTT 180  
GCGGGGCCCTG TCTCAGTGAT TCGNTTTTGG TATTNGTTTG TAGCTTTCCT GGAAGTCAAA 240  
TAAATGTTTC CCCCCTCCA AA 262

SEQ ID NO:3689  
SEQUENCE LENGTH:256  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04345

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## SEQUENCE DESCRIPTION:

GATCTCAAAT GTGAACAGTT TACTAATGCA CTAAGAAGT TTAAATCTGT GGCACAATCA 60  
 ATGTAAGCAT GGGGTTTGTT TCTGTAAATT GATTCTAAT NTGAAATTAC TGAACAACTC 120  
 CTATTCCCAT TTTNGCTAAN CTCAATTCT GGTGTTGGTA TATATCCATT CCAGCTTAAT 180  
 GCCTCTAATT TTAATGCCAA CAAAATTGGT TGTAATCANA TNTTAAATA ATAATAATTN 240  
 GGCCCCCCT TTAAA 256

SEQ ID NO:3690

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04346

## SEQUENCE DESCRIPTION:

GATCTAAAAA GCTGAATAGC ATGTNAGTTA CTTGGTTTCA ACTTGAGTTT NCTTTTAATG 60  
 TTAATAAGAT TGAAACTTTA GTATTTAGTG GGGAAATGGAA AGAGTTGCCC TTGTTGCAAG 120  
 TAATGAAGCC TGATTTGATT ATGAAGCTGC TTAATCACTC TTCATGTGTT CAGAATTACT 180  
 GTTTTTNTTG TTTGTTTNC CTTTNGTCA CTGTGGTACA TTAAAAATTT NGGGAAGATG 240  
 CTTTACCTAA A 251

SEQ ID NO:3691

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04347

## SEQUENCE DESCRIPTION:

GATCCCAGAC CTGTNGTCTC TCCCACCCCC TCCCCAAAGC CACTGGAAGG AGCACATACT 60  
 ACCTAGAAGT AAGANGNNGA GCCTCAGAAG AAAACAAAGT TCTATTTTAT TAATTCCTA 120  
 TGTGTTGTGT TTGTAGTCTT GTCTTAGCTC TGGACGTGAA ATACTTCGAT GATGATGATG 180  
 ATGATGATGA TGATAATAAT AATAATAATA ACAACAACAA CAACAATAAT AAAGATGTGA 240  
 AAACTCGAAA 250

SEQ ID NO:3692

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04348

## SEQUENCE DESCRIPTION:

GATCTCAGAT AACTCAGTAC AGATAGCAAT TAGTCAGCTG ATTTGATTAC AATGGAGTAA 60  
 CCGACAATAT ATTTATTTAT AAAGCACATA TTCATAATAA CGAGAAGAAT TCAGAAAACC 120  
 ACTTAAGCAA GACCCTTCTG AAATAAAANN TGTNGCTTTT TAAATAGTTT GTCCTAAGGT 180  
 GTTTAAANCA TGCAACCTT ATGTAAGGNN AANTTTCCTG GTCCAANTAA NGTTGANGTT 240  
 TAAGGAAA 248

SEQ ID NO:3693

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04349

5 SEQUENCE DESCRIPTION:

GATCCTGGTT GGAAGGATGG GGAAGGATGG GGAAGGATGG GGAAGGATGG GGAAGGATGG 60  
 TTATAAAAGG AGGGCAGCAG CTGAGACTGA TGAGAGGAGG GCAGCCTGCT CTGTTCTTTC 120  
 AGGGCCCCC ACCCCCATCT CCCCTACCCT AGCCCACCCT AGGGCCTCTA CCCAGCGGGA 180  
 10 GGGGTTGAAG ACCAGGCCTG GTTTTATTAG AATTCATTTT GTAATAAAAG CCTTTTTTAG 240  
 TGGTGAAG 248

SEQ ID NO:3694

SEQUENCE LENGTH:248

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04351

SEQUENCE DESCRIPTION:

20 GATCCTATTT TNATGAAATG TCCAGAACAG GCAAATCCAC AGAGACAGAA ACTAGACGAA 60  
 TGGTTGCCTG AGGGTGAGGG GAAACAGGGA GTGACTGATG ATGGGTTTTG TGTGGGGGCA 120  
 ATAGAATGTN CTAAAATTTG ATAGTAATGG TTATACAACT CTGAATATAC TAAAAGCCAT 180  
 TGTACACACG TTA AAAAGGG TGGATTGTAT GTGAATTCTA TCTCAATAAA GCTGTTCAAA 240  
 AATTCAAA 248

SEQ ID NO:3695

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS04352

SEQUENCE DESCRIPTION:

35 GATCCACTCC GCCATCGATG CATCCAGAC CCCCAGATGTC GTGTTGCGAA GCATCCTAGC 60  
 AGCCTTCTCC AAAGCCACAT GTAAAGACTT GGTTATGTTT ATCTAATGTT GGGTCCAAGA 120  
 AGGAATTTCT TTCCATCCCT GTNAGGCAAT GGGTGGAAT NATAGGACAG GCAAAGAGAA 180  
 GCTTCCTCAG GCTAGCAAAA ATATCATTTN ATGTATTGAT TAAAAAGCA CTTGCTTGAT 240  
 GTAAA 245

40 SEQ ID NO:3696

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS04353

SEQUENCE DESCRIPTION:

50 GATCTCAAAA CCACTATTTT TATTATTTCA TTATTTTCA GAGGCCTTAA AATTCTGGAT 60  
 AAGAGAAATGG AGGAAAATAC TCANCGGTAC TTCATTATTT NATTCCTTT TATTA AAAAAA 120  
 TTA CTCTAT GTTTNATTG TCTCTTGAGC CTTAGTTAAG AGTAGTGTAG AAATGCATGA 180  
 NCTTCATCCT AATAAGGATA AANCTTAAGG AAAACCACAA TAAACCATGA AGGTGTACAC 240  
 AAA 243

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SEQ ID NO:3697  
SEQUENCE LENGTH:241  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04354

SEQUENCE DESCRIPTION:

GATCTNTCCA CGGTAGCACT TGNCCTTTTC GACGCTTAAC CTTTCCGCTG TCGCCCCAGG 60  
CCCTCCCTGA CTCCCTGTGG GGGTGGCCAT CCCTGGGCCC CTCCACGCCT CCTGGCCAGA 120  
CGCTGCCGCT GCCGNTGCAC CACGGCGTTT TTTTACAACA TTCAACTTTA GTATTTTAC 180  
TATTATAATA TAATATGGAA CCTTCCCTCC AAATTNTTCA NGTAAAAGGT GGCTTTTCAA 240  
A 241

SEQ ID NO:3698  
SEQUENCE LENGTH:239  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04355

SEQUENCE DESCRIPTION:

GATCAGCACT GCACTNTTAG CTGAGAGTGC GGGCAAGACA TAAACTGTCC AGAGTTTNA 60  
GNTTCTNGGA AAGACCGGAG GGCTTCTCCC CACAGAAGGC GGAGAGAGCT GGGNCTCAGA 120  
CATGGNTGTG CACCTTAATA AACCTGTCTG TCTGCCTCCC TGACTCTGCT TCTNNGGAGC 180  
ATGGTGAGCA GCCCTNGTGC TCANCAGCCA TACCTATGGG ACACACACTA CGNAAAGGN 239

SEQ ID NO:3699  
SEQUENCE LENGTH:236  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04356

SEQUENCE DESCRIPTION:

GATCACAGGT GATTCACACG TACACACATA AACACACCCA CCAGTGCAGC CTGAAGTAAC 60  
TCCCACAGAA ACCATCATCG TCTTTGTACA TCGTATGTAC AATGCAATCA TTTCATACTT 120  
TAAACTGGTC AAAAACTAA TTGTGATTTC TAGTCTTGCA AAGCTGTATG TAGTTAGATG 180  
ATGTGACAAC CNCTAATATT TATCTAATAA ATATGTATTG AGATGAAACC TGTA 236

SEQ ID NO:3700  
SEQUENCE LENGTH:235  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04357

SEQUENCE DESCRIPTION:

GATCCATCCT TTATCAGGAA GTCTGAAGCG ACTATAAAGG TTTTNNANTT CAGATTTAAA 60  
AACCAACTTA TAAAGCATTG CAACAAGGTT ACCTCTATTT TCCACAAGC GTCTCGGGAT 120  
TGNTTTTGAC TTGTGTCTGT CCAAGANCTT TTCCCCCAA GATGTGTATA GTTATTGGTT 180  
AAAATGACTG TTTTCTCTCT CTATGGAAAT AAAAAGGAAG AAAAAAAGG GNAAA 235

SEQ ID NO:3701

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04358

SEQUENCE DESCRIPTION:

GATCCGTGTT CTCCATTTAT TAATGCATTG TAGACCAATT TAACTGCTGT GTTTCAGGAA 60  
 AATTCTTCCT AGTTTAATAA GCAAGCTAAA AGTTTTATTT TTTATATTTA GTGCTTAATC 120  
 TTTGCCCTCAT GTTATGTAAA ATTAGCCTGC AGATATTTTC TCTCAATTCT GTAGACTCTC 180  
 GCAAGATAAA CATTCAAACA GTGAAACAAA CANTAAAATA AATAAACCTA AA 232

SEQ ID NO:3702

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04359

SEQUENCE DESCRIPTION:

GATCCATCTG AACTATGAAG TGAGTACCTG GAGGAACTCC TACATTTAAG GCTTTCAAAG 60  
 GTTACAGGCT TTTCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGCGTTTGT AGAAAAATGG 120  
 AATTCAAACA CTGTNNNTAG AATGTATGTT TACTTATATA GAATTAATGA ATNTATATAA 180  
 TAATAATNAC TGTATATAAT TNTAAAATAT AATAAAGTCT CTTTATCCAA A 231

SEQ ID NO:3703

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04360

SEQUENCE DESCRIPTION:

GATCTGGAGT TGAGAGCCAT GGGTTTGGAC ATGACTGGCA CAAACAGCTG TCATATGTTC 60  
 ATGGTCAGAT GTCATACATT CTCAGCTGTC TTGTTCCACC AGTATTTACC AGGAAAACAA 120  
 AGAATGTGTT AAGGGATGCT CCCCCACCCC ACATCTTAAG TCAGTGTGCC AAGTACTGAG 180  
 ATGATTTTAG GGACATTTTA TTTTAAATTA AATTTACAAT CTAATGGTAA ATTGAAA 237

SEQ ID NO:3704

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04361

SEQUENCE DESCRIPTION:

GATCATCAAC AAGATTTCTT TGTGCAAAAT ATTTGACTAT NCTGTATCTT TNATCCTTGA 60  
 CTAATTCGT GATTTTAAAG CAGCATCTTC TGGTTTAAAC TTGTTTGCTG TGAACAATTG 120  
 TCGAAAAGAG TCTTCCAATT AATGCNNNNT TTATATCTAG GCTACCTGTT GGTTAGATTC 180  
 AAGGCCCCGA GCTGTACCA TTCACAATAA AAGCTTAAAC ACATTGTCAA A 231

SEQ ID NO:3705

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04362

SEQUENCE DESCRIPTION:

GATCAAAATT GAACCATTGT ACAGTTTGGN TTCTGTTTGC TTCAAAATAT GTAGAATTGT 60  
 GGTGATGAT TAATTTGCGA GACTAACTTT GAGAGTGTA CANTTTTGAN GAAAACATTG 120  
 AATGTTTTGC AAATGAAGGG GCTTCACGGA ATGTTACANT GNTACTAATA TAATTGGGCT 180  
 TTNNTNATGC AAATNGTTAA CACCAGCTAT TAAAATATAT TTNGTAAA 229

SEQ ID NO:3706

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04363

SEQUENCE DESCRIPTION:

GATCGCTACC CACCTTCCTT CCATGGTTCC CACCCTCCAC GTTATTTTCC CTTTCTGCAG 60  
 CGGTTGCACT ACAGGTAGCT ACTGTGTATT ATGGACAAAT GAGAAATGAA TTCTTTTCT 120  
 GGCTGTCCAT CTATTTTATT TCAAATAAGG AAAAGTGAT TTGGATTTTG TGAAATACA 180  
 TCTAGTGATG NCATTTTTC AATGTTTNA AAAACCGTGT ACAGTAAA 228

SEQ ID NO:3707

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04364

SEQUENCE DESCRIPTION:

GATCCTCATC CAATTGGTGT TTTTCAGAAG TTTCCAATA TTATGAATTC TGTGTTGTGG 60  
 AGAAAAGCAA CCATGCATTT ACTGGTCAAT GCCTTCTTGT ATATGTAATT CAATACTTTT 120  
 ACTTTTAATA TCCTCACCTT ATCTAATCTT TGATTTTGT CATGTAATTT ATTGCTTCAT 180  
 TAAGGTACT TTTGTTATA CAAAATAAAA GCTGATATCC AAGGCAAA 228

SEQ ID NO:3708

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04365

SEQUENCE DESCRIPTION:

GATCTATGAA AATNTGTTTT GACCAACTT AGTATTAGGC AGGTACACAG ATAAGATTTT 60  
 CCATTCTNAA CATTCTCACT GTAATGCACG ACATTTGANG CACCTGNATG TGCTATCAAT 120  
 CAGGTGGGAA ATTTAGCATT ATATATTGGA AGCATTGAGA AACATTGGTC TNTCATTCT 180  
 ATTTNNTTTT NCCCCTCCTN TCCTCCTCCT GCCCCACANT ATATNN 226

SEQ ID NO:3709

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04366

SEQUENCE DESCRIPTION:

GATCCTGAGA GCTTTGAGAG GGTGTTGCCA GTTTTAAGCT GAGATGGCCC ATTTGGAGCC 60  
TTACAGAACT AGACCAGAAG ACATTTGTGG ATAAATCTGA ACTCACTTCC TGTGTGTAAC 120  
TTCTAACTTC ACTGGTTCCT CCCATCTGAA TTGGCCACAT GCTTGCTGAA GAGACTTGTT 180  
TTCTTCTTCT AAGACAGTGG TTTTGT TTTT TGGGTTTTTT TAAA 224

SEQ ID NO:3710

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04368

SEQUENCE DESCRIPTION:

GATCTGGGCA GAATCCGCCA AGCGGCTGGG CCCAGGCTGT GGCATGATGN ACGGAGNAAN 60  
GAAGCACCTG GACTTCTAGG GATTCCTCCT TAGTCGCTGC ATGCAGAATT CTATGACACT 120  
CTAATNATGA TTGCTAATAG CTTATGTAAA TATTTNNNTT AACAAATTGG NCCTNCACTC 180  
CTTNAAAAAC ACAAGGATTA TAAAATGGGT GCCNGCATT NTN 223

SEQ ID NO:3711

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04369

SEQUENCE DESCRIPTION:

GATCGTATTC NTNATAAACT ATTACCAGTA CAGTAGCTAG TAGATATNNT GTGACTGCCT 60  
CATTGTTTAT CTTGCTGCTT TGGTCCCTAT GGCTCTAGTA TGAACATTCT CGTGTCTTCT 120  
GTGGAAATGA TTTCTGTGTT ATAGTTNCAN CTTNGGTAGA GGTGGGGATG ATTGTATTTT 180  
GTTTTAGTTG ACATCATTCT CAACTNTTAG AAATACTGTT N 221

SEQ ID NO:3712

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04370

SEQUENCE DESCRIPTION:

GATCAGTTTG CGAGTTTTGA TGAGNTTGT AAGGTTNTN TTTTACAAAC TATGAATCAG 60  
CAAATNTTTA AGATTGTACC ACATAGCAAA CATACAGCTG TTGAAAAATA ATGTATATAA 120  
AATGCATATA ATAAATATTA AATNGTGTAC CTGTATGTTA CTGTTGGCTA CATCATTTTG 180  
TGTTGAATAA TAAAGTGCAA TACNNCCTT CTCCATAAA 219

SEQ ID NO:3713

SEQUENCE LENGTH:214



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04371

SEQUENCE DESCRIPTION:

GATCATTCTG TATATACATA TTTTAAATTA TGCAAGCAAA CTAGGAGGAG AATGTNCAAT 60  
TTTAAGGGAT ACCTAATTTT CNTTCGGTTA GGGGATATTT TCCANCCTCT TGCTTTATAC 120  
TCTGATATGG GGTGTNTTTA TGANCITTTT AATGTTATTT ANTCATGCAG ATTTCCAATC 180  
ANTGTATTGC NCATTCCTG ACAAANGGG NAAN 214

SEQ ID NO:3714

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04372

SEQUENCE DESCRIPTION:

GATCCAAAAN ATAAACTTG AAGCTATTCT GGAACATAA TGGAAAAATG AAATGGCTAT 60  
TGTTTAAAAA AATGATAGAA ATACATTGTT GATGGGATAT GAGTTAAGTT TATTTTCTAC 120  
AAACCTGTAA TTGATGACGG CATGGATAAT ATCTTCATGT TTCTGACNAG TAATCTGTAT 180  
GTGGGGGGAG GGGATAATAA ATATTCTAA CCAAA 215

SEQ ID NO:3715

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04373

SEQUENCE DESCRIPTION:

GATCAAAAGT GAACACCCTG GCCTATCCAT TGGGGATACT GCAAAGAAAT TGGGTGAAAT 60  
GTGGTCTGAG CAGTCAGCCA AAGATAAACA ACCATATGAA CAGAAAGCAG CTAAGCTAAA 120  
GGAGAAATAT GAAAAGGATA TTGCTGCATA TCGTGCCAAG GGCAAANTG AAGCAGGAAA 180  
GAAGGGCCCT GGCAGGCCAA CAGGCTCAAN GNAGAAGNAC GANCCAGNNG ATGAGGAGGA 240  
GGAGGAGGAA GANGNAGATG AAGATGAGGA GGAAGAGGNT GAAGATGAAG AATAATTGGC 300  
TATCCTTTAA ATGATGCGTG TGGAATGTGT GTACN 335

SEQ ID NO:3716

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04374

SEQUENCE DESCRIPTION:

GATCAAATGT GCTGCAGCTT TTGCAGAAAA CAACTCAGAA ACACAAAACC CCCCAACAGC 60  
TCAATTATTA TTTTTCATG GTTTTCCTAC AAGAGCCAAG TAGCACCATG TACAGAAGAC 120  
GCCTTTTTTT TTGGAATATT GAAATCGTTC TGCATGTAAA ATATGGGATA ATGACCTGTT 180  
TATATTAAAA TTCTGATTAA ATTATCTGAA A 211

SEQ ID NO:3717

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04375

SEQUENCE DESCRIPTION:

GATCAAGAAT TCTACCATCC CTTGGGTCTT TGTGTATAAA CAATGTATAA TACCAGGTAG 60  
 ACTCAGTCTT TAAGATATTA GACAGTTTTT TTAGTCCATG GGNTNNNNAA TATAAACATT 120  
 AACTTTCCTA TAAGANTATT TTGGCTTTGT AATCTATAGC CTCAAATTGG TATTTATTAT 180  
 GGNTTCACTA GACAAACAGC TGTTTCCTTA TTGTNTTTTN NCTTTAGTGT TTCTGATTTG 240  
 CTATCAGTAG CTGTTTTTAA AGCCGNCCAA GGNAAATANT TATTTGCAGT TTTTGAAGT 300  
 CACTTTTGA GCCCTCATNC AAGCTCTCAT TGTGGNTGGG GAGGGATACC NTTTTGGTT 360  
 GTTAAAAGGC CTATNATTGG TTAAAGGGCN 390

SEQ ID NO:3718

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04377

SEQUENCE DESCRIPTION:

GATCTTAGAG CTGAGGAATT GGCCTCCCAA TCCGAACAGG TGTTATAATC CTTTCTNAAT 60  
 AGGTTGTGCT GTGGACCCAA TGTNAGGGCT GTNCTGGTGT AAATGGTGAC ATATTGAGCT 120  
 GGGGGGATGC TTTCGGGGTG GGGGGACTGG TTCCATTCCA TCAAAAGGCC CTCTTGAGAG 180  
 TCTATCCNGG GNCCATTGG TTNAATTAA CAGGCCAGNA AAGANGGTTG NTNNN 235

SEQ ID NO:3719

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04378

SEQUENCE DESCRIPTION:

GATCTCCTGA GCTCAGGCAA TCCGCCACC TCGGCCTGTC AAAGTGCTAN GATTACAGGT 60  
 GTGAGCCACC ATGGGTGGCA TCTTAAATAT AGATTTATAA GGCCCNNTG TTATATATT 120  
 NNAAAAATC AAATTA AAC TANATCCCA AATGTCCNT TTATTAATGA AGTATTTGT 180  
 CANATGGATG TTTTAAAGCT GTGTATGTN 209

SEQ ID NO:3720

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04379

SEQUENCE DESCRIPTION:

GATCTAGGAT TACTCTGGAC CTCATTCGGG TGTTATGAGT ATCCCACGAA GGCCAGACGC 60  
 TGATTTNATT TNCTCATTC CACAGATTGA CAAGGATAAG TCAGNNGTT GTAAACTCTA 120  
 GGTAGCAGAT GAGAAATAAT TGACTTAATA TCAGAAATAT TTNCCAAACA CTTTCCTTNA 180  
 TTTTTCCTTC TGANTAAATA GANANCCNN 209

SEQ ID NO:3721

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04380

SEQUENCE DESCRIPTION:

GATCCAAGGA ACGTTTGGGG TTTCCTAGGT GGGCCACATC CAATCAGTGG AAGGTCTTAA 60  
GAGCAAAANC TGAGGTTCCCT CAGAGAAGAA GGAAATGTTT TAAGACTTCA GCATCAATTC 120  
CTGCCTGAGT TTCTAGCCTG CTGGCCTGCT CTACAAATTT CAAGCTTGCT AGCCCTCACA 180  
NTCACATGAA TAAATTCCTT AAAATAAA 208

SEQ ID NO:3722

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04381

SEQUENCE DESCRIPTION:

GATCCTTTCC CCATGGACAG TGACAGAGCA ACTGGGCCGC AATGGCATAG GCAGAAGAAA 60  
ATNTAATCAC TCTGGGGGTG ANTGGTGGTT AAAACGACTC ATGTAATTAT TTGGATTGTA 120  
ATTTCTTAC ACATATTTNT TTGCTTAACC CAGCATGTNA GATATATNAT NTAATCTAAT 180  
AAAAGATACA AACTTATGGG CACACAAA 208

SEQ ID NO:3723

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04382

SEQUENCE DESCRIPTION:

GATCACCTG GAGCTGTGGC TTCCCCGAGC AGCTGAGAGT GAAAGGAGGC AGTTCCTTTA 60  
CTGTGAGCTC TCACGGCACG GTGCTCACGC CCCACACAGG GGCTGCCTTC ACTCGGCTTC 120  
AGCAGCNGTT GACTTTTAAA TCATAAAAAG CCGCTCTATA TACAGTTTAC TCTGTTGCTA 180  
GAAGGCAGTG GAACATAGGT ATTTAAA 207

SEQ ID NO:3724

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04383

SEQUENCE DESCRIPTION:

GATCCACGTA CAGTTTGGAT TTTCCTTCTA GCCTTCATGT GTGGCCCAAG CATCTATTTT 60  
AGACTGTCAT GGTGGGCATT GTTCTCTGAG GTTCTGTCTT CCCTTCGTGT TTCTATGAGC 120  
TTTAATTTGT ATGGTTCTTG TTCTGTTAAT GCCACTAGGG ACTATGTATT CCTGATTCCA 180  
CCATGACAGC TACAGTAAAA CAGTAAA 207

SEQ ID NO:3725

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04384

SEQUENCE DESCRIPTION:

GATCAAGCAG GCACTTCAAG CCTCAATAGG ACCAAGGTGC TGGGGTGTTC CCCTCCCAAC 60  
CTAGTGTTCA AGCATGGCTT CCTGGCGGCC AGGNCTTGCC TCCNTGGACT ANCTGGGGGG 120  
TTCCGGGTCT CAAGAAGACA AGGGTGCTGG NCCTCCCTAA GCCAAGGAGA GGANTAAAGA 180  
CAAAAAGCTN AAAAAAAG GAAA 204

SEQ ID NO:3726

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04385

SEQUENCE DESCRIPTION:

GATCTCGAAC TGTACAAAA TACATGGAGA CTAACAAACA GAACCACATG GAACTTTCAA 60  
ACTGAAAAAA AAATTTGTCA CAAAACTTT GTTGTCTAG TTAAGTTGAT TGTAGATGGT 120  
AATTGAATAT ACTCCTTTGA AAATATTTCA TCAAGTATGT TTCCTGCTCA TTGTGATACA 180  
TTAAAAAAA ANTATGGGCA AA 202

SEQ ID NO:3727

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04386

SEQUENCE DESCRIPTION:

GATCCAGAAG GCTTACGAGT ATTTTATTAT CTTGTCCAGG ACCTGAAGTG TTTGGTCTTC 60  
AGTCTTATTG GATTACACTT CAAGATTAAA CCAATCTAGA CTGAATATTG GTGTGGACAT 120  
GGGGGGTGGG TGGGAGTAGA AAATTTTGTG TATATCAGGG CAGTATTTT TTATGAACTA 180  
TAAATGATTG TCTTTAATAA ATATGTGATA AAATCCAAA 219

SEQ ID NO:3728

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04387

SEQUENCE DESCRIPTION:

GATCATATTT AGAGGATATA ACAATTAGAA ATCTAGAAAA TAATTATCAC TTTNATAAAA 60  
TNTTNAGTCA ACTGTACAAA TAATTACATA AAACATCAAT TAATNATGCT TAAAAATCAC 120  
TAATNTTCAT AATATATAAT CACTATTTGT AATCAAAAAGT TTAATTTTAT NTNAAAAAAT 180  
AAAAAATGCT TACTTGGAAG 200

SEQ ID NO:3729

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04388

SEQUENCE DESCRIPTION:

GATCAGCCGA ACTCTAGGGA CTTGGTGTG CTTGGAAGGC ATCCATACCT GCATTTTGCA 60  
TTCTTCGTAT GTAATCATAT TGCCAAAGAC AAATATTTC ATCATTTATT GTAAATAACA 120  
CTTTTCCCA GACCTACCAT AAAGTTTCTG TGATGTATTG TCTCCAGTT GCAATAAAAA 180  
TTACTGAGTT GCATCAAA 198

SEQ ID NO:3730

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04389

SEQUENCE DESCRIPTION:

GATCTAAGAT TAATTCCTCA ACTGTTTTGC ACTCAACAAA GACATACCTC TGAGTTGGCA 60  
ACCAGCAGGG TGGATAACGG GCCAGTGGTG ATAAATCAA AGAATAGGTA ATGAAACAAT 120  
CATCCAGTTA ACAATCAGCA AGGTTCTTCA GAGCCTAATT AATGTTTAAT TCTAAATAAA 180  
TTGCAACAAT TAAGAAA 197

SEQ ID NO:3731

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04390

SEQUENCE DESCRIPTION:

GATCCAAAAG TTAAATTAG TGCATACATC ATGTCATTTT ACCTCCTGTT CCTAGGAACT 60  
CTCCATTCCC AAGCATTGCC AGTGTTCCTC AGATAATCTT AGCTGTTGTC TTGTGCTGTG 120  
GAAATGGAAG AAACCATCTT CACAGACTGT AGGAGAATTC AACATATAAT TTCTTAATAA 180  
ATACTGTTTC TTTTAAA 197

SEQ ID NO:3732

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04391

SEQUENCE DESCRIPTION:

GATCTAAGGG AGTCCACTAT CTGTGCAATT GTATTTGGNT TTTTTTGCA CTGTTTCAAT 60  
GCTGGTAATT GAAACCATT TAATATATTT GGTGTATTC ACTTTATATG TCCTTCCAAA 120  
AATNTGTTG TGTACAAACC ATGNNNNNGA ATGTTGGCTT CCAAGTTTTT AAATAAGAAA 180  
CTTTTGTAT TTAAA 195

SEQ ID NO:3733

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04392

SEQUENCE DESCRIPTION:

GATCCACGGA GCAGAGGTCA TCTGTCCCCA GCTTGGCCCA CTGAGGCCAG CATGGNTGGG 60  
CCCAGGATGC TTGTCTCTCA GCTCCCATCC TGTGTACTTC CACATTGGTT TAACCAGAGG 120  
AAAACCGAAA TCTACAATTG TNATAAACAC ATTTAAATGT GCGTAGAATC AGCCATACAA 180  
ATTGTGAAAC ATAAA 195

SEQ ID NO:3734

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04393

SEQUENCE DESCRIPTION:

GATCAACTCC CCCAAGGCCC GAAAGGTGCT GCATACCACG TACCANAGCC AGGAGCGTGG 60  
CACACACAGC CTGGACATCA AGTGGTGAAG TNAGGCCAGG GNCTTCCAGC TGCTCTTGGG 120  
GCCAGAGCCA AGAGCCTCTN AGTAGAGGGA GGGGCTGCCC TGAGTGGAGT ATTAAAGACA 180  
CTTAAGAAAA CAAA 195

SEQ ID NO:3735

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04394

SEQUENCE DESCRIPTION:

GATCCTGTGC CCTAGGAGCA CCTAGGAAGA CTTGCTCCAT CTCCGCCCGC ATATCTGGGG 60  
CACCAAGAGA GACAGAGTCG TGAGCCAGGC TCGCCTCATT CCTCGTCTTG GGAGAACCGG 120  
ACCAACTTCC CAAAAGGCC TTGCCGTGCA GAATTGGCCT GGTTTAATAA AGAACAGACC 180  
TGNCCCAAGN AAA 193

SEQ ID NO:3736

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04395

SEQUENCE DESCRIPTION:

GATCTGGCCC TCCCCAGAAC AATCTGGATT TCACGGAGAC AGCAACCAGA AGTTAAACCA 60  
TGTGACTAAA AATGCATCTG GCTACTTTTT CATGTATGTA TGAGACAGAA ACTAATCCTT 120  
ACTATCCTAT TAGGATACCA CTTTTCATTG CAAAGTTTGT GTCAATAAAG TCATTAATTT 180  
TAAACATAAA 190

SEQ ID NO:3737

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04396

SEQUENCE DESCRIPTION:

GATCATAAGT AGTGGAGGAT TTAAAACCAG GCTGGCTGGC TCTTAAGGCC TATGCTCTTA 60  
ATTNACCATG TNGAATTAAT TTACCATATT GAATTACACT TATGTNCACC AAGTNAGGCA 120  
TTTNGGCAGC CATTGTTTAC GTTTTANTTT TGGAATAATT TAGAAAAGTT ACCAGAGTAA 180  
TATGAAAGCN 190

SEQ ID NO:3738

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04397

SEQUENCE DESCRIPTION:

GATCCTCCGC ATCCCGTGCG AGGAAGAAGA TGTGGAGATG AGTGAGGACG CCTACACGGT 60  
GCTGACCCGC ATCGGGCTGG AGACGTCAC TGCCTACGCA NNNNNGCTCA TCACAGCTGC 120  
CAGCTTGGTG TGCCGGAAAC GCAAGGGTAC AGAAGTGCAG GTGGATGACA TCAAGCGGGT 180  
CTNNNNN 187

SEQ ID NO:3739

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04398

SEQUENCE DESCRIPTION:

GATCTGGCCC TAAACTTGAA ATACCTCCTG CTCCTTTGGG GACTGGNCTT TGCNAAGAGC 60  
ACCTGGGGAG GAGACTGGTG CTAATAAGC CAGTAAGTAA GTCCACTCTT TGGNTGCAGC 120  
TGGTGCAAGG TCTACCCATA CCTTTTATT TNCAGTGTTT AATAAAANTC CAGTGNGCAA 180  
AGACAAA 187

SEQ ID NO:3740

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04399

SEQUENCE DESCRIPTION:

GATCAAGTTC TGCNCTGAN GAGGCTGCCA AAAGTCAAAA GNNGGGCCTG GGAAGGCAAG 60  
CTCATTCCTC ACAACGGCCT TTCCAGGCC NGTTTTTCCC TTCCGGCAGC CTCTTGGCCT 120  
CTAATTTGTT TATCTNTNGT GTATAAATCC CAAAATATGG AATTTTGAA TATTTCACC 180  
ATTAAA 186

SEQ ID NO:3741

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS04400

SEQUENCE DESCRIPTION:

GATCTGCCTT CCTGCTGAAA CTTGTTCCAC CTCAGTCCCC TCATCTGTCA CACGCATGTG 60  
GGGTGGAGTA GGGAGATGCG GGGAGCAGGG TGGGCAGGAA TACTGTTATC TATGTNACGG 120  
GGCAGTCGTG AGGCTGAGAT GAGAATGCGG ATTAAAATGC CTGGCGTGCT CACCGTAACA 180  
CCAAA 185

SEQ ID NO:3742

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04401

SEQUENCE DESCRIPTION:

GATCCCATCT NTACAANAAA CTAAAAAATT AGCCAGGCAT GATGGCACAT TCCTGTAGTC 60  
CTAGCTACTC AGGAGGCTAA GGTAGGAGGA TTGCCTGAGC CCAGGAGTTC AAGGCTGCAG 120  
TGAGCTAAGA ACGTGCCAGT ACACTCCANC NNGAGCCACA AAGTGAGACC CTGTCTCGCA 180  
AA 182

SEQ ID NO:3743

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04402

SEQUENCE DESCRIPTION:

GATCAAAGTG GTAAAGACAA TGTAATAATT AACATTTTAA TACTGATGTT GTACACTGTT 60  
TNTACTTAAC ATTTTGGGAA GTAAGTGCCT CTGACTTCAA CTCAAGANAA CACTTTTTTG 120  
TTGCTAATGT AATCGGTTTT NGTAATGGCG TCAGAAATAA AAGGATGCTT ATNATTCAA 180

SEQ ID NO:3744

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04403

SEQUENCE DESCRIPTION:

GATCTNCGGA ATGATGAGCA CACAAGGCGG GAGCTAGCCA AGATGAAGCA GGNGCCGGTG 60  
AACCTGAAGA AGGCAGAGAT ATGGCAAACA GGATTNGCGC TTTTGGNNAC ATGGAGTGTT 120  
CAGCAAAGAC CAAAGATGGA GTGAGAGAGG TTTTNAAT GGCTACGNGA NCTGCTCTN 179

SEQ ID NO:3745

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04404

SEQUENCE DESCRIPTION:

GATCTGAGTG CCTCAAGATG GTTTTCAAAA AAATTTTTTT AAAGAAAATA ATTGTATACG 60



TGTCACACACA GCTGGCTGGA TGATTGGGAC TTAAAAACGA CCCTCTTTCA GGTGGATTCA 120  
GAGACCTGTC CTGTATATAA CAGCACTGTA GCAATAAACG TGACATTTTA TAACGAAA 178

5 SEQ ID NO:3746  
SEQUENCE LENGTH:332  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS04405

SEQUENCE DESCRIPTION:  
GATCCGAGTT CCTCACC GCG GGCCGGGATG TGACCACCCT NTTCAGAGGT TGGACCCAG 60  
GCTTCAAGCA CCGAGTGAGG GGTCTGTTGG GCCCCCTGGG AGAGTCTCTG GTGTGAAGTG 120  
GCTTAGGTCT GGA CTGGTCA GCTGTGGCAC CAGCCGGTCC TGCCACGCT TCAGGATGGC 180  
15 CGGGGGCTGC CCCTGTGGGA GAGTTGCCAA GACTCGGCGA TACCAAGGAT GGAAGCCAGA 240  
GGCTGTGGCG AGGGAGAGCC AAGCATATTC CCAGCACCAG GGCCACTGCT GGCACGTCGT 300  
AGACATCCAA TAAATATTTT TGGAAGGAGA AA 332

20 SEQ ID NO:3747  
SEQUENCE LENGTH:177  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

25 CLONE:HUMGS04406

SEQUENCE DESCRIPTION:  
GATCTNNATA CTGTGAATAG CAGAATGTAC AGATGAAGAA TATTAATAATN AGGGGCGTCC 60  
ACTCCAAAAC ATATCACCAG AGTGACAACT TCAGCCCTCA GCCTCTGCAA TCCATATATA 120  
30 TNCTGGTCTT GGGAGTCCAT AGAATACTGT TTCCTTCTAA TAAAGGTTTC AAACAAA 177

SEQ ID NO:3748  
SEQUENCE LENGTH:186  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

35 CLONE:HUMGS04407

SEQUENCE DESCRIPTION:  
GATCAATAAT AGTACCTTN ATTATACATT TATTATTGTN TCTCTCTCTG ATGTACTGTG 60  
GATTGTACAT TTAACCTTGG AATGGCTTTG TAATAATCAG TCTTAAGAAA ATNTTGACAA 120  
40 GCTCTGGTTG CTTATTTTGA GAAATAAGG ACATTTAATA ATAATAAAAA AAAAGGGATT 180  
AATAAA 186

SEQ ID NO:3749  
SEQUENCE LENGTH:175  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

45 CLONE:HUMGS04408

SEQUENCE DESCRIPTION:  
GATCCCCAGT GGATGCCTGA AACCGCAGAT AGTACTGAAC CTTATATATA CTGTTTGT 60  
50 TCCTATGCAT ACATATCCCT ATGATAAAGT TTATGAATTT GGCACCTAAC AGCAGAACTA 120

55

ATAAGATGAA AGAGTTGTAA CAATATACTC TAATAAAAGT NATTTAAAAT GTAAA 175

SEQ ID NO:3750

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04409

SEQUENCE DESCRIPTION:

GATCAACAAT GAGCAGAAAC ATCATCAGTC CTTCCCAAGG ACCATGGCGT TTAATGTCTT 60

GGGCACCCCT TGGAAATCAC AGAAAGTCAG CNGTACTGGC CGTGTGGAAC TTNCATCCCA 120

AGACCTACTT TNCAACTGAG TAAGAAGGTC ATTGTGCCCN CTGCATTNNN NN 172

SEQ ID NO:3751

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04410

SEQUENCE DESCRIPTION:

GATCAAAAAA TGTTTATNCT GAATTCTNTA ATTTAAAAA NTCATACCTA TNAGGTGTGC 60

TACAGGAATT CAGATACAAT AAGTTGCATA TAAACCCGA CCTCANN 107

SEQ ID NO:3752

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04411

SEQUENCE DESCRIPTION:

GATCTGACCA ACAAGGCCAC AGGAAAATTA ATAGCACAAG GAAGACACAC AAAACACCTG 60

GGAACTGAG AGAACAGCAG AATGACCTAA AGAAACCCAA CAATGAATAT CAAGTATAGA 120

TTTGACTCAA ACAATTGTAA TTTTGTAAAT AAAGTAGCAA AACCAGAAA 169

SEQ ID NO:3753

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04412

SEQUENCE DESCRIPTION:

GATCTNCTTG GCCAGCAGGA CGTCCAAGGA CCAGAGCCTG TGTGATGTCC TNGAACAGGT 60

NTGCGGCGTC CTCAAGCAGG GGAGCTGAGC CTTCCANAGG CAGGGTGGGC TCCAGTTGTC 120

TTGAGGTGCC GGATGGGCTC AGGTAATAAA GAAACGGAAG CAGCAAA 167

SEQ ID NO:3754

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS04414

SEQUENCE DESCRIPTION:

5 GATCTGGGCT GTGGGGCCCT TGGGCCACGC TCTTGAGGAA GCCCAGGCTC GGAGGACCCT 60  
GGAAAACAGA CGGGTCTGAG ACTGAAATTG TTTTACCAAC TCCCANGGTG GACTTCAATG 120  
TGTGTATTTG TGTAATGAG TAAAACATTT TATTTCTTTT TAGGTAAA 168

SEQ ID NO:3755

10 SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04415

15 SEQUENCE DESCRIPTION:

GATCTATGAT TTATNATGTC TTAATAGACC CTAAATTGTT CTTTAATTAC AAGAGTGGCA 60  
GTCTCTGAAG TCATTGTGA GCTTGTATGA CTTTGTATT TAGCAATGTT GCATGCTCAC 120  
ATAATTGAAA ATTAAAAGTA ACACATTTT CTGAAATGTA AA 162

20 SEQ ID NO:3756

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS04416

SEQUENCE DESCRIPTION:

30 GATCAAAACA TAATTGTTTT AATTCTACAG CTGTAGGAGC TTTGTATTGC TGAACCTTCA 60  
TCTGGAAAAG TTTCACAGTG ACATTTTAA AAGAGAATTT TTTTATCTGC CGAATTCTAC 120  
CAGTGTAACC TTTTNTNNTAA ATAAACAATA GTTTTNTCAA A 161

35 SEQ ID NO:3757

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS04417

SEQUENCE DESCRIPTION:

GATCTCAAGA AGCCCCACAT CTCCTAAGG GGCCCCATGG CCTNNTTTGG GNGCAGGGTA 60  
GGTCCTGGGG CACTGTGGGC CGCCTGCCTG CTGATGTGGG CTCTAGGCCA GCTTGTGTGC 120  
40 ACGTACGTGG TGTGAAATAA AGCCCAAGCA CTNGNTGAAA 160

45 SEQ ID NO:3758

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04418

50 SEQUENCE DESCRIPTION:

GATCCTGGGT GACTTTGGGT GCACAGGGTG ACCGAGCATT TCTGCCCTG TGAATGTGGC 60  
50 ACTAACACTG TGCACGTCT CCACCAAANA AGGTTTCCAC TGAGTTTCT CTCATGTTAC 120  
TGGGTTTGTA AATGAATAAA CACATTTTAA CTA CTACTCTAAA 160

55

# EP 0 679 716 A1

SEQ ID NO:3759

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04419

SEQUENCE DESCRIPTION:

GATCAATAAG AAGANCCTAG TCTAGAGACA ATGATGCTAG TTTGCATATG TTTTCCTATG 60  
CAATAGTTGT TTTCCCAGTN ATNCAAAGCA GCTTTCTATA TG TAGAGATG CAAATNATTA 120  
AGTTGTTNCC AATACAATAA ATAAAAGCAT CNGTTNTN 158

SEQ ID NO:3760

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04420

SEQUENCE DESCRIPTION:

GATCAGATTT GTAATTTNCC TGTATTAAAT GCCTAGAACT CTACAGTCAA CAGATGGCGC 60  
TCTAGTTCCA ATTGTNACAG AAGTNCTCTG CCCATCCGCA AGCAAAGCGT TGTTTTCATC 120  
AGTGAAAAGA GAATAANCAC TGTGCTTTAA CTTTAAAA 158

SEQ ID NO:3761

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04421

SEQUENCE DESCRIPTION:

GATCTGTATG GTACTATAAA ATACTTATTT NATAATTCTG TAACCGTATG GCAGTGTTAT 60  
GCCAAAAATG TATAAGAGC AATAGTTTTT GTTGCTTACT GCTGTATTTT AAAATATTGT 120  
TTCTAAAATA ATAGNGTTAG AGTTCCTTTT GAGTAATTAT TTTAAGGAC TATTGCCAAA 180  
TATACATCCT GTAAAACCTA ATAAAAGCCA CTCCATCTTT NGGTAACCAT TTTAGCATTT 240  
GTGCTTGGNG TACATNNTGG GTGGTTTTTG CNCGNTTAAN NANNTTANNN 290

SEQ ID NO:3762

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04422

SEQUENCE DESCRIPTION:

GATCCCACCC TCTNTCCAC CTGGGCNACT GACGCTCTGG CCTCTNTGGN AATNACACTG 60  
GGCTGACCTG GCATTGGGAG AGGGAGGGAG GAAGGAAGGG AGGGAGGGGC TGGAAGATAC 120  
TGAAGGATTC CTTTTTNAAG GGTTTTTTTT ATTGTAAA 158

SEQ ID NO:3763

SEQUENCE LENGTH:157

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04423

SEQUENCE DESCRIPTION:

GATCCAAGTC CCCTGCCTGG TCCCCACAA GGNCCTCCCAT CCAGGCCCCC TCTGCCCTGC 60  
CCCTTGTNAT GGACCATGGT CGTGAGGAAG GGCTCATGCC CCTTATTTAT GGGAACCATT 120  
TCATTCTAAC AGAATAAACC GAGAAGGAAA CCAGAAA 157

SEQ ID NO:3764

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04424

SEQUENCE DESCRIPTION:

GATCATTTTN CATCTGTNCA TAGCGTTTCT NCAGAAGGAA CAGTAGTCTC AAATCTTTCC 60  
TCATAATGAT AACAAAATGC TCTTGCATGA TTTTNTAACA ATATATTTAA NCAGGAAGTT 120  
GTCACTGATA TACTTTATTA AAAGGATTTT AATCAAA 157

SEQ ID NO:3765

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04425

SEQUENCE DESCRIPTION:

GATCGTGTGT TGCCATTTNG TCTGGCTGTG GCCCCTCCTT CTCCCCTCCA GACCCCTACC 60  
CTTTCCCAAA CCCTTCGGTA TTGTNCAAAG AACCCCCCTC CCCAAGGAAG AACAAATATN 120  
ATTCTCCTCT CCCAAATAAA CTCCTTAACC ACCTAGTCAA A 161

SEQ ID NO:3766

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04426

SEQUENCE DESCRIPTION:

GATCTTGAGG TTGTTTGATG CTTTAAATTT TTNAATTATA TTATTTNNTA GGTGTTTATT 60  
GGTACATTGC AGTTTTTTTT TTNAATTTA AAAATTTCTG TAAACTTTG TTTTCAAGTA 120  
ATCTGACAGC ATTAAATATT GCATTTAAAA ATTAAA 156

SEQ ID NO:3767

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04427

SEQUENCE DESCRIPTION:

GATCCGCAAG AACAAGTACC GCCCGACCTG CGCNGGCAGC CATCCGCAGG CCAGCGCATC 60

CTGCGACAGA AGCCTGTAAT GGTAAGAGAA GCGACCCGCC CACCAAGAGT CCTGAGCCCC 120  
TGCCAGAGA ATAAAGCAGC TGGCTTTCTA CCAA 155

5 SEQ ID NO:3768  
SEQUENCE LENGTH:155  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS04428  
SEQUENCE DESCRIPTION:  
GATCCCAAAA CATCATNAGG CATTTTNAAG TTGGTCACGT CGCAAGTCG ATATCACAAC 60  
TTAATTGTAA AAGGAGGGAA TCTGGTTTTG TNACTTGGCA GTGGTTTTTT CTCACCCCTC 120  
CTTTTAAACA ATAAATCCC ATTTGGGTCT TGAAA 155

15 SEQ ID NO:3769  
SEQUENCE LENGTH:155  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS04429  
SEQUENCE DESCRIPTION:  
GATCTATTTG ATAATTTNT GGGTTTTTTG AAGAATTAAT GAGCATGTAC ATAGAAATAG 60  
25 TGACTGCTTG ANTACTGTAT TTNCTTGAC TCTTTCAGTA CATCAAGATT CCTGTATATN 120  
TNAGNGTATA ATAAACACA GATGTGAGTT GTAAA 155

SEQ ID NO:3770  
SEQUENCE LENGTH:153  
30 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04430  
SEQUENCE DESCRIPTION:  
35 GATCGGCACA AGATGCTCAG CTAGATGGGC TGGTGTGGTT GGGTCAAGNN CCCAACACCA 60  
TGGCTGCCAG CTTCCAGGCT GGACAAAGCA GGGGGCTACT TCTCCCTCC CTCGGTTCCA 120  
GTCTTCCCTT TAAAAGCCTG TGGCATTITT AAA 153

40 SEQ ID NO:3771  
SEQUENCE LENGTH:153  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04431  
45 SEQUENCE DESCRIPTION:  
GATCTGAAGT GTGAGTAGAA TGTATTCAGC TGTTTAACAT GTAGTTTAGA TATTCAAAAG 60  
TATGCATGTA GAGTTTAAAG AATATGTAA AANTNATTAA TTTTAATATT TTGTTTGAA 120  
AAGCATGTTA TAATATAATG TTTTCACTAT AAA 153

50 SEQ ID NO:3772  
SEQUENCE LENGTH:152

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04432

5

SEQUENCE DESCRIPTION:

GATCTGGNAC TCCTTG TAGT AAGCTGTTTT CTGCTCAGCC ACTGGGCTCT TTCAC TTTTTT 60

TAGTTCTTAA AAATTTATTT TTAAGTTCTA AAATAAAATA AAAATAAGTT CTAAAAATTT 120

ATTTTTTTCC NGAATAAATT GTATTTGGTA AA 152

10

SEQ ID NO:3773

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS04433

SEQUENCE DESCRIPTION:

GATCGCAAAT CACAGCTCAG ACAGCCAGCT CTTAAGTGAG ACCTGAGTGC CAGAGAGGGG 60

TGGATACAAG GCCAACAGTT ACTAAATGAA TGAAAATTGT GATTCCGATG AAGCCTGCCA 120

20

GAGAAATAAA GCATTTTTTA AAAGATGGAA A 151

SEQ ID NO:3774

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS04434

SEQUENCE DESCRIPTION:

GATCTAGCCA TAAACTAGT AATCTTGAAT TCCTCTTGAG CTGGATGGTG ATTAGCCATT 60

30

GTGAAAACAG ATTATATGGA AATTGTGCAT ATTGCTAAAT TTAAAAACAT GGATTTATCA 120

ACTGATAATA AAATATATCT TACAAGATAA A 151

SEQ ID NO:3775

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS04435

SEQUENCE DESCRIPTION:

GATCTTTAGC TGCCTTTGTA TCAACTTCTN TGGAGCTTAT GTGATTTTCC AGAAAATATC 60

40

CAAGGCATAG TTTTGTCCCT AAGTCCCATG AATATGTAAT ATNTNGTGTC TCTCTATTAA 120

AATAGCACTT TTNGTGCATN CCATTAACAA A 151

SEQ ID NO:3776

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

45

TOPOLOGY:linear

CLONE:HUMGS04436

50

SEQUENCE DESCRIPTION:

GATCCATCAA AAGGTTCTTT TTNATAATC CCTTTTGAAA ATAATAATCA AAGGAAGAGA 60

55

TGTGGTGT TT GGCATGTGG AAACTCAAT GTATAATTAA GACGTCTNTC AAAAATCCGA 120  
 CAAATAAAAT NAAGCTGGAA CGAAGGCAAA 150

5 SEQ ID NO:3777  
 SEQUENCE LENGTH:146  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 10 CLONE:HUMGS04437  
 SEQUENCE DESCRIPTION:  
 GATCCNAAAG CACACCAGGA AGATGCTAAA GATGCTTATA CTTTCCTCA AGAATTGAAA 60  
 GAAAAACCCA AAGAAGAGCC AGGAATACCA GCAATTCTGA ATGAGAGTCA TCCAGAAANN 120  
 NNNGTCTATA GTTATGTTTT GTTCNN 146

15 SEQ ID NO:3778  
 SEQUENCE LENGTH:168  
 SEQUENCE TYPE:nucleic acid  
 20 TOPOLOGY:linear  
 CLONE:HUMGS04439  
 SEQUENCE DESCRIPTION:  
 GATCAGAGAA GTTATGCTC ACTGTCTGAT GCAACTNTCT GGTCTATTTG TNAGTAAATA 60  
 25 ACAGGGAAAT CATTTCACCT TTTTGTTAAA AATAAGGTAT TTACAAGCAT ACCTTGAGT 120  
 TATTGTGGGT TCAGTTTCAG ACCACTGCAA TAAAGTGAAT ATCTCAAA 168

SEQ ID NO:3779  
 SEQUENCE LENGTH:149  
 30 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04440  
 SEQUENCE DESCRIPTION:  
 35 GATCTGACCC ACCAGTTTGT ACATCACGTC CTGCATGTCC CACACCATT TTTTCATGACC 60  
 TTGTAATATA CTGGTCTCTG TGCTATAGTG GAATCTTTGG TTTTGCATCA TAGTAAATA 120  
 AAATAAACCC ATCACATTG GAACATAAA 149

40 SEQ ID NO:3780  
 SEQUENCE LENGTH:144  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04441  
 45 SEQUENCE DESCRIPTION:  
 GATCGGGACC TGACCTGGGG CTGGCCTCAG GCCCAGGTGC ACGTAACTGC CCTCTGTGGA 60  
 AGCCAGCTTA AACCTAGCC CTNTNAGAGC TTCCTGTGCC CAGCAGGAAG GAAGTCAAAT 120  
 AAACCACACT GACTACCTGT GAAA 144

50 SEQ ID NO:3781  
 SEQUENCE LENGTH:144

55



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04442

SEQUENCE DESCRIPTION:

GATCTAGGGG GAAAGAGGAG CATTATCAC AAGTTTCCTA GAGAGAGGAG ACAAATCGGT 60  
GTGCCATTGA CAACATGAGC CAGGGTAAAG GCACCCTTNN NNNTTACTGA TTTCAAAGAT 120  
TAATAAAGTA ATTCTATTTT TAAA 144

SEQ ID NO:3782

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04443

SEQUENCE DESCRIPTION:

GATCTATGAC TCATTGACA GAGAAGCCAA GGAAAAAAG CTGCTTGGC CCATTAACTC 60  
AAATCCACCA AATACTTTTG TCTAAGTTCT CATTCTTTCA ATTGTTATGC ACCAGAGATT 120  
AAAAAGCTTT AACTATAAA 139

SEQ ID NO:3783

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04445

SEQUENCE DESCRIPTION:

GATCTGTGTC TTGAAGCAGC TGCCCTCATT CCGACTTCAG AAAATCGAAG CAGCTGGCTC 60  
CTCCCTTGT TCTCTCTCCC ACCCTCCCCC AAATCTGTTT TCATGTAAAA GACAAATAAA 120  
TGATGACTTC CCCCAA 137

SEQ ID NO:3784

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04446

SEQUENCE DESCRIPTION:

GATCAAAATA AAAATGTACA TGACGGGGAA GGGAAAAACC TGTGGAGTT GCTTCCAGCC 60  
AGCCACGCTC CGGGCCAGCA TGTGGAATC CAGCGTGGAG CAGATGCAGT AAAAATATGG 120  
TTGGTTTCTG TGTGAAA 137

SEQ ID NO:3785

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04447

SEQUENCE DESCRIPTION:

GATCTCTCTC TCNTTTTACC CCCCTTAGGC TGAGGGTAAA AAGCTGGGAT TGGTAGGCTG 60

GGTCCAGAAC ACTGACCGGG GCACAGTGCA AGGACAATTG CAAGGTCCCN TCTCCAAGGT 120  
GCGTCATATG CNGNNNN 137

5 SEQ ID NO:3786  
SEQUENCE LENGTH:133  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS04448  
SEQUENCE DESCRIPTION:  
GATCGGCCAA GTATGCTNTT NTTAGAGCA ATGTTTGGC CTAGAGANTT GTAAAATTTA 60  
TGTNATGACT CAGTACATAT GTGTTCGTAC ATATATGATN GGAATAAAAT GTTTATGAAA 120  
15 TATTNACTCA TAN 133

SEQ ID NO:3787  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear

CLONE:HUMGS04449  
SEQUENCE DESCRIPTION:  
GATCTGTGTG ACCTCACCTG CATTTGATTG AAAAAAGTAT GCGCGTAATT GTACCCACCC 60  
25 AGTTCAAACC CGTGTGTAAG GGTCAACTGT AAAAAAAGT TTGTGAAATA AACGTACTGG 120  
AGAATCTTTA AA 132

SEQ ID NO:3788  
SEQUENCE LENGTH:130  
30 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS04450  
SEQUENCE DESCRIPTION:  
35 GATCAGTATT TAANATTATA CCAGTTTNA TTAAACCCTT TCCCTCCCCG ATAAAGAATG 60  
TTCTATTCT GCCTCCCTT AAAGGGGAGA CCTCAGAAGT AAAGNAATTT NATGTTGTGT 120  
TTTTNTTAAA 130

40 SEQ ID NO:3789  
SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

45 CLONE:HUMGS04452  
SEQUENCE DESCRIPTION:  
GATCCCCCTT CACCTTTTGC CATGGTCATA AGCTTCCTNA GGCCTCCCTG GAAGCTGAGC 60  
AGATGCCAGC ACCATGCTTC CTGTACATCC TGCAGAACCA TAAGCCAATT AAACCTTTTT 120  
AATAATAAA 129

50 SEQ ID NO:3790  
SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04453

5

SEQUENCE DESCRIPTION:

GATCCNCCAT GGTGGACACG TCTGTNCTGT ATGTAAAAGG CATTACAAAT GTTTTTTAGC 60

AGATGAGACT TGAAGCCTTT CCACAGTCCT TGTNCTCTGA GATGGCTGTN GAGCTCTGCT 120

CANCTGTTN 129

10

SEQ ID NO:3791

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS04454

SEQUENCE DESCRIPTION:

GATCCCTACC CCTCANCAAC TAGCTCCCCT GTCGGCCAGC TAAGAGAGCT GGGACANTGG 60

AGGCTGGCAG AAGCTGAGAC GTGACTGTCT AGGAGTAACA CTCATTAAAG CTTTCNTTTT 120

20

GGCAAA 126

SEQ ID NO:3792

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS04455

SEQUENCE DESCRIPTION:

GATCTGAAAA AGCAACCCAT TTCCTAAATT CATATTTTNC CTAAACTTT ACTATGTTTT 60

30

NATTTTAAGA GGTTCCTGT TATATACACT TTTNACACAT GCAAATAAAC TTTATACCAA 120

GTGAAA 126

SEQ ID NO:3793

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS04456

SEQUENCE DESCRIPTION:

GATCTGTTTA GAAAATACCT TTGAAAACGA GGGTAACTTT AAAAAATGGA AACTTTCAAA 60

40

TCCATTTATA TTTNNTTAT AANCAAACT TAATTAAAAG TTAAACAAAC TGGCTGAAAA 120

CTCAAA 126

SEQ ID NO:3794

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

45

TOPOLOGY:linear

CLONE:HUMGS04457

50

SEQUENCE DESCRIPTION:

GATCACTGAG CTGCCCNTCA AGGGGACCTG GANNCCGGGT CCTGGGGTCA TGCTGCCTCC 60

55

EP 0 679 716 A1

NAGGCTCCAA GGTGAGGGTC ATCTTCACGA GCAAAGAGAA CCAATAAAGT GACAACGNAC 120  
GTCAAA 126

5 SEQ ID NO:3795  
SEQUENCE LENGTH:123  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS04460  
SEQUENCE DESCRIPTION:  
GATCCAGGGC TTTCGAGGCC TCTCCTCATT GAGTTCAGAG TCACATATCA GAGGNTTAAA 60  
TCCAAAAGAA ATATGCACAC CCCTCTCCTC CCTCCCAGTA AAAATAAATC GCTCCTCTTG 120  
AAA 123

15 SEQ ID NO:3796  
SEQUENCE LENGTH:125  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS04462  
SEQUENCE DESCRIPTION:  
GATCTCTGTG CTGTAACTA AAACAAATTG TGCATTCCTT CCGGGGCCAT CGTCTTTGTT 60  
25 TTCTTTTTTG TCTTGAATGA ATTTTAAAAG GAAATATATA ATAAAAATGT TAACCAGAAG 120  
GTAAA 125

30 SEQ ID NO:3797  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04463  
SEQUENCE DESCRIPTION:  
35 GATCTGGGGG CCCCCCAGC TGGCGGGAAC CCCAAATGGA CACAACTGT ACATTTGCCA 60  
ATGGGTTTTT TTCAGACCAT GGTTTTTACT TGCAAATAAA CCTGAGTTCT TTTCTGAAA 119

40 SEQ ID NO:3798  
SEQUENCE LENGTH:133  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04464  
SEQUENCE DESCRIPTION:  
45 GATCTAAAAAN NATACTNTGT TCCCTCATAT GCATGCCCTT CCTTTCTATA TCCTTGACAC 60  
CTTACTTTCC CATTGTAACA ATAAAAAAG TATCAATAAA ATAATTATTG GCAAATAAAT 120  
TGGTGAGTTG AAA 133

50 SEQ ID NO:3799  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid

55

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS04465

SEQUENCE DESCRIPTION:

5 GATCCTGCAG TGATGGAATG TTCTGTCTTG ATTGTAGCAA CACCAATATN CTGATTGTNA 60  
TATTATACTA TAGTTTTCGA TAACAGTTAC CATTAAAGGA AATTGGGTAA AAGGCTAAA 119

SEQ ID NO:3800

10 SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04466

SEQUENCE DESCRIPTION:

15 GATCTCTTAG CAAATAGGAA TCTAGGTGTA GAATTTATAC ACATATATAT TTTTAAAAGT 60  
ATAAAAATGA GAAAGTATGT ACAAAAAATC ATCCTAAATC TTAGAAAGGA GACATAAA 118

SEQ ID NO:3801

20 SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04467

SEQUENCE DESCRIPTION:

25 GATCTGGGAG CCAGCAGCTG GATGCTGTGG CTGGCCAGAN ACACCTCCAG GCTGTGGCCT 60  
GGGGGCTGGG GGGAGCCCCA GGCTGAAAAG GGTCCAATTA AAACAAATGG AGCCAAA 117

SEQ ID NO:3802

30 SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04468

SEQUENCE DESCRIPTION:

35 GATCACATTC CAGCCCTCGC TGCTGGGGTG CACACCCCTT CCTTAGNTGA TGTGCTTGGG 60  
AAACTCCCTC CCCCTCCTC CCAAGAGAGA AATAAANCA CCTTCGCCTA GGNCAAA 117

SEQ ID NO:3803

40 SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04469

SEQUENCE DESCRIPTION:

45 GATCCTGACC TCCTCCAAGG AAGAAATCCA GAAAGCCTTA AGACTAAGAC AACTTGACTC 60  
TGCTGATTCT TTTTTCCTT TTTTITTTNN AAAANAAAAA TACTATNANC TGGAAA 116

SEQ ID NO:3804

50 SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

55

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS04470

SEQUENCE DESCRIPTION:

5 GATCAGAACT CCAAAACCAC TCCCACCCCT GAAGGTCGGG AGGGTCTGAG CAGCCCTGGT 60  
GGCTNCTTGT GCTCAGGTCC TCAGTCCAT GGGAAATAAA AATGGCACCC TGAAA 115

SEQ ID NO:3805

10 SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04471

SEQUENCE DESCRIPTION:

15 GATCAACATA TTTAGCTTAT ACAGAAATAA AATTAAGTCA ATCCACTCAC AAAGAATTTC 60  
TATTTTGTA AAATGTAGCT TGTATTTCAG TATAATAAAA TCTGATGTAA GAAA 114

SEQ ID NO:3806

20 SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04472

SEQUENCE DESCRIPTION:

25 GATCANAGCT NTCCCAAAGA GGGAAAGCGG TGAGGTTTNA GGAGGGGCAG AAGCAGGGCC 60  
GGCAAAGNTT GTACCTNCAT AAGGTGGTAT GGGGGGTTGG GGTGAGGCC TGAN 114

SEQ ID NO:3807

30 SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04473

SEQUENCE DESCRIPTION:

35 GATCGAAAGA CTCAGGGAGA GCGGTCCTNA CCACCTGGAA GTAAGTCCA CCTGGACCTT 60  
ATNAAACTA CTCACTCCAC CTGGGCCCT GCTGAAGCCN NNTTTTAAAA TN 112

SEQ ID NO:3808

40 SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04474

SEQUENCE DESCRIPTION:

45 GATCTGTTTC GTGCATTGGA AGACCCACCA CAAGCTTGGC ANACTAANTN TTGTATCCTG 60  
GGGCTCCNT CATCTCCAGG GAGACCAAAC CCCGGCCCTA CCAGNGCCCG N 111

SEQ ID NO:3809

50 SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

55

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS04476

SEQUENCE DESCRIPTION:

5 GATCAAGACT AACAAATAAC TTTGTGATGA AAATNCTTCA AAAATATAGC TACTCTTTTC 60  
AAGTATACCA TTAAATATAT TTCATCAGGC AGAGCCCTGA CCAGGAAA 108

SEQ ID NO:3810

10 SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04478

SEQUENCE DESCRIPTION:

15 GATCAAGAAN ANTNAAGACA ACGAGAAAGT TTAAAGTTTC GAAAGCAGCA AGATNCCTTT 60  
CCCCCTGGT CAATCNCTGA CACAAGAGAA GGCAGAGACC CTGAAGCN 108

SEQ ID NO:3811

20 SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04482

SEQUENCE DESCRIPTION:

25 GATCTTCAAG CAAGGGAAAT GATTCTTAAA AGGATTATCT GAAATTGAAA AACTAGTAAG 60  
CAAATAAATG ATAAACATAA GTAAATTAA NCTGTTGTTT GTATAAAACA ATTATAATGA 120  
NGTGTTTATA AGANATTGTA AACAAATGTA AANCTAAATN ANCATTGTTA TGCAACATTA 180  
AA 182

SEQ ID NO:3812

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04483

SEQUENCE DESCRIPTION:

35 GATCTCCCA AACTAAAAAG TACAGTACTT GGAATTGTGT TCTTTATGGT TGTAGTGTG 60  
GTAAAGCACT AATATGCAGA AAATAAAGGA ATTACACAGT GCAA 105

SEQ ID NO:3813

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04484

SEQUENCE DESCRIPTION:

45 GATCCNAAGC AGTGAACATG CTGTTAATAC TTGTAAGACT CCTAGCAAAC TGCATTTAAT 60  
TTTTTAAATT AGTTTGTAGT TACATAAAGG CATGTNTTN CCAA 105

SEQ ID NO:3814

55

EP 0 679 716 A1

SEQUENCE LENGTH:105  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04485  
 SEQUENCE DESCRIPTION:  
 GATCCATGGG ATTNATAATT GAAATAGAGA TTGGAGACCC TCCTATTCAN TTCATAAGCA 60  
 ATNGCACCAC AGGTCANATG CAGTTATCTN AACTCCAGGA AATTN 105

SEQ ID NO:3815  
 SEQUENCE LENGTH:104  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04486  
 SEQUENCE DESCRIPTION:  
 GATCTTGCTA AATTATTAGT TCTAGTAGCT TTTTGTAGA TTCATTAGGA TTTNTACAT 60  
 ACACAATCAT GCTATTTGCA AATAAAATAA TGCTTTTATC CAAA 104

SEQ ID NO:3816  
 SEQUENCE LENGTH:104  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04487  
 SEQUENCE DESCRIPTION:  
 GATCGAGTCC AAGGNAGACT ATGTCCTCTN CTACCAACGN CAGGNCGTGG CGCGACGCCT 60  
 GCTGTCCCCG GCCGGCTCAT CTGGCGCCCC AGCCTCCCCT GNCN 104

SEQ ID NO:3817  
 SEQUENCE LENGTH:103  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04488  
 SEQUENCE DESCRIPTION:  
 GATCAGCACT GTGGTGAGCT CCAAGGAAGT GAATAAGTTT CANATGGCTT ATTCAAACCT 60  
 CCTTAGAGCT AACATGGNTG GGCTGAAGAA GAGAGACAA NNN 103

SEQ ID NO:3818  
 SEQUENCE LENGTH:103  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04489  
 SEQUENCE DESCRIPTION:  
 GATCCCAAAC CTNAGCTCAA TCAGTATTGC CAGANAGGGG TAAGACTGGT TGGAAGCTGA 60  
 CTGCAGACTT NNTTCCCCT TAGTATGTNC TGTGTTGTAA ATN 103

SEQ ID NO:3819



EP 0 679 716 A1

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04491

SEQUENCE DESCRIPTION:

GATCACTAAG CAAAGCTGCT AGTGGGATTC TATATTTTCGT GTCATCTTTT TTATNATAAT 60  
NTATTGCAAA TATTTTCTG AATAAATATA TGTGTGTGA AA 102

SEQ ID NO:3820

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04492

SEQUENCE DESCRIPTION:

GATCCTGCCA CCAGGTTNT TTTGAAATAG TACCACATGT AAAAGGGAAT TTGGNTTNA 60  
NTTCATCTAA TCACTGANTT GTCAGGCTTT GATTGATAAT TN 102

SEQ ID NO:3821

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04493

SEQUENCE DESCRIPTION:

GATCTTGTC AATCGGAAAC CCCC GTTACC TCCTCTTTT CTTCTCTTT CTTTTTTTTT 60  
TTAACTNAA ANATTTTAT GATGATTAAG ANGGAAGTNG TN 102

SEQ ID NO:3822

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04494

SEQUENCE DESCRIPTION:

GATCCCAAAC ACTCNATCCT GTAAGNCGGG TACAGTCCTA TTGTNTGTTN NCACACTGAT 60  
GATGTGAGCC TGTGAGATGA GCCAATCACC AGTTGTTATG TN 102

SEQ ID NO:3823

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04495

SEQUENCE DESCRIPTION:

GATCTCATGT ACTGAAAAA AATTCTTAAT TTTATTGGAG TTTATACCAC TGTGAACTG 60  
CAATATGACT GTAAGAGAGT AAAAAGATTG TNACATCTAA A 101

SEQ ID NO:3824

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04496

SEQUENCE DESCRIPTION:

GATCTGGGAG TCTGAAATGG TAGCNTTTTG TCCCTGTCTT CACACTATCA TAGGGAGAAT 60  
 CAAAAGANCT AACAAATATA ANCATGCTTT GTGAATNNCC N 101

SEQ ID NO:3825

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04497

SEQUENCE DESCRIPTION:

GATCTNTTTT NTNTCTATTT TTTGAGGTAC ATGCTACATA CATTTTNTNT GTAAACAACT 60  
 ATTTAGCATA TTGAATAAAA TAACATTTTA AAAATAGAAA 100

SEQ ID NO:3826

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04498

SEQUENCE DESCRIPTION:

GATCCACGG CNAACACTCA CCACNCGCTA CCATACGCCN TCCCAGAGCT AGGGGCTGCC 60  
 TTAAAGGAAA TTGTAGCCTA AGTAGGTCAT GGCAAGN 97

SEQ ID NO:3827

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04499

SEQUENCE DESCRIPTION:

GATCAGCCAC ATCAACTCAG TTGTCCACCA CAGGGGAATT TTNAATGTCT TTTGTTTTTG 60  
 TTTGTTTTTG AAAAATAATA AACAGGCAAC TGTAAG 96

SEQ ID NO:3828

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04500

SEQUENCE DESCRIPTION:

GATCTATTTG GCCTCTCAA TGAAGTGA TTCTGTAA AAAAGATTGA TGTATTGTC 60  
 TCTTGTAGAG GAAACTAATA AAGCTGCAGG NGAAA 95

SEQ ID NO:3829

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04501

SEQUENCE DESCRIPTION:

GATCTATCAT AATTGCTTTT CTGATGCATT TAAAAATAAA TGGAACACTT AAATGTATAT 60

TACCGATGCA AACTGTGGAT AAAGTTGAAA GAAA 94

SEQ ID NO:3830

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04502

SEQUENCE DESCRIPTION:

GATCACAGGC CTGGCCGCGG TAACAGACTT TTACATGGAA TTGTTTAATT ATTTGTACTT 60

TTCATGCCAG AAAATAAAAG TTCAGAATCT TAAA 94

SEQ ID NO:3831

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04503

SEQUENCE DESCRIPTION:

GATCACTACG ATTAACGACG GTCGTAATGT TAAGACGTCG TCTCCATGAN CTTTGGGGGG 60

ACTTTAATNT GGAATAAAGA AACTATCACT NAAA 94

SEQ ID NO:3832

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04504

SEQUENCE DESCRIPTION:

GATCCAGATN AAGTGCTGAA GAAAAGAAAA AAGAAGTGGA GAAGAGTATG NTTATNCTTC 60

TCCTTATTAA AGAAATTNC TCAAAACAGC AAA 93

SEQ ID NO:3833

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04506

SEQUENCE DESCRIPTION:

GATCTATCCA GTGACGTGGC CTGGTGGGCG TTTCTCCTTG TACTTATGTG GTTTTTTGGC 60

TTTNAATACA GACATTTTCC TCCAGAAA 88

SEQ ID NO:3834

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04507

SEQUENCE DESCRIPTION:

GATCCCAAAA TATGGTAAAG TGAACCCATC TGTCTGCATT TTCTACTCTG AGCCCATTTG 60  
TTAATAAACA CTTATTTTTA TATAAA 86

SEQ ID NO:3835

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04509

SEQUENCE DESCRIPTION:

GATCCGGGCC CCAGGCTGCT GCCGCTTTTT ATAACCTTAT ATTATTTTNN TTTTAAGAAA 60  
AAAAGCTCTT TAAAATACCT CAAA 84

SEQ ID NO:3836

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04510

SEQUENCE DESCRIPTION:

GATCTGAGGA GCAAACCTCC GTGGCACACA TTTACCTGCA TAACAAACCT GCACATCCTG 60  
CATGTGTACC CCAGAACTTA AA 82

SEQ ID NO:3837

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04511

SEQUENCE DESCRIPTION:

GATCCAGGAG GCTCAAAGAG AAGCCAAGTC AGCTTTGTTG TGATTGATT TTTTTTAAAA 60  
AACTCTTGTA CAAAACCTGAA A 81

SEQ ID NO:3838

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04512

SEQUENCE DESCRIPTION:

GATCGTACT GTTATGTGGG ATTATTATTT CTAAATNTTA CTCATTGAAA TAAGCATACA 60  
ATAANANGCA TTTATTGCAA A 81

SEQ ID NO:3839

EP 0 679 716 A1

SEQUENCE LENGTH:80  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
5 CLONE:HUMGS04513  
SEQUENCE DESCRIPTION:  
GATCAAAACA AGACCCAGCT TATTTTCTGC TTGCTGGTAA ATTAAGCAAA CATGCTATAA 60  
TAAAAACAAA ATGAAGGAAA 80

10  
SEQ ID NO:3840  
SEQUENCE LENGTH:78  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
15 CLONE:HUMGS04514  
SEQUENCE DESCRIPTION:  
GATCTGGTTG AAAATTGTAT TTCTATGTAA ACTCAACGAT ATGTTTGGTT TTCCTGAAAA 60  
TAAATAATTT TAAATAAA 78

20  
SEQ ID NO:3841  
SEQUENCE LENGTH:75  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS04515  
SEQUENCE DESCRIPTION:  
GATCCTCACA CCTCAGCGTC CCAGAGTGCT GGGATTACAG TTGTGAGCCA CTGTGCCTGG 60  
CCTTTTTTTT TTTTN 75

30  
SEQ ID NO:3842  
SEQUENCE LENGTH:74  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS04516  
SEQUENCE DESCRIPTION:  
GATCAGAAAT CTGAGGTTCA ATGAGGCCAG AATAACTCAG CTTCAAAATG AATAAATGTG 60  
GAAGCCAGCA CAAA 74

40  
SEQ ID NO:3843  
SEQUENCE LENGTH:72  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
45 CLONE:HUMGS04517  
SEQUENCE DESCRIPTION:  
GATCTCCCCT TGGACTGATA CCCTTTTCCC ATTCATTAC AAATAAATTA CAATGGGTGC 60  
TGAGAACTTA AA 72

50  
SEQ ID NO:3844

55

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04518

SEQUENCE DESCRIPTION:

GATCTGTGTC ATGGTTTAT AACCTTNTN TTTTGTAAC CTTGAATGTT CAAAATTAAC 60  
ATGCTGTTTA CTCTGAAA 78

SEQ ID NO:3845

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04519

SEQUENCE DESCRIPTION:

GATCAGGAAG AACTAAACAA AACCCACACT CCAAAACTA ACAAAGAATA AATAAATAAT 60  
ATAAAATAA A 71

SEQ ID NO:3846

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04520

SEQUENCE DESCRIPTION:

GATCTCAGAA CAGANTTAAA ATATTGTGAA AATTACAGCT TAATAAATGT TTATTGTAAT 60  
TTTNTTGTA A 71

SEQ ID NO:3847

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04521

SEQUENCE DESCRIPTION:

GATCTAGGAC TTGCCTTATT TTATCATTTT TCTTTAATAA TCTCCAATAA ACTTTCTTTA 60  
TTCATTAAA 69

SEQ ID NO:3848

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04522

SEQUENCE DESCRIPTION:

GATCACCCT AAAGAACTTA CTCATATAAC CAAATACCAC CTGTNCTCCC AAAAACCTAT 60  
GGAAATAA 69

SEQ ID NO:3849

EP 0 679 716 A1

SEQUENCE LENGTH:69  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
5 CLONE:HUMGS04523  
SEQUENCE DESCRIPTION:  
GATCAGTATG CTGTTTAAAT AATTATGTGC CATTTTAATA AAATGAAAGG GTCAACGGCC 60  
CNNTTTAAA 69

10  
SEQ ID NO:3850  
SEQUENCE LENGTH:67  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
15 CLONE:HUMGS04525  
SEQUENCE DESCRIPTION:  
GATCTACACT GATGATTAAA TCAAATTGGC TAAGATTATT CGTTCTAATA AAAGCACTGA 60  
CTCCAAA 67

20  
SEQ ID NO:3851  
SEQUENCE LENGTH:67  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS04527  
SEQUENCE DESCRIPTION:  
GATCTCTTCC TGTTTTGTAC ATAGATTAT TTTTCAGTTC CAAGAAAGAT GAATACATTT 60  
TGTNAAA 67

30  
SEQ ID NO:3852  
SEQUENCE LENGTH:67  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS04528  
SEQUENCE DESCRIPTION:  
GATCTAGCAT ATGTATCTTT TTAAAGGTA TTGTTAATAA ATATNCTGTC ATTTGTAAAG 60  
ATANAAA 67

40  
SEQ ID NO:3853  
SEQUENCE LENGTH:66  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
45 CLONE:HUMGS04529  
SEQUENCE DESCRIPTION:  
GATCCATCTT CAAATCAAGG GCTCCCTGGC TACCAAATNC TGTCTAGTAA AAATNATTCG 60  
AGCAAA 66

50  
SEQ ID NO:3854

55

EP 0 679 716 A1

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04530

SEQUENCE DESCRIPTION:

GATCTATTCA ATGTACAAAA TATTTTGAAA GTTCTGTGA TTAAATGTNC TTTGAAAACA 60  
TAAA 64

SEQ ID NO:3855

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04531

SEQUENCE DESCRIPTION:

GATCTGTTAT NAACACCTTT GTTGGCTTGG TTCAGTAATA AATATGTNAG ACTTTTCATT 60  
TAAA 64

SEQ ID NO:3856

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04532

SEQUENCE DESCRIPTION:

GATCTGTGTA AGCTCTGAAT GAACTTCTTT ACTCAATAAA ATTAATTTTT TGGCTTCTTA 60  
AA 62

SEQ ID NO:3857

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04533

SEQUENCE DESCRIPTION:

GATCCAAGAT ACGTCATTT TGTATTGGCA AAATGCCACT ATTAAAGTGT AATTCTTGAA 60  
A 61

SEQ ID NO:3858

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04534

SEQUENCE DESCRIPTION:

GATCTCAAGT GCTTAATGAT AAGGTGTTGA CTTGTAAAT TAAACCATTT GGAATACAAA 60

SEQ ID NO:3859

SEQUENCE LENGTH:60



EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04535

SEQUENCE DESCRIPTION:

GATCAAATGC CCTAAAATGT AGTGACCCGT GAAAAGGACA AATAAGCAA TGAATACAAA 60

SEQ ID NO:3860

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04536

SEQUENCE DESCRIPTION:

GATCTGAGAC TTTGAGTCTC CAGAACTGTG AGAAAATAAA TTTCTGTTTC TTAAGCCAAA 60

SEQ ID NO:3861

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04537

SEQUENCE DESCRIPTION:

GATCTTTCCT GTCTTCCCCA AGTTTGCAAT TCCGACATTA AAGTTTACTT TTNAGTTAAA 60

SEQ ID NO:3862

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04538

SEQUENCE DESCRIPTION:

GATCAATCAG GGAGAAAATA CAGAAGAGAA TAAAAAGAGA CTCATTCAGT GGAAGCAAA 59

SEQ ID NO:3863

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04539

SEQUENCE DESCRIPTION:

GATCTGAATT AAGCTGTCTG CCATTTGGAG AAATTTAAAT ACTATTTTAA ACACACAAA 59

SEQ ID NO:3864

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04541

SEQUENCE DESCRIPTION:

GATCCACCCA GGCCTTTCNG TGAAATAAAA GCTCCAAGT TGGGTACAAA CCAGGAAA 58

EP 0 679 716 A1

SEQ ID NO:3865  
 SEQUENCE LENGTH:57  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04542  
 SEQUENCE DESCRIPTION:  
 GATCCCAGTC TGAAGGATTA TTGTGAAGAA TAAATGAGAG AATGTGTAAA TGGCAAA 57

SEQ ID NO:3866  
 SEQUENCE LENGTH:56  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04543  
 SEQUENCE DESCRIPTION:  
 GATCTGTGTA TTTGATTTTG TACTTTAAAT GTGACAAATA AACCTTTTGG GAGAAA 56

SEQ ID NO:3867  
 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04546  
 SEQUENCE DESCRIPTION:  
 GATCTAATTC TGAAAACATT GTAATAAAAT AATNAGCTAT AATGGTATTT TCAAA 55

SEQ ID NO:3868  
 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04547  
 SEQUENCE DESCRIPTION:  
 GATCTCGAGC GTTTATCTCG GGCTTTAATT TGCTAAAGCT NTGCACATAT GTAAA 55

SEQ ID NO:3869  
 SEQUENCE LENGTH:85  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04548  
 SEQUENCE DESCRIPTION:  
 GATCTGCCAT GCACTCCAGC CTAGGCAACA AGAGTGAAC CTGTCTCAA ATAAAATAAA 60  
 ATAAAATAAT AATAGTAATA ATAAA 85

SEQ ID NO:3870  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS04552

SEQUENCE DESCRIPTION:

5 GATCAAAGGT CATTTGTGTA GATGAGTAAT TAAAAAATAT TTAAATCACA AA 52

SEQ ID NO:3871

SEQUENCE LENGTH:51

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04556

SEQUENCE DESCRIPTION:

15 GATCAAATAG AAACAGGGTT TGCAAGTNTC CATACAGATG CCTCTACCAA A 51

SEQ ID NO:3872

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS04557

SEQUENCE DESCRIPTION:

GATCCTATGT AAAATATATA TTTATGTATT AAAAATACTG AAAACATAAA 50

25 SEQ ID NO:3873

SEQUENCE LENGTH:443

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS04597

SEQUENCE DESCRIPTION:

GATCCTATTT TATAAGGAAT CTTTTTTATA CGAATGTACT TATTCTTTTA GATATCAGTT 60  
 CTTGAATGTA TACTCCTTAT GATATACAGC AAGAGATTCT TGAGGTTCCC AAGAATTGTC 120  
 35 CTGGAAAGAA AATTGATTTT GAATTGAGAT TAGCAGTGTT TTAATTTTCGC TGAGATAACT 180  
 CCTTTAACTC AGCACTTTCA CAAAACCTAA ATATTAAATA AATTGAATTT GAGGCTGGCA 240  
 TTCTTCTCTA AATTGAATTG GACTGGTTGT TTGCTGAGGT ATGAATGGAG CAGCTCGGAA 300  
 GTATTATAAT TCCGTAGCTG AAACAGGACG CTTATTTATG TATGNTCCAA TCTCTNCTCA 360  
 TTAAAAATG NCTCAGCATT TCCNGCCATT TAGATAGGTA AATNAATAGT CCATTANNTT 420  
 40 TGNTNACCTA CCATAANTAT TTN 443

SEQ ID NO:3874

SEQUENCE LENGTH:423

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04598

SEQUENCE DESCRIPTION:

GATCTATGGT ACAGTTCATT GGCAGAGAAT CCAAGTACTG TGGACTTTGT GATTCCATAA 60  
 50 TAACCATCTA TCGGGAAGAG GGCATTCTAG GATTTTCCGC GGGTCTTGTT CCTCGCCTTC 120  
 TAGGTGACAT CCTTTCTTTG TGGCTGTGTA ACTCACNNCC CTACCTCGTC AATACCTATG 180

55

# EP 0 679 716 A1

CACTGGACAG TGGGGTTTCT ACCATGAATG AAATGAAGAG TTATTCTCAA GCTGTCACAG 240  
 GATTTTTTGC GAGTATGTTG ACCTATCCCT TTGTGCTTGT CTCCAATCTT ATGGCTGTCA 300  
 ACAACTGTGG TCTTGCTGGT GGATGCCCTC CTTACTCCCC AATATATACG NCTTGGGATA 360  
 GACTGTTGGT GCATGCTACA AAAAGAGGGG GAATANGNAG CCGAGGGAAA TAGCTTATTT 420  
 TTN 423

SEQ ID NO:3875

SEQUENCE LENGTH:413

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04599

SEQUENCE DESCRIPTION:

GATCCAAATN ACCATCATCT CTGATGGAGA TGGGTTGGGT ACCTGGCCTT CATGGCACCT 60  
 TCACTGCTAG GGATGCTCAA GGGGCAGGCC TGGGGCCTTC CCTCCTGTCT CTTCTCGGTC 120  
 TTTCTCTCT GAGCANCCTC CTACCTCCCC TGCCTGAGCC TCACTCCACA GCCCTCCCAG 180  
 GTACCTAGCA GAGGCTGTCA GTCCTTGGCT CACCTGGAAC AGGGCTGGGG CTGGGTTGGA 240  
 ACAAGGTGTG TGCCNACCA CATCTCTATG ACTCTGTTCT CCCTCCCTGC ATTGTGGCTC 300  
 TTGTATTTGA GGGCCTCAAG AGAGTGAGGC CCTACCATCA CTGTCCATAT TAAGTCCAAG 360  
 CCAAGTGNG GTTCCTCTGT TCCCTCNTAA GCAATCAATN GTTNAGTTTC TAN 413

SEQ ID NO:3876

SEQUENCE LENGTH:410

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04600

SEQUENCE DESCRIPTION:

GATCCACCTG CCTCGGACTC CCACAGTGCT GGGATTACAG GTGTTAGCCA CCACCCCGAC 60  
 ATTATTTGAA ACTTTTATTT TATCATGAGA GAGTTCCAGG AGTCAACTGG AGAGAGATTT 120  
 TTGGTATGAA AATTACATAT GCAAAAAGAC TGATTCCAGT ACATGAAATT AAATTCAACA 180  
 TTTACATTAA ATGCCTTCAA ATATGGTAAA ATGGTTTCTT TTGGCACNNT ACCTCATTAT 240  
 GTTTTGAATG ATTTGGTCTA TCATATGAAA TAACTTTTAT AAATATAGTA NCTCAGGCCT 300  
 GGGCACAGCG GCTCAAGTGG GAGGNCTGCT TAAGCACCCG AGTTTNAGAC CAGCGTGGAC 360  
 AACATGGGGG GACCCCTTNC TGTCCCAAAA NTAGCTGAGC ATGGCAGCGN 410

SEQ ID NO:3877

SEQUENCE LENGTH:402

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04601

SEQUENCE DESCRIPTION:

GATCCCAACA ATGGAACTTT CCTTCTCTGC TGTCAACAAA GGAATAAAAA ACTTCTGTGT 60  
 GATTTGATAC AGACAATTTA GAAAACTTTT GTTTCAAAGT TTCCCATCCA GACTAGCCAA 120  
 GGAGAGCAAG GGAGGGNNNC TAATAAGCCC ATTAAGGTGT CTTCCCAAAC AAATGTTTTT 180  
 TTTGTCCTTC TGCCCAAATG CAGAAACAGC TGCAGCTTTA AAAANTAGCA TACTTTTATC 240  
 TTTTGANGGA AATATGTGAA AGTTTTAGCA CTGTTGTCTT TTGGTTGGCA AGAAATTGTT 300

NAGTGTATN NATTNCTTCC TATTTGNCTG AATTTTNCCA AATTGTCCA CAGCAAGCAT 360  
 GACTACTTN NTCATATNAA ATCTCCANTG NATTTATGCA AA 402

5 SEQ ID NO:3878  
 SEQUENCE LENGTH:393  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 10 CLONE:HUMGS04602  
 SEQUENCE DESCRIPTION:  
 GATCTTGTC CTAAATCTA ATTTATATCA AATTTATGAG AGAAAGTATT TTCCTAATNA 60  
 TGGTCAAATA AATTGGTTA ACATCCTAGT GATTCTCTTT CTATATAATA AGGCAATTAC 120  
 AGTTTTCAAA GCATTAAGTC TAACATAACT TTAAACATTC TCTTAGGTTT CAAGACACTT 180  
 15 CTATTTAATA TTCATTGGGG AAAAGTTGTC CAGCTATCAG CTAGNGAAAA CACATGCAAA 240  
 TATGGTTGTG TAAAGTTAAG GGTATANGG NANNANANAT CAGTAGAATT ACATAATACT 300  
 AAANGTTGCA GTTGAAGGAA TATCCCAGTN TGTGTTGGTA GTNCTNNAA GNNTNTAGC 360  
 TGTNATTGCC TTGTTTTNT AGCCCTTNGT TTN 393

20 SEQ ID NO:3879  
 SEQUENCE LENGTH:392  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 25 CLONE:HUMGS04603  
 SEQUENCE DESCRIPTION:  
 GATCTNAAGC TTNCTNCTTG GACACCCCAT ACCCANAGTC CTCCAGGCCA CCCTTAAGTA 60  
 CAATGTTCTC CTACCTAAGA AGGCATCTGG ATTTTNTCTT TCCTTGGAAG TAGTAAAGAA 120  
 30 CTACTCTTTG ACTGTTTTTG ACCTCACAGT GAACCTCAA TACTTGGA TCGCAATAA 180  
 ATCCAGTATG GTGGTTATAG ATGTAAAAAT GCTATCAGGA TTTACTCAA CCATGTCATC 240  
 CATTGAAGAG CTTGAAAACA AGGGCCAAGT GATGAAGACT GAAGTCAAGA ATGACCATGT 300  
 TCTTTTCTAC TTGGAAGATG TTTTGGTCG AGCAGACAGT TTCACTTTT NCTGTTGAGC 360  
 35 AGAGCAACCT TGTGTTCAAC ATTCAGCCAG GN 392

SEQ ID NO:3880  
 SEQUENCE LENGTH:385  
 SEQUENCE TYPE:nucleic acid  
 40 TOPOLOGY:linear  
 CLONE:HUMGS04604  
 SEQUENCE DESCRIPTION:  
 GATCTCACCA CTGCACTCTA GCCTGGACGA CAGAGGGAGA CTGTCTCCAA AAAAAACAA 60  
 45 AGAAAGAAAG AAAAACTGT AAAAAAAT TTNCTGCAAT GGNCTTAATA TGTGTGCCC 120  
 TTAAAAATGT ATATATTGAA ACTCTAATCC CAATGTGATG TTATTTAGAG GTGGGGCCTG 180  
 TAGGAGGTAA CTGGGTCCTA AGGGTAGAGC CCTCATGANT GAGATTAGTG CCCTTATAAG 240  
 ANGCCCCAAA GCTAGCTACC TCTNTTCCA CTATGTAAG NTACAAAGNG AAGTTGGCTG 300  
 TCTGCAAACT AGAAGAGGGC TGATACAGTT TGGCTGTGTC CCCACCCAAA TCTTCATCTT 360  
 50 AGGTTTTTAA CTNCCGCAAT TCCCN 385

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SEQ ID NO:3881

SEQUENCE LENGTH:383

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS04605

SEQUENCE DESCRIPTION:

10 GATCTTAAGG TAATTACAAA AGGGAAATTC CAAGAATGCA TAACACAATG ACAACATGGT 60  
GAGAAAAGTG CAGTACTACT TCCAAGGTAG CTAGTGTAAG GGACACTTGA GTTTTTAAAA 120  
CTGTGGTTAA ATGTTTTATG TGGAATTTGA TGAGTTTGTA TATTAAATAC CACTGCTTGC 180  
TGCTTTTACT AGAATCAAGT TAAGGGNCAC GTTAGAAATA GAACAGCTTA ATATCACTGG 240  
CTTCAGAGCA AAATGAGCTC GGGTGACTGC AGATTATGAT GGTAAATATG GCTTTAATTA 300  
15 CAAACATGNG GNATGATTCA CTGAAGGTGA AAAGNTAGGG CGGNTGTGNT ATTGAAAAAA 360  
AACCANCAT TTTTGGCATT GAN 383

SEQ ID NO:3882

SEQUENCE LENGTH:383

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04606

SEQUENCE DESCRIPTION:

25 GATCTATTTC TCAGTAATGA GTGTGTNCTC ATGCCTGTTT CAATATTGGG TTTTGGAGCA 60  
TTATTGTACC AGGCTGTGTA TTGCATACTG TAGAAGATTT GATGTTTANA CTGGTTCTTC 120  
TTCATATACT ATGTTTNGTC TCAGTTNCTA TGCTATTGGA TGATACTTCA TTTGTTGTTC 180  
TGGTGCTGAT GAAAAGGGNA ACCTGCTCTC CTCTATTTAG ACCTTGACAC TTATTACTGC 240  
TCAGTTGTTN CTGGAGCTGA AGNAATGAAA NGTCTGGAAG GAACAGCTAT CAGATGTGGC 300  
30 CATTTGGATT GTNACAAATG AGGAACCCTG TGTACTGGGA CAGTTGCCAN AATAATATAT 360  
GTGGCCTNCT ATAATGTGCA TTN 383

SEQ ID NO:3883

SEQUENCE LENGTH:380

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04607

SEQUENCE DESCRIPTION:

40 GATCTGAAGC CAGAAGGGCT GAGTGTATTG TNAACTTATT CTTGCATGTN GCTGTCTGGG 60  
AATGGACCAC ACTACAGCAG GTAGTNCTGG GGGCGATACT GCCGAAAGNC CGANCACATG 120  
TATTTTGGCT GCAATTGAGG NNCTTGGGAT GCTATTAATT TTGTATTTC GCAACTGCCC 180  
CTTCTCCTAT CCCAAAGCAC CAATTACTNC CCTCTGCCTC AGNGGTACCA GTATAAGATG 240  
45 ACATTCCAAA GACTGGAGGC AACTCAGCCT GAGTTAATTC ACAAATATAT GCCATGCTGG 300  
GGCTTGAGCT TGAGCTTGGG CTTAGGCTTG GGCTCAGCTT TTGACCCTCA GGCATCTCCT 360  
TTNCCTTNCT GTCTTNCTTN 380

SEQ ID NO:3884

50 SEQUENCE LENGTH:377

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS04608

SEQUENCE DESCRIPTION:

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5  GATCTGTTCA CAAGCTGGTG TTCAGGAACC AATGTGTGAC TGGTCCATGC CCACTTCTGA 60
   TTATATGGAC TCAGAGACAA TGTACATGGG AGTGCTTTGC CAGTGGTAAA GTTTCTACAA 120
   ATGGGAGGTA ATTGCATGGC AGGTGTAAAG TTATTTGGAC CATTGAGGCC AGAAAAAATG 180
   TAGATTTAAA ATATACTGAT ACTGAAAGCA GANCTGTTTG ANCTAATTGC TAATTTTAAAG 240
10 GNATTCAGAC ATTCATCCAA AGGNTTTAGG CCAAATGTTG CCTAAATTGT TTCTCTATTG 300
   CATATGAAAG TGATTTCNGC GGCTTAACNG TTCTCTNCTN TTTATGTGCA TGGCCATAGC 360
   TGGTTGTNTT CACATGN 377

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SEQ ID NO:3885

15 SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04609

20 SEQUENCE DESCRIPTION:

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   GATCAAGGTG AAGCTCACAG TGTCAGGCTT TCTGGGAGAG CTCACCTCCA GTGAAGTCGC 60
   CACTGAGGTC CCATTCCGCC TCATGCACCC TCAGCCTGAG GACCCAGCTA AGGAAAGTTA 120
   TCAGGATGCA AATTTAGTTT TTGAGGAGTT TGCTCGCCAT AATCTGAAAG ATGCAGGAGA 180
25 AGCTGAGGAG GGAAGAGAG ACAAGAATGA CATTGATGAG TGAAGATGTC GGCTCAGGAT 240
   GCCGAAAAAT GACCTGTAGT TACCAGTGCA ACGGGCAAAG CCCCACAGTT TAGTCCTTTG 300
   GAGTTATGCT GCGTATGAAA GGATGAGTCT TCTTCCGAGA AATAAAGCTT GTTTGTTCTC 360
   CCTGAAA 367

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30 SEQ ID NO:3886

SEQUENCE LENGTH:360

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04610

35 SEQUENCE DESCRIPTION:

```

   GATCAAAGTA GCTTACTATA TCTAAACTGT AAAACAATAT AGTTTCTCCT GAACACCTGC 60
   TTTCCTTCTG GGAGTCTGGA ATTTTGGTAT GTGCCAGGCA GAGACTACCT TTGTGACCAG 120
   CTCCCAGTAA AAACCCAGG CACTCAGTCT CTAACAAGCT TTTCTGGTTG ACAGTGTTTC 180
40 ACAAGTGCTG TTACAACTGG TTGCTGGGAG AATTAAGCTC ATCCTCTGTG ATTCCACTGG 240
   CGGAGGATTC TTGGAAGCTT GCACTTAGTT TCCCCTNGAC TTCACCCCAT GTGTCTTTT 300
   TCCTTTGCTG ATTTTGTTTT GTATCCTTTC ACTGTAATAA ATCATGGCCG TGAGCAGAAA 360

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45 SEQ ID NO:3887

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04611

50 SEQUENCE DESCRIPTION:

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   GATCGCAAGT GACTGCTTCC GCTTCCAGGA CTGGGCCAGC TAGTGGGGGT GGCAGAGGTC 60

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TCTTTGCTTC ATTCAGCCCT AGCTCTGTAG AGAAATGCAA ACCTCGACTC TCAAGGATGT 120  
 GAGGAACACA AGTTCATTC TGTGTGTCG GAGACACTGC AGACTCCACT GTGCCGAGGT 180  
 TGAACCTTN NTTGTTGCTC AAGTTCTAGG AGTCCCTTTC CTGAATATAT ACTTGTTTGT 240  
 CATAGTTTCC TTNNCAAAGT AGTAAACTTT TCTATTNNTC TACTTGCCCA GTAGAGACTC 300  
 TTGATTCTGG AANATTCTNG NCAAAATAAT TTTAATAATA CACATGGTTG CTTCTTAAA 359

SEQ ID NO:3888

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04612

SEQUENCE DESCRIPTION:

GATCACTGA GGCCAGGAGT TCAAGACCAG CCTGGGCAAC ATAGTGAGAA TGCATCTCTA 60  
 CAAAAAATAA AAAAAATTAG CTAGGCATAG TACCTGAGGC CAGGAGGTCC AGGCCGCAAT 120  
 GAGATGTGTT TGTGCCATTG CACACCAGTC TGGGTGACAG AGAAAGACCC TGTCTCANGG 180  
 GCANNTTAAA TAAATATCT TCATATATAA ATTAAGCTAA TTTAAANTAT TTTTCCCTGT 240  
 ATTTNTTTAN TATTTTCTAA TCTGAACCCA TATNCAGCTG ACTANTTCAT TCTTAGAANT 300  
 GTGTTATCTG TAATCTNTCC TAAACAGTGT AGCCCAACAAG GNTCCATGGC ACTTTTTAN 359

SEQ ID NO:3889

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04613

SEQUENCE DESCRIPTION:

GATCTAAAGG GGACACTGTA CTCAAGCTTT TNACCTCATG CCTTGTGTAG TAAAAAAGGA 60  
 TTTGGGGGTT TTGTTTGGTT CCTGAGAGGG TTGTGTTTTG TTTTGTTC CTTTGTTTA 120  
 TGTTTTGGCC TTTCTCTTT GTCTTCCAT GTAGACCAGA TATTTGAAAG GGCAGACGAT 180  
 GGCTAGAGGT GTAATGTGCA GCTTGTATAT ACGGTATTTT GGGAAACTTA CCTTGGATGG 240  
 GAAATCGAAT CGTGGATTCA CCAGGCCGGT GCTGGCACAC TCACCCTCGC CCTTCCCTC 300  
 CGGTTTCAGTA CCTATTGTTT CTCCTTTCAA ATATGTGATT GTACTAGCTC TTTCCATAN 359

SEQ ID NO:3890

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04614

SEQUENCE DESCRIPTION:

GATCTGATGG GCTCTAACAG TGCTTACTTG CAGCCTTG TG TCCACCACCA ACTTCTCATC 60  
 ATGTTTCTCT CCGTTGGCCG TTGGGTTTCC AACTCTTCAA NCTTCAGGGT CTGGGNCAGG 120  
 GAGTGGGCCC ACCATTTGTG GGGAAAGTAT CATTCTCCA CCTCAGGCTT GGGTAGATTT 180  
 GGAAGAAANAC AAGGTNAGGA TACGCCTGTT TGAGCTTTGG GGNATGAACT TTGCTTTTTA 240  
 TATTTANCTA NGGNTACTTT TATATGATGG GTGCTTTGAG TGTNATTNAG CAGGNTCTCT 300  
 TNGTTTCCCG AGGGNCCTGC TTTTGNAAGG TGACCNNNGT TACTTAAGCT AAGGNTTN 358



SEQ ID NO:3891

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04615

SEQUENCE DESCRIPTION:

GATCAACCCA CATTAGAGTG TCTAAGGACT CCTGAGAATT CCTGTTACAG TAAACAAAAC 60  
TAACGTAATC TACCATTTC TACACTATTT GAGCATGGAA ATCATAGTCC CCACTCTGTG 120  
AAACTTAAC GCTTTTTTGA AGACATTCT GTAGCATGTC AGTTTGGAGA AATGNNTGNG 180  
CTACGCCTTG ATGAAAGAAC CGTGTGGTG CTGCTAAGTT TAGCCATTAT GGTTCNCCT 240  
NTCTCTCTCT TAAGCCTTAT TCTTCAACTA AAAGATGAGG ATTAAGAGCA AGANGTTGGG 300  
GGNGATGTG AAAATAATTN TATGNGGTG TCTAAAATAA AGAGTAGTTT CTTAAA 356

SEQ ID NO:3892

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04616

SEQUENCE DESCRIPTION:

GATCTACAAA TGTACGTTGT TACAGGGCTG CTCCTAAAG ATTTTTTTTA CCTCAGGTTT 60  
CTCTTAATAT AGTTCTCCAG TCACTGACCT TGAATTGACT TACATAAATT ACTGCCAATG 120  
TTTAAATTGC CCTTATGTTT ATATTTATTA TGCAAGCCA ATTCGTACAT ACAATTTGGA 180  
ATCAAATGTC ATAAGAATTT ATTATATAAA TTTNTCAAGA ATAAAAATGC CTCTCCAGCC 240  
TTAAGTATTT ACATGCTCCC AGGTCATTGT CAGTTTATGG TATTATGTTG TTTTATTAA 300  
AGCATTGAAT TGATAGAAAA AATTGCTCTG TAATAAAAAT CTACTTTCAC ATAAA 355

SEQ ID NO:3893

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04617

SEQUENCE DESCRIPTION:

GATCTCATTG TTTTATGGC TGCATAGTAT TCCATGGTGT CTATGTACCA CATTNCTTN 60  
ATCCGGTCCA CCACTGGTGG CATTTAGGTT GATTCATGTC TTTGCTATTG TGAATGGTGC 120  
TGCGATAAAC ATGCATCCAT GTGTCTTTAC AGCAGAACGA TTTATATTCC TTTGGGTATT 180  
TTTTTTGAGT ATAGTAATAG GNNNNNNGG TGGAGTGGCA GTTCTGTTT AAGTTCTCTG 240  
GGAATCACC AAAGTCTTT CCACAGCAGA TGAAGTAGTT TACTCTCCA CCAGCAGTGT 300  
ATAAGTGTT CCTTTCTCT GCAACCTCAC CAGCATCTGT TATTTTATA N 351

SEQ ID NO:3894

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04618

SEQUENCE DESCRIPTION:

GATCTTCTTG TAAGCACATC CAGAGTGAGA CTTTTCTATG TTTGAAAGAA GAATGTGTGT 60  
 ACATTTCAAG AATTTGGGTT TTTTGAGGG AGGAGGAACT GTTACGTTT TTCCTCCACA 120  
 CGTTTGATTT TTGACACATA CACCCCTAAT TCCTCAACAG CAGACCTCCT GCAGCCACCA 180  
 GGGGCCAGCT CTGTGTAGGA ACCAGATGGT CTTTTTCCAA GCNGCATCTT CAGCTGCCAG 240  
 CTAAACTCCA ACCCCAGNCA GGGAGGGGCA GGCTCAAGTC TTNCAGAATC ACACAGGGGC 300  
 AACACATGCA NNNNCCGGNA CCTGTNCTGT ACNGTCTNGG TTTNTTCNTN 350

SEQ ID NO:3895  
 SEQUENCE LENGTH:348  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04619

SEQUENCE DESCRIPTION:  
 GATCCATAGG AGGGTAAAA GTCCGTTTTTTC TTCATTAAAA CTCTCAGCT CAAATTTATA 60  
 CTAAAGCATA TCCAGGAATT AAAAAAAG GTTTTGATGA TATTTGCTTT CTAGTTTAAT 120  
 AAGTTTTAAT ACTGAATAGG TTAATTAAT ACAAAATAAC ATAAATGCT AATATTTATT 180  
 GAGTATTTAC TTGTGTACCC ACTACGNITT TAAGTAATTT ACTGGGATTA TTTTATTTTA 240  
 GTTTAACAAT GCAGGTAGCT ACTATAATCG TCCNGGTTTT ACACTTGAGG AACAGGCTA 300  
 AGAGAGATTA ANTTAGTGGC CCAAGGTCAG AAAGCTCGTA ATTCTTGN 348

SEQ ID NO:3896  
 SEQUENCE LENGTH:347  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04620

SEQUENCE DESCRIPTION:  
 GATCCCAAAT ACTGCCATTG TGTTGTCTAC TTATGAGTTA ATTGTGTACC TGTTAGAAGA 60  
 CCGTACTCAG TAACAGGCCG GAAATTTGTG CTCTAGAAGA ATAAACTGA AAAACTCTAG 120  
 AGAATTTTTT TTCCCATTTG ATGTTTAGAA AGTTTGAGAC TGAACAGGA AAGGCCATAA 180  
 AATATCTGGT TCATATCACC TGTTGGACAT TTCCTTTTGG ATTCATGCTT TCTGGAAGGT 240  
 TTAAATTCAT TAACGTAAAT AGTTAATTAT AACTNTTNT TTAACCTAAG AGGATTCAGG 300  
 GTTAAGCACC AACTAAATTA AATCATGCTA TTAAATTTAN GTATAAA 347

SEQ ID NO:3897  
 SEQUENCE LENGTH:345  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04621

SEQUENCE DESCRIPTION:  
 GATCTAGAAT CTNTNCTNGG NTAAGCATAT AGGATGCCAC TTCTTGCTAC CTCCACAGCA 60  
 ATACATCACC TGGACAGCTT GCCACTCTTT GTTGCTTGA ACTTCTCTGA TGTTTAGGCA 120  
 GCCCATTTCTG GTACTGAGAA CACAGTGAAT GAGCTACATC CTCCTGCTTT CTCTTCTAT 180  
 TATNACTTTT ACCTGATTTT TTCTCAGGAG GAAGCTGTAC ATTTTAACAG GACAGATAGG 240  
 AGGAAAAGCA ACTATTTTTC TGCCGAGATA ACAATTGACA ACTTGGGGCA GTATGTGCAG 300  
 AGTTTTCTCTG GAGTTGTATT AAAAATTATC TGATAAGCTG CCAAA 345

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SEQ ID NO:3898  
SEQUENCE LENGTH:342  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04623

SEQUENCE DESCRIPTION:

GATCAGTGTA CTGTTACCCG GACATACCTA TTCCTTCACA AGTTCTGGTT CTTCAAGTGT 60  
GCTTACTATT TTGGTAACTG GGCCTTTCTT GGGGTATTTT TGATTGGATT AATTGTATCC 120  
TGTTGTAAAG GGAAGAAATC GGTTATTGAA GGAGTAGATG AAGATTCAGA CATAAGTGAT 180  
GATGAGCCCT CTGTCTATTC TGCTTGACAG CCTTCTGTCT TAAAGGTTTT ATAATGCTGA 240  
CTGAATATCT GTNATGCATT TTTAAAGTAT TAAACTAACA TTAGGATTG CTAACNAGCT 300  
TTCATCAAAA ATGGGAGCAT GGCTATAAGG CCAGCGATAT TN 342

SEQ ID NO:3899  
SEQUENCE LENGTH:410  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04624

SEQUENCE DESCRIPTION:

GATCTGGTGC CCCTCTTCTC CTGGATTCAC ATCCCCACCC AGGGCCCGCT TTTACTAAGT 60  
GTTCTGCCCT AGATTGGTTC AAGGAGGTCA TCCAACGTAC TTTATCAAGT GGAATTGGGA 120  
TATATTTGAT ATACTTCTGC CTAACAACAT GGAAAAGGGT TTTNTTTTCC CTGCAAGCTA 180  
CATCCTACTG CTTTGAACCT CCAAGTATGT CTAGTCACCT TTTAAAATGT AAACATTTTC 240  
AGAAAAATGA GGATTGCCTT CTTGTATGC GCTTTTTACC TTGACTACCT GAATTGCAAG 300  
GGNTTTTAT ATATTCAATA TGTTACAAAG TCAGCANCCT CTCCTGATTG GTTCAATNAT 360  
TGAATGTGCT GGNAAATTNA AGGTCGGTTN NANTTTAAAN CAAGGNTNCN 410

SEQ ID NO:3900  
SEQUENCE LENGTH:338  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04625

SEQUENCE DESCRIPTION:

GATCAAGATA TAGAGCATCT CCATTTATAA AGTTCCTTCA TGCTCCTTCC CAGCCAGCAA 60  
TTCTNCTTAC TGTCCTGCTG ACTCCTGTTT TCACCTTCAT CACCATCAGC TCATTNGCT 120  
TGTNCTTGAC TCATAAACAG AATCATATAG TAGGTGGTTC GTTCAATGTA GGCAGTCTGT 180  
TTTNGCTTTA ATCATTACAT GAGTATACAT CCATATNGTG TGAAGCAGTA GTTCTTTNGC 240  
ATTGCTGTGT AATATTCCAT TGTATAATTG TATAAATATA TGTGGTATAA ATGTAAGTAT 300  
AGCACANTTG ATTCCTTATN GGGCCACTTG GTTTATTN 338

SEQ ID NO:3901  
SEQUENCE LENGTH:238  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS04626

SEQUENCE DESCRIPTION:

GATCCACTGG TAAAGGGCAT CCCAGAGGNC AAAAATCCCT TCAAGGAGCT CAAAGGAGGC 60  
 TGTGTGATTT CATAATACAA ACAAAAAGAA AAAAAATTAN ACAAATTCTT GGAAATATCT 120  
 CAAATGTTAA TAACAATATG ANTTTTTCTC ATGCATACTA TTACTACTAA GCATGTACGT 180  
 GANTTTTTTAA ATGTATAGAT GTAAACTTTT ANTAAANNTT GGGGTGTGGT AACCCAAA 238

SEQ ID NO:3902

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04627

SEQUENCE DESCRIPTION:

GATCTCTATA AGTTATTAAT TTAACCTGAA ACCAAAGTGG TCTCCATTTA AAGTTACTTA 60  
 ATCCCTTTGT ACCACCTATT TCTAGTTAAA TATATGTNGC TANNC AAATA GGTAAGTGC 120  
 TTCCTTGCCA TGATGGTAAT GGATTGGAAC TATGAAGGCT CTCAGTGTAT TGGCTTCTGT 180  
 AAAGATGAGG CGTCTCCTCA GAANCCCNAA CTTTTCACAT TTCTGCTTAC TAGACCTGGG 240  
 TTGATGTACA TGGTAAGTCT CAAACAGATG CAAGCTATGT GCAAAANGGA ACTTTAGCCA 300  
 AATGGAAATA GCTGGATGCT TTGNGAATTG N 331

SEQ ID NO:3903

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04628

SEQUENCE DESCRIPTION:

GATCCAAACT GTGTTGTTCT TAAATCAAAA ATTGGNTAAT TTTTAATATN TATGTATTAA 60  
 TCACAAA 67

SEQ ID NO:3904

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04629

SEQUENCE DESCRIPTION:

GATCTGCCGG AGTCTTGAAA TTCAGCTGAT TGGAAAGTGGT TTCTTTGACT TTCAAGGTCA 60  
 TTCCCTATCA GTTACTACTA AGAGTTCTCT TACTGTCAGA ATCTCTCTTG CAGTACAGCT 120  
 CAAAATAGTG GATGCATTTT AAAGTTGACC ACCTTTTCCT ACCAGCTAGT TAGAAGTCAT 180  
 CAATATTTCT CTACATTTNG TTTATCTGTA AGTCCTTTAA ATCTATTTTN GCTAGGCATT 240  
 CATTATGATT AATAGTAGAC TTTTAAGACA ACATTTNTGT CACTCCCCAC CTCCTCATAT 300  
 TTNATAAAGG AGATATTTAC CTTGAAA 327

SEQ ID NO:3905

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04630

SEQUENCE DESCRIPTION:

5 GATCAAAGAC CAAAACATTT TCTTAAATAT ATTTTATGTA ATATTTTATT TGTATACAGT 60  
 GTTGTGATG AAATATTTAA CTAGAGCATG ATATTTTAAA TGTTAAGGTG TAACATATGT 120  
 TAAATAAAAC TGTATTTTN GAATTTNAAA ATTNGTTTTT NGGGGGTATG ANCTACTAGA 180  
 GTTTAAATTT CTGCCAACT ATTACTTATA TGTNCTATTG TGTAACATAC TTNCTNGAAA 240  
 10 TATTTNGGTT TATAGAATTG ANGTTCTTA TCAGATGGGA TACTGGGGAC TATAACAAT 300  
 GGAAATAAAG CCACTGTATT TNTAAA 326

SEQ ID NO:3906

SEQUENCE LENGTH:325

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04631

SEQUENCE DESCRIPTION:

20 GATCTAATTA AGCTAAATTT TGGTGCACAG CAGGTTGTAC ATGATTCAT GTTTATGTAG 60  
 CAAATGTCAT TGAAATGTAT TAGTGTGAA ACATACATGT AAAGGTAGTT GTGGAAATTG 120  
 TTATATTTNC CTTGTGTGTC ATTTATTTAG AGCATAAAGG TTTTTTTTAT TCAGCCNNNC 180  
 TGAATAAGGC TAAATGAATA CTGTAATTGA AAATATATTT NAAATCTTTG TCATGAGTTT 240  
 25 TTTTAAAAAA ANCTATTGCA AATTGTATCA TTCCTGATTA CACAGAACTT TGTGGGTGGT 300  
 TTTAANTAAN TNTNNTACTT CTAAG 325

SEQ ID NO:3907

SEQUENCE LENGTH:324

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04632

SEQUENCE DESCRIPTION:

35 GATCTGGCCC GAGCTCTCCT CAGACCTCCC CAGACCTGTC TTCTCATCAG CCACCGCTGT 60  
 TTTCTTTTGC CGAACGATGG TTGCATCTCT CGGACACAGT GTACCCCTC CCAAGCCCTC 120  
 CCTGAGCCGT TCTCTGAGT CCCTGAGGGC AGACACAGCT CCAGGGACCC AGGCCGGCTG 180  
 CCACACCCNC GACACTNCTG NTGTCCACTG GCCTTAGCTC CTGCAAGTTC CCCAGTGTCC 240  
 GCACCTGTTT CNTTCCCTGA CTTACCTTN CTGGGGTCTG TGACTGACTG GAGATAAAAN 300  
 40 TAAAAGCAAT TGTGACANCT GAAA 324

SEQ ID NO:3908

SEQUENCE LENGTH:319

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04633

SEQUENCE DESCRIPTION:

50 GATCAAATAC CGAAATTGAA CTTTCTAAAA CCTACACATA GCATGCGTTT AAATTCTATT 60  
 ATATAAGCC CCAAGTGCTT TACCTTCTAA AACATGCTTC TCTATAGGTG CAAAGTTATA 120  
 AGATATGTAG AAGAAAACAT CCATCAGAAT CTNCTGGAGA NTATGGTCAG AGTCTTAAAC 180

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AGGCCCAGTG CTGAGTNCTT TGTCCACTTA GTCACACATC TTTTGTGGGA ATGGGAAAGG 240  
AAGGAGACAG CCAAACCTCTG ACAANGGCTT TTCCTTATAG ATTAACCCAA AGCCTAGGTG 300  
AGGGTTGATA TATTAATGN 319

SEQ ID NO:3909  
SEQUENCE LENGTH:317  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04634  
SEQUENCE DESCRIPTION:

GATCTGAGCA AAATGTGAAC TCAGTATGTT TACTATTGCT CTTACTTGAA AACTTTTTTT 60  
CAAAAAAAGC ACAAATTAAG GTAGTAAATT CATATCCATA GATAGTTCAT TCATTCAACA 120  
AATATTTACC AAGTTCCTAA TATAAGTGAA GGNCCACTTC TCAGATTACT AAGTCATTTG 180  
TATGAATATG TGTGGCAGTG AAGAGAACAG GTCTTTCAAA AAGCATTGGA TTATCTTTAT 240  
TTNTTTTAAA TACACTCTCT NATNTTNCTA CTTGTTTTTT TGTTAATCAT AGCAGGATAT 300  
GACAACTCTT ATTTGAN 317

SEQ ID NO:3910  
SEQUENCE LENGTH:317  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04635  
SEQUENCE DESCRIPTION:

GATCTACTCA GATGTCATNA TACTCCATAC CTGCTTTTCC CATGGCCGCC CTACGGAAAA 60  
TCCCATCCAC AGAGGCCAGG GCTACCCAAG NCCCTCCAGG TGAGCTGGGC CTTTCCTTTA 120  
TGAACCTCCA TCCTCCCAGC CAGCTACAGT AGGGCCTCCT CACCCCGTAC CCCACAGCTA 180  
GACAGTGTCA GCACTCATCT CCTCCTCCCA CATTTNTGGA GCTTTTTTTT TCCTTCCNCA 240  
TTGACCTTTG TGGTCTTCTG TGATTATTTA TGCTGCCTCC NAAGGATAGA ATTGAAATAA 300  
AATGTTTTCA ACTTAAA 317

SEQ ID NO:3911  
SEQUENCE LENGTH:316  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04636  
SEQUENCE DESCRIPTION:

GATCAAAGGT TCTTCATTCA AAAAGAAGCA ATATCCTTTT GCCTGATATG GGGTGGGAAG 60  
GGTAGGTGGC GATGATATTT CAAATGAATT AGAAACCACC TCCCATTTGA TGATAGCTGG 120  
AGAAATGGAC TGACCTAGAA GTTACAGGAC CAGAAACTAC AGTCACCACT AACCTTTCTA 180  
CGTGGCACCC AGCCCCACTT GGAGACATTA TTTTTCATC AAACACAACC GTACTGCACA 240  
GACATCTTCA CTGTCTGTTG CAAAGATTGG AATACGTAGA TTTCTGTTCA AAATTAAATA 300  
ATATTTTAAA TACAAA 316

SEQ ID NO:3912  
SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04637

SEQUENCE DESCRIPTION:

GATCCACTGG TAAAGGGCAT CCCAGAGGAC AAAAATCCCT TCAAGGAGCT CAAAGGAGGC 60  
 TGTGTGATTT CATAATACAA AAAAAAGAA AAAAANTTAA ACAAATTCTT GGAAATATCT 120  
 CAAATGTAA TAACANTATG ATTTTNTC ATGCATACTA TTACTACTAA GCATGTACGT 180  
 GANTTTTAA ATGTATAGNT GTAAACTTTT AATAAAANTN GGGGTGTGGT AACCCNGNGG 240  
 GNCTATGTTT TNNTTAACAT AGCTGGCACA GGGTTTAACA CATAATNGCC ATAANTATTG 300  
 CTTAAGGTNC TTAAA 316

SEQ ID NO:3913

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04638

SEQUENCE DESCRIPTION:

GATCCACCTG CCTTGGCCTC CCAAAGTGCT GGGATTACAG GTGTGAGCCA CTGTGCCCCG 60  
 CCAAACCAAT TTTGTTAAT TTCATTTCTA CATGGTCGTC AAACGTGCCT ATCCAATGAA 120  
 GCCTTCATAG AAGGCCAAG AAGACAGAGT TTGGGGAGCT TCTGGATAGC GGANATGTGG 180  
 AGGTTCCAGG AGGGCAGGGT GCCCAGGAAG GGCATGGAAG CTCCGTGTCC CTTCCCCATA 240  
 CCTTGGCCTA TGCATTCTT CATCTGTATC TATTGTGATA TCCTTNACAA TAAACTGGT 300  
 AAACATANAT AAA 313

SEQ ID NO:3914

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04639

SEQUENCE DESCRIPTION:

GATCACCAGC TCACGTCATG TTGCCTTCTC TTTTCTTTGT GTGTGTGTTT ATTTAAGTNA 60  
 TTTTCTTCC TCCTCTCCCT TTTCTTTTGG GCCCTCCCTC CCTCCCTCTN CTGCCATGTA 120  
 ACTGGAGGAT GTGCTATGAG TTTGCAAACA GCTGGACTGT CAGGCTGCTT TTTTCCAGA 180  
 TGTTCTCCT CTGCCTCCC TTCCCTCCT CTCCCTCCT TTTCTTCCT TCCTTCCTT 240  
 CCTTGGAGCA CTGAGCACCA TTTGGAAGCT TGAGAGAAAC CAAAATTAAGAGAGAAAGA 300  
 GAGAGCGTGA AA 312

SEQ ID NO:3915

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04640

SEQUENCE DESCRIPTION:

GATCTAGAGG AAGTACAGCC ACCCACTGAC ATCTGANTTT ATATACCTNT TGAGTTTTGA 60  
 GTGCACCAA AACTCGATA AACCAGGTGA AGAAATTTAG CTTCCATGTT CTACTTCAGC 120

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TAAACAGCT ACATACAACC TAGTACCCTT GANGTCAGAC AGACATTTCA GTTGCTTACC 180  
TCCAGTACTG AGCCTTGCTT TGGGAAACTA AAAGATTAG ACCAAGTCAC TGCCAGTTT 240  
NGCCTTNGTN GCATTNGTA CAGTTTTTAT ATNNGGATA TCTTGTAAT AAAGACAGCC 300  
AGCTTTTCAA A 311

SEQ ID NO:3916  
SEQUENCE LENGTH:308  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04641  
SEQUENCE DESCRIPTION:

GATCAAATCT AAAATAAGTA TAATGCATTG TAATTCCAGA GATAAATCCT AGACCCCTTCT 60  
TGGCCTCCTT CTNACATAAT TCTAATCCTA CAGTCTCAGA GATGCTGTTG TATCCTGCCC 120  
CCCAACCCCA TGATAGTNAT AGTGGTTTTT GCCTTGAAGG AATTGCTTTG TATTTAGCTT 180  
TTCCCCCTCT AGATTTCTAG TTCCTTTTCA GTATTGGATT GGATTGAGA TTTGATTAAAC 240  
CTAGTACTCA GGTTCAGATG CTCGCCTCTT TGCAATTTTA ACACTCATTG GACAATAAAG 300  
TCAGTNGN 308

SEQ ID NO:3917  
SEQUENCE LENGTH:306  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04642  
SEQUENCE DESCRIPTION:

GATCTAATGC ATCCTATATC CAGTAAGTAG AATTATCTCT TCATCTGGGA CCTGGAAATC 60  
CTGAAATAAA AAAGGATAAT GCAATAAACA CAGTTGCAGG AAAGTATGTT AGCTATATAC 120  
TATGAAGTAC TCTTAGTTTA CTTATGTTGA ATGGCTTAGC TATTAATACT CAAATTGAGT 180  
TAAATGAAA ATTCCTCCTT AAAAAATCAA ACGTAATATG TATTACATTT CATGGTACAT 240  
TAGTAGTTCT TTGTATATTG AATAAATACT AAATCACCTA GGTGTCTATG TTCTATCACA 300  
TCTAAA 306

SEQ ID NO:3918  
SEQUENCE LENGTH:306  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04643  
SEQUENCE DESCRIPTION:

GATCAGCTGC AGCAGGNTGG GTCCCTCTGC ATCTGTCCAT CACTGCGACT GATGGCAATG 60  
ACTGAGTATA ACACCTTTCT TCATGGTCAA CTCTACCCAG GAACCACGTA GGGAAGGAAA 120  
TTCTGGAAAA CAGCTCCCAG CCTTAGCCAA CTTGACATAT CATAATCCAA CAGANCTCAA 180  
CCTCTACCAA CTTGGAAATC ATGTACATTT GTCAGGACTG TATTTAATTT CCACATAGAG 240  
AGAAAGCAAA ATTATACTTT TGACCAAACT AATAGANTTA TCCATTAAAC ANACAAAAC 300  
GTGAAA 306

SEQ ID NO:3919



SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04644

SEQUENCE DESCRIPTION:

GATCCTCCCA GCTCTGTCTC CCAAAGTTCT GGGATTACAG GCATGAGCTA CTNTGCACAA 60  
 GCTAAGAATA TGTGCTTTTA AATCCCATAA GGAAAAAAT ATTTTGGTA AATAAAATTA 120  
 AAGCATAAAT ATCATGATT ACCTGACGTT TACCGTAAGC AACATAAAAG ATATGTGATA 180  
 CTGAATGACT AAAANGTAGT TTTGGTTAAA GAGAGTTCTA GTTCCATGA GGNCTCTGAC 240  
 AATGCTGCAT TTTATTTTNC TTTTAATGT GCACATTGGT ACANGTTTAA CTACTCTACT 300  
 CCTGTN 306

SEQ ID NO:3920

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04645

SEQUENCE DESCRIPTION:

GATCCTGTTA TGAAAAGCCC TAAAAAATAG GGTATAGAGT TTGGGCATAT TTCAGAGGTA 60  
 ATAAGAAAGC ATTCTGCATT TTTAAAGTAA GGTTTAAAAA TGTTTCTAAT TAGNGATACA 120  
 GCAAAGTTGG TGTGAGAGGA TAAAGCTGAT ATACATAATC TGAGGAGTTC ATGAAAATTC 180  
 ATGTAAANCT GTAGTATGAA TTGGCCTAGG NGCAGCAGCT NAGGGCATAG NGACTTTAAG 240  
 ACTTTTCCAA GAGAGTGNAG GCTGGNGATA AATTGTGACT AAAATATATT TTGTGTTTGN 300  
 GAAA 304

SEQ ID NO:3921

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04646

SEQUENCE DESCRIPTION:

GATCAAGTAA TTCTTTTCACT AGGTTGGGTT TGGGGAGGGG GGAAAAGAGG GGCTTTTCCT 60  
 AGGAGAACGA TAAGAAATGG AAAGACTCCT TGAAGTGTTG CAAGGGAACC TCCTAGCACT 120  
 GTGAAAGTCA GAATCGCCTC AGCATTTCCA TGACGCACAT TATGCAAATC TTTTAGCAC 180  
 TATTTTAAGT TTGAAACTT TAACAATGAA GGGGAAGGGG AAGNTTTCCA CCAACTGANT 240  
 CATTGTGCA CGTGTATAGC TCAAAGNGCT TAGACTTCAA ATATATCTGG TGAATGACAA 300  
 A 301

SEQ ID NO:3922

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04647

SEQUENCE DESCRIPTION:

GATCTGCCTG CCTCAGCCTC CCAAAGTGCT GAGATTAGAG ACGTAAGCCA CCATGCGTGG 60

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CCAATAAGAC TGACTTTTAA TTTTCCTTTC TTGTACTGTT CTTGTCTTGT TTTGGTATCA 120  
 AGGTTATATT AGCCTCATAA AAGGAGTTAA GAAGTGNTCG CTCTTCTAT TTTCTGAAGG 180  
 AGTCTGCTAA GTATGAGAAC TCTCTATTTT ATGAATGATT GATAAACTC TCTTGGAAAC 240  
 TGTCTAGACC TTATGGAAAT ATTCAGTAA TAGTTACAAA GCTATTCAAG TTGTCTGGTT 300  
 N 301

SEQ ID NO:3923

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04648

SEQUENCE DESCRIPTION:

GATCTCAGTT GGATAGTTGT ACCTCAAAAA AGTAGGTGAG AACTGGCTTC CTCATTGTCC 60  
 CAGGATGTCA AATACTAATG ACATAAGAGC TCACTTACGT GCCAAAATTC ACTTTTATAC 120  
 TAGTTTTTCA GTGCTTTAAT ATTTGTAAC NAAATTTNAA AACTCGTATT TACAAACACT 180  
 ACTGTAACTN CAGTGAAACT GAATTGTGCG ATTGANGCTT TTTGCTTATC ATAGTATNTA 240  
 TTACACTACT TANTTCAGTA AATATATAAA NGTAGCCTNC AATTGANGTG TNTATTGAN 299

SEQ ID NO:3924

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04649

SEQUENCE DESCRIPTION:

GATCAGAAAG GTGAAATGTT TCGAATTTAA AATGTTTAAA GCATGTTTGG TTTTATTATT 60  
 TTTACATAAT TGTTTACCAC TAGTTTTTCC ACTAGCTTTT TATTATATAT GTTTAATTAT 120  
 GTAATTGTTA TTCACTAGCT TTTATTATAT AATTCCTTTT AAATAATACT ACTATTCATC 180  
 AACTCTGTG GCATAAGAAT TGCAGTTTTT TCTACCAAAC TTTTACTTCA TCTATGAGTC 240  
 GTGTTAGAAA TAGTCATTGA AAAAATATAC AGTAAATAT CTAGCAAAAT AAA 293

SEQ ID NO:3925

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04650

SEQUENCE DESCRIPTION:

GATCTGGTGA AGGCCTNCTG GCAGCATCTT CTCAGTAAGA CCTCATGTGG CAGAAGGAAA 60  
 GGGAGCTATC TGGAATCTCC CTTATAAGGG CCCNNNGGCC ATTCATAAGG GCTGCACCCT 120  
 CATGACCTAA TCACCTTCCA AAGGCGTCAC CTCCTGGTAC TGTCACCTTG GGC GTTACGA 180  
 TTTTCATATA TGAATTTTGG GACGGCATAT TCAGTCCACA CCAGGAAGTT CTTGCACNTC 240  
 ATAGTCGAAA GTCAGTTTTG TGGCTATAAA AATCTTGTTT CCATTTTCCG CTN 293

SEQ ID NO:3926

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04651

SEQUENCE DESCRIPTION:

5 GATCCACCCG TCGTCGCCTC CCAAAGTGCT GGAATTACAG GCGTGACATG CATGCCCGGC 60  
 CAACATATAA TTATTATACA ACCCAGCCAC TGCACTCTTG GGCATTTATT CTAGAGAAAC 120  
 AAAAATTAT CCCCACTCAA AAGCATGTAC GTGAATGTTT TTAGCAGTTT ATTTTATAAT 180  
 GGTCAATATC TGGAAACAAT CCAAATGTCC TTCCATGAGT TAATGGTTAA AATAACTGTG 240  
 10 GTGCACCCAT ACCATGGAAT ACTGTTTCAGC AATAAAATGG TATGAAATGA AA 292

SEQ ID NO:3927

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

15

TOPOLOGY:linear

CLONE:HUMGS04652

SEQUENCE DESCRIPTION:

20 GATCCTATCT AAAAATATGT AGTTATTAAT CATTCTGTGG ATATTGTNA ATAAGGTAGT 60  
 TNCTATGGTC CGAATATCTG GGCCTGCCCC CCCAAATNAT GCTGAAACCT AATCACCAGT 120  
 GTGATGGTAA TAGGAGGTGG GACTGAGCTC TGATGAATGA GATTAGTGCC CTTATAAATT 180  
 ATGACCAAAA GAGCTCTTCA CTCCTCCTAC CATTTGAGGA TACAGTGAGA AGCCTTCATC 240  
 TATGAACCAC AAAGTAGCCC TCATCAGACA CTGAATCAGC CAGTGCCTTG N 291

25

SEQ ID NO:3928

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS04653

SEQUENCE DESCRIPTION:

35 GATCTCACAG AAGTTATTCA ATCTCTAGGT TGCTTTAGCA TCTACTTGTG TAGTGAGAAG 60  
 AGTTATTTAC TTATATTGTG CATGAGGCCG TTTAGATATG TTAAATGCAA AACAGAACTC 120  
 TTGCTAGCTA AACACAGTAG AACTTGAATT TTTTTTTTNA GAGGTTATTT AATANCAAAA 180  
 TCAGGTTATT TGTGACTTGG TTGAAGTAAA CGGTGTCTCA GATAAANTAA TTNGTTAAAA 240  
 GAGTTGCCA NTTTATGTCT TATANCTTNA ANCAANTANN TANTAATAAN 290

40

SEQ ID NO:3929

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04654

45

SEQUENCE DESCRIPTION:

50 GATCTGGGAT GTGAGTGAT CAAATCTTAT CAAATCCATT GACAAATCAG TGGTGCTATA 60  
 CTGGAAATGG CTACTCCTTT GGATGAAGGA CCTCATTTCC CAGTTGCTTG GAACAAANGA 120  
 GAATTTACAT NNNNCTGTAA GAAGGGAGAG ACGGCAGTTG TTGGTAGACA CACAGNNAAG 180  
 GGTGCCCAAG AATAATTCTG TCTGGATTAA AGGTCCCAGG GAAGTGACGG NGCCATTTCT 240  
 GTACCAAGAG GTGAATATAA TTTGCATGTT NGNGTGCAGT AATTAAA 287

55

SEQ ID NO:3930

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04655

SEQUENCE DESCRIPTION:

GATCCCAAGA TGAAGGGGT GGGAGGTCTT GCTAGAATGG GAAGGGTCAT AGAAAGGGCC 60  
 TTGACATCAG TTCCTTTGTG TGTACTCACT GAAGCCTGCN TTGGTCCAGA GCGGAGGCTG 120  
 TGTGCCTGGG GGAGTTTTC TCTATACATC TCTCCCAAC CCTAGGTTC CTGTTCTTCC 180  
 TCCAGCTGCA CCAGAGCAAC CTCTCACTCC CCATGCCACG TTCCACAGTT GCCACCACCT 240  
 CTGTGGCATT GAAATGAGCA CCTCCATTAA AGTCTGAATC AGTGCAGAAA 290

SEQ ID NO:3931

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04656

SEQUENCE DESCRIPTION:

GATCCTGAAG GGAAGGGGCA GGGATTTCTC CTTCTTCTTG GTCCTGGCTC CCAAGGGCTT 60  
 CTGTCTTCAT CTCTGCATGA GCTCTCCTTC CCAGAGACCA ACTCTTTTN ATTTNATTN 120  
 ATTTNATTTT TNAATTTATG TCTGGAGCCT GGCTACTCTG CATTGGGNT TGGGGATGCT 180  
 GGGTGGGTGT GTGGTCCATG TTCAGCGTTC TAGCAACACG TGTGTGTGTG TGTGTGTAAA 240  
 GGCTATGCAG CAAAATACC ATCTGGCCAG ACGGGCCAC CCACAAA 287

SEQ ID NO:3932

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04657

SEQUENCE DESCRIPTION:

GATCACCTGT TCCTACAGTG ACAACTGGAC CTGGCCCGAA CCCCTGGCAT CTGGCAACAT 60  
 TATTACCTGT CGAAACAGAA GTAGAGATTT GAAATAGAGG ATGCCAGTTC CCATTCCTC 120  
 CTGCTGTCTG GAAGGAAGTC TGGCTTTCCA GCCCAACTCT AAGCTCATCT TTACATACAA 180  
 AATAAGGGTA TGTTTACATG GAAAGCAAAA ATAGAACCAT GGATTTACAG AAGGTTCCAT 240  
 AGCAGCAAAT ANCAGTGCTT ATGAAATAAA CATTTTAAAT ATTAAA 286

SEQ ID NO:3933

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04658

SEQUENCE DESCRIPTION:

GATCTAATTG TGAAATCGTT CACCTTGTTA AACATCTAAG TAAGTCTGTA GTCGCTCTGC 60  
 AAACAGCCAT TATATTATT TACTCTAGAA GAACTGTAG AGTAGTAATT CGTGCTAATG 120  
 AGAAAAACAA AATACCATGT TCAAAACAGA TGTATTTGAA AACTTAATGA CATGGTTCCA 180

AAAACTAGAG CATGTATGTA TGCTGTGCAT CATCTCAGCA GACCTAAAAT ATCCCCAAGT 240  
 TGTCCTTTA CAGCCATCAA TATATTNAC ACTCTGCGGC AAA 283

5 SEQ ID NO:3934  
 SEQUENCE LENGTH:283  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

10 CLONE:HUMGS04659

SEQUENCE DESCRIPTION:

GATCTGAGTC CTAGGNCGC CCTCATTAC TAGCAGTAAG AATTTAAGTG GTGCATGGCA 60  
 CATAGCACTG TACTAGATTC TGCAGGGGCA CAAACATAGA GCCAAACACT CTCCTCTTG 120  
 GAGAATTTCA GACCCAGAAA AGGCCACGCA GTTCTAACTT TTGTCATCGG TTCCTTTTGC 180  
 15 TAAAAGGCAA AGGGTATGTT CCTTGCCTAT TGTCCAACAT ACCCCTTCCA AGATTGTGAG 240  
 AAGATGGGTA GCTGGGCATC ATTAAATATT GAATCAATTG AAA 283

20 SEQ ID NO:3935  
 SEQUENCE LENGTH:281  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04660

SEQUENCE DESCRIPTION:

25 GATCCACAGC TTGCAGGAGA AAGTCAGTGG CCCCAGACAC ACGTAACAGG GTGAGCACTG 60  
 AAATAAGAGC ACGCTGGGGC GTCCACACCA AGGGACTACG CCCCAGTCTG CCCACCTATC 120  
 TTTTCTCCAT CATTAAACCA GCGCTCTTTC TCCCTGGACT TCCAAGTACC AATGACCTTG 180  
 GGGCTTCTTT GCAGTTTAAA GGGAAAATGC TCTACAAANT AATTCACTN TCAAACANNT 240  
 30 CAGCAGAAGA ATAAAATNTT TTTTCTGGNA TATCTAGTAA A 281

35 SEQ ID NO:3936  
 SEQUENCE LENGTH:280  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04661

SEQUENCE DESCRIPTION:

40 GATCCAATCA CATGGCAAAT GCCTCCTTTC ACAATAGAGC ATGGTGCTGT TTCCTCACTT 60  
 GANCTGAAAC TTCATAGAAG ACCAGGTGAG ACCACAGAAT ACTAGATGNN AATGTTTCATG 120  
 TAGGTAAGCT TTATATTTCC TTCCAAGCTC CATTGCTACA AAGGTGTAAA TAAAATACAT 180  
 TTTTATGAGT TGAAGTAACT TCATGGTAGA AAATAATAAC TCTGCCTTCA AAAGCAAATA 240  
 ATGGTTTCTT TGTTAACCAA TAAAGCATAA GANAATGAAA 280

45 SEQ ID NO:3937  
 SEQUENCE LENGTH:278  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 50 CLONE:HUMGS04662  
 SEQUENCE DESCRIPTION:

55

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GATCTTTAAA TTTTGTCTCT TAGTTAAGTT CTGTATTTAG TGAATTAATT GCATCCTAAA 60  
AAGTCAAACT TGAAAAGCAC ATTTTAAATG GCAAATCTAT TTTTACATG TTTGTGAAGT 120  
TTTTATTTT TAGTAAACAG ACCATCAGAA GAGAACAAATG GTACAGAGCA GGGGTCAGCA 180  
GATGGATTTT GTANNGCATC AACTTGTAAG TATTTTCAAG TTTATTAGCT GTATGGCTCT 240  
GGTTTCTGTT CCTGTTCCTA AATGTAAAG TCTACTGN 278

SEQ ID NO:3938

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04663

SEQUENCE DESCRIPTION:

GATCGACATT TAAAAAATGA GGTGAAAGAA AGCTATAGTG GCATAGAAAA AGTATAAAGC 60  
TCAGTTAGTT TTTTATTAT TATTATTATT AAAAGTTAAT TCAGGACTGA TGTGACCTAC 120  
CAGATTTTCAG AACATGTGTT AATAGTATAT ATGCCACTGA AACTTAGGT CCTGTATCAT 180  
ACTTTTINCT TTAAGACTTT TTAAGAAATA TTACTTAAAC ATGTGGCTTG CTCAGTGTTT 240  
AATTGCAAGT TTTCAATCTT GGACTTTGAA AACAGGATTA AACGTTAGTA TTCGTGTGAA 300  
A 301

SEQ ID NO:3939

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04664

SEQUENCE DESCRIPTION:

GATCTCCCTT TTACAGATAT CAGAAAGCAT GAAAAAATA GAATTGGATT TAATGCTTTG 60  
CAGATATTCT GTTTTTTTC CCAATTATTT GATTTACCT ATATACATAT TCTTTNNTCT 120  
TTTTCTAGC TTTAGAAGCA AACCAACAAA AGCAGTTTGG ACTTTAGTAA CTTTTTTTAA 180  
CAGCAGCATT TAGAACAGTT TGCATGTTCT GAGGAATATT ATATGTGTGT TGGGGGGAAA 240  
GGAATTCACA CTGAATAAAT TTTAGAAATA ATTAAA 276

SEQ ID NO:3940

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04665

SEQUENCE DESCRIPTION:

GATCTTACTG CAAAGGAAAC TGACAGAAGA AAAAGAAAGT GCTTTTGAAT TTNTTTCCTC 60  
TGCCTGACTA GACAATGATG TTAATAAATG CTTCAAAGCT GAAGAATCTA AATGTCGTCT 120  
TTGACTCAAG TACCAAATAA TAATAATGCT ATACTTAAAT TACTTGTGAA AAACAACACA 180  
TTTTAAAGAT TACGTGCTTC TTGGTACAGG TTTGTGAATG ACAGTTTATC GTCATGCTGT 240  
TAGTGTGCAT TCTAAATAAA TATATATTCA AATGAAA 277

SEQ ID NO:3941

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04666

SEQUENCE DESCRIPTION:

GATCCTAAGC CATAGACAGG CTAATTGCCC ACCACTCCCA GGAATATTGA AATAGCTACA 60  
TGACCATAAT GTGTTTAAAA TGTGGTATGC TCTTGAGATA TTTAAAGTTT TGGCAGTAAA 120  
ATACTCTGTT TTAAAGTATG AATGTATTTT ATTCATATTT CCTCTCACAA AGGAAAATGA 180  
CTTCAGTATA GATTTGTTTT TATTTAAATG CATTTTTTAT TCTTAAGTGG TAGGAAGCAA 240  
CATCCAAAN TGCTTAATAA AATGCTTTTA AGCTGCAAA 279

SEQ ID NO:3942

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04667

SEQUENCE DESCRIPTION:

GATCAACTGG CTTTCTCTA TTATGACTTT AGATGAATCG TTTAATAGA TTTGCTAATG 60  
TTAAGACATC TCTGCATTTT TACAAGAATC TGATGTAGTC ATAGTATACT ATTCTTTTAA 120  
TATACATCTC CTTTCAATGT TAACAGTGGT TATTTATGAT TGGTTGGTCC ATAGTAGATT 180  
TTTATTTTGT GTTCTTATC TGNACTTTCT GATTTTCCTA CAAAGATNNG NGNNTACTT 240  
GTATAATAAA AATAAGAGCT TTAAATNGTG AAA 273

SEQ ID NO:3943

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04668

SEQUENCE DESCRIPTION:

GATCGCGTCC AGATGGAAAA CGGAAGCAGA GGCTTCTAAT CGTCGCATTT ACTGGCTCCA 60  
GTGCAACACA TCCATCTGAA AACACTCGGA AGTCTGGTGC TTGGAGAGGG TGCCATTGTC 120  
TCTTGACAT AAGGTCATGA CGTGTCTATG TCAAAAGTTC TTATATATTT CTTTATAAG 180  
CTGAAAGAAG GTCTATTTTT ATGTTTTTAG GTCTATGAAT GGAACGTTGT AAATGCTTGT 240  
CAAACAATAA AAATAACGAA AAGTGAAA 268

SEQ ID NO:3944

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04669

SEQUENCE DESCRIPTION:

GATCTNGTGC CTGGAAATAG CCTGAGGTGG CTCAGGAAGC GGAGAAAGGG TGCCAGACCA 60  
TTCTCTGGCG GGGACCAGGG CCCAAGGCC CAGGGCTGGA AGNAGACCAA GGGGCAGCCG 120  
CCCTGGAGGG ACATCAGTGC TTCCTCTTCC ACCCAATTCC CCCACGCGGT TCCATGTTTT 180  
CCCACCAGCC TGTTGGCGAA GTTGCTGCTC CGGCATTAG TACCTNNTNN NNCCAGAGAA 240  
ATANNNGAG TTTCTATTTT ATGTTAAA 268

SEQ ID NO:3945

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04670

SEQUENCE DESCRIPTION:

GATCAGATGG TTTAAGGCTA CAACACGAGG CCAATATCTG TATGTNAAGG AGACAGAAAC 60  
 ATCAATGTTT GGAGTATATA TTGACCTTCA TTCTTACTTT CTCCTTATTC TCTTATGTAA 120  
 CTGTTAATTT TTCCCTTCCT TGGCTCTATG TATTTAATTA TAATAAGCTT TACCTACAAG 180  
 CAAAACAAAC CAAACATGAA CAATGAAAAC TACTTTTGGT CATGTAGCAG AAACAGCAGT 240  
 CAATAAAGGA GAGAATGAAA CTAGAAA 267

SEQ ID NO:3946

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04671

SEQUENCE DESCRIPTION:

GATCCTGTGA AAGCTGATGC CCATGTGCCC TGAGAGCTGC CTCTCAATCC CTGTCCCAAG 60  
 CCACAGCTAT GGCCTTAATG TCACCAGTGT TCTCACCCTC TAGGCCCTGT GCCTGGAGGT 120  
 GCCTCCACAG CCGACCAGCA GCCACCCCGC CTGCTTCATC CACATCAGGA GGGTCCGGTG 180  
 AGGCTGCAGC AGTGGTTAAG GAGTAACACC TTCTTGATT AAGGAATTTT AAATAAATA 240  
 AAATGTATGT TGGAGATACT GTTAAA 266

SEQ ID NO:3947

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04672

SEQUENCE DESCRIPTION:

GATCCCTAGG TCTTGGGAGC TCTTGGAGGT GTCTGTATCA GTGGATTTC CATCCCCTGT 60  
 GGGAAATTAG TAGGCTCATT TACTGTTTTA GGTCTAGCCT ATGTGGATTT TNNCCTAACA 120  
 TACCTAAGCA AACCAGTGT CAGGATGGTA ATTCTNATTC TTTCGTNCAG TTAAGTTTTT 180  
 CCCTTCANCT GGGCACTGAA GGGNTATGTG AAACAATGTT NAACATTTTT GGTAGTCTTC 240  
 AACCAGGGGT TTTTCGGTT TAACN 265

SEQ ID NO:3948

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04673

SEQUENCE DESCRIPTION:

GATCTAGNAA ATGCATATAT TTAGCGGGTA TTTGAAAGAT AGAAGCATT TTTATAACTG 60  
 AAGAGTATAA CACTTATCTN CTTAAGTAAA TGCTCTCATA ACTTGATAC ATTTTNCAG 120



GTACAAATTC AAAAGTATGT AAGCATTGTA TAATGTGACA ATTGTATAAT TTATGTAATC 180  
 TGATGCATGA NTCAGAATTT TTATATAATA TATGATTATN GACTTATAGT TGATTAANGT 240  
 GTTTAANCTT AAAANANAAN ANNNN 265

SEQ ID NO:3949

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04674

SEQUENCE DESCRIPTION:

GATCTCTAAA CTAGCTCTTT TGTTAGTATC GTCTCACAAA CTGATTATTT TCCTCTTTCT 60  
 TTGGTAAGGT CAATAACTGG GAGATGGACA AACTAGAGAT GGAAGATGCA GTCACATTTT 120  
 TGAAGACTAA AATCTATTCA GTAGAAGCTC TTCCTGTTGC TGCTGTAAAT GTGCAAAGCA 180  
 CACAATAAAG TGAAAATCAA CCTTTTCATA TTAGGAGACA TGCATTTGTA AAAATTAATA 240  
 AAGATGACAA GTCAGTTNTC AAA 263

SEQ ID NO:3950

SEQUENCE LENGTH:261

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04675

SEQUENCE DESCRIPTION:

GATCCACACA CTACAGGAAA CAGTTGGCTT TGGAAATCCA TCTTTCTGAT ACCCCTCCAG 60  
 CTGAACAATT TTCTGCATGG GACTCTGAGT TCCTTTCCTT CCCAGAGAGT TTTACCGTAT 120  
 GAAGCCTGGA GCTGGAGAAC GAAAGAATCT TCACTATAAA CAGAGACCCA TTCATTTATT 180  
 TCCATTGGCT GTGTTACTGG ATGTTTTACT GGTGACGAG AACTGGGTC ACAATAAAAA 240  
 AATGGAGATA TGAAACTCAA A 261

SEQ ID NO:3951

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04676

SEQUENCE DESCRIPTION:

GATCTGTTTG TAATACAAGG TATTTGGNCT TGTCTTTAAC TGTATAGTGA TTTGTGGGCA 60  
 GGCTGCAGGA GCCAGGATAA AGAATGCATG TTTGAAATCT NCTCTATACA AATGCATCCA 120  
 CACTCTCCNG CAAAGGGATG AGTTTCTTAG CCGTTTTTAC TTGATACAAA TGCTATTGTT 180  
 TCCTTTGGAN GGNGTGAAAA ANTGNANGCT CCACCTGCTC CGTGAGTAGC ATTGCTCTCA 240  
 ACTGGTGTTT CCAGCCGTTT ACATGTCTAC CCATTCTCTC CTTTANGGTT TTCTTAGGGN 300  
 GCNGGNGGNT GNNTN 315

SEQ ID NO:3952

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04677

SEQUENCE DESCRIPTION:

GATCTAAACT TGATATGTTA AATTTAAATT TAATTTCCCC AAGTGTGAGT ACTATATGTN 60  
ATTGTAGATA ATTTGCAAAC TACAAAAAAT AAAAATAATT GGCTGGGCGT GGTGGGTCAT 120  
GCCTGTAATC CCGGCGCTTT GGGAGGCCGA GGTNGGTGGA CCACCTGGGG TCAGGAGTTC 180  
AGGACCGGCC TGGCCAACAT GGTGAAACCC GTCTCTGCTA AAGGTATAGA AGCTNGCCGG 240  
GTGTGGTGGT GGGCACCN 258

SEQ ID NO:3953

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04678

SEQUENCE DESCRIPTION:

GATCCTCACT CAACGAAAAC TCGNTTGGAA ACTGTTCCGN CTGGCAGTCC TTTTTTGTG 60  
TTTTCCATCT CATTTCCCTT CCATCTGAAA GTGGCATTCA GCTGACTNGC TCATTTAGAC 120  
NGTTCACGGA GTCTGAATCT GCCAACGTGG TGTGGAGGC TCCACCTGA AAAGGGCCAC 180  
AGTCAGGGCA ACTTTCCCA TACAGGAAAA CTTGAAAATT ACATCAACAG TCTACGTCAC 240  
AGCCAAATTA TATTTCCN 258

SEQ ID NO:3954

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04679

SEQUENCE DESCRIPTION:

GATCCAGTGG CTGCAGCTTC AATCCCAGTG CTGNANTCAC ACATCCATTC TGCCCTGGGG 60  
GACCCTGGAG CCTACTTGTG CGCTTTGCAT TTCATTGATT GACGNCTCCC TTCAACAAGC 120  
ATTTACTGNG CGCCTACTAT GTACTAATGC TAGANGTTAG ATGTACAAAG AAGACAGTTT 180  
TCATCCTCTA GGNACTCATA GGCTAATGGT GAGACACACA GACANACATC ATTATATTAN 240  
AATANGCTAA GNGAAAA 257

SEQ ID NO:3955

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04680

SEQUENCE DESCRIPTION:

GATCTACAAG GCCACACAGA TAATTNCAAA TACATCTCAT TTCCTTCTGA TTCAGGCCTC 60  
GGNAGACCCC AAGGGGAAGG AGTTCTCATG GGNCACTATA ATCNATGAAG CTGAAGTTGN 120  
AATATAGANG GCAGATTTAA AGTTACCATT TTTTTTTAAA CACCAGCTAT GGTCCCTTCA 180  
AAATTGTACA AGCTGTCAGT ATCACCTGCA CATGAGCAAT TTAGTCTNNN GGNGGNGTGA 240  
GAAGTTTtagg TCTTTNN 257

SEQ ID NO:3956

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04681

SEQUENCE DESCRIPTION:

GATCTGCCCA CCTCGGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCAT GAGTGCCCAG 60  
 GCAGAGAAGT CCTACACCAC GTGTCAAACCT CGGAACACAA AGGGNCACTG TCTTATTGCT 120  
 TGGTACAGTA CTCCTGTTTG TTGAGAGCCC ATTTACTAGA GCAGCTCTGT TTGTGCTTAA 180  
 TGAAAGCTCT TTTCTGAGAG GCAACAGAGT GTGTTCTATC ATAAATGAAG CGCTCTTCAA 240  
 GAACTTCCTG AGCAAA 256

SEQ ID NO:3957

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04682

SEQUENCE DESCRIPTION:

GATCCACCGT CGGATTCCGT CTGCAGAGGA GGACGTAGGG GGCCGTCACA CCCACCAGGC 60  
 CTCCCTGCTG TGCTTTAACA CAGGCAGAAG AGGTTTCATGG CAATATAATA GTCAATGAAC 120  
 TTTCAGTTTA AATTGTGTAC ATTTTAAAT TGTAAGATT TTACTGTATA TTGATGCATA 180  
 GTGTGATTCA ATAAATTGCT TGTAATTTAA AACTATTTA ATATTCAAAA TAAATATAGT 240  
 TATATATTTA TAAA 254

SEQ ID NO:3958

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04683

SEQUENCE DESCRIPTION:

GATCTGTTTT AAAGTTGGGG GGTGGGAAAT TTAGCTGACT AGGGACAAAC ATGTAAACCT 60  
 ATTTTCCTAT GAAAAAATT TTAAATGTCC CACTTGAATA ACGTAATTCT TCATAGTTTT 120  
 TTAAATCTAT GGATAAATGG AAACCTAATT ATTTGTAATG AATTATTTAG ACAGTTCTAA 180  
 GCCCTGTCTT CTGGGAGTTA TCANTNTTAA AGAGANCTTT TGTGCAATTT CAAATGAAGT 240  
 TTTTATAAGT AN 252

SEQ ID NO:3959

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04684

SEQUENCE DESCRIPTION:

GATCCGGAGT CTTGAGGCC ATTNTTGAAC TACTAATTCA ACTAATCCTG AACCACCATA 60  
 TTTTCATATT CATCCATGAA GTGTAAAGTG TTCTTATGAT TTAAACCACT TAGCATTGGT 120  
 TTTTATATTT CTTGCAGCCA AAATCTTCCT AACAGTAAAA TAAAGTTTCA AGTTTCATAA 180  
 GTGCCAATGA TTTTAAATG TTAATAAATT TGTACTAAAT AAAAATGGCA ACAGGAGCAG 240

GTAAACCTAA A

251

SEQ ID NO:3960

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04685

SEQUENCE DESCRIPTION:

GATCTTCTAA CTTATAAATG TCAAATATAT TTTTGTATTA GATTGTGCCT ATNATGAGAG 60  
AAATCTTTAA TGTATATTTN ATGTATGCTG AACACATTTT TATAATTTGN CACACTTGGA 120  
GGCATGGTCT AGTAATAATA ATGTAATATG TACCTTGCTG GTTANTATAA CTAAGATTTT 180  
GCCTTTATTG GGTTAGGTAT CTNTTNTTTA TTNTNGCACC NGNTAGCTGN CTTCTACTGA 240  
GTAAAGANTT N 251

SEQ ID NO:3961

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04686

SEQUENCE DESCRIPTION:

GATCCAACCT CAAAGTAAAA GTTGGAAAGG GCAAGAGTCT TTAAAGCGGA ACTTCAATTC 60  
TNTTNNCATG GTTACTTATA TATAATGAAT ATAAATAGAC AAATAGGACT TGGAAAATGT 120  
GGTATATTCT AAGTCAAGAT GCTATGAAGT TGTTATAGTT TAAGGGNCAT TCTTAAGAAG 180  
GAATTACTTA AGTNCATTAC TCTNCTCATT TCAAGGACAT GAAAAAGTAA AGGATGGTCT 240  
GGCACTATTT N 251

SEQ ID NO:3962

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04687

SEQUENCE DESCRIPTION:

GATCCTGGAG ACGCCATTTC CGAGATTGTT CTGCATATTC ATTTGCACAT TGTTGTCTGG 60  
GTTGGACATG CGTGTGGGCT TCAGTGTGAG GCTTTTAATA TGTATATCCT GTTATCAATA 120  
AAACAATTAT CCAAGTGGTT GAATCCTGTG AGACTTGGCA AGTGTGTGCA AATNAAGTAT 180  
ACTTGACTTT TCAACCTCTT CTTTCAATGT NGCNNTTATA TGANATAAAG TAATCCATT 240  
ANCAGTTAAA 250

SEQ ID NO:3963

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04688

SEQUENCE DESCRIPTION:

GATCGACATG AGATACAGAC GAGAGATTAT GTCTCTTATG GCTTTATCAT CAATTAACT 60

TAGCAAAGTC TGTTAAATTT ATTTTCAGAGT CTCCCAGCTG TGAAAAGTAG AGTTCCACTT 120  
ATGTCATCCA TATCTGCACA GTAATCTTTT TTTTAATCCT AAACCTTCTT AACAGGTTTC 180  
TNTCCTNAT TCTAGACAAT AATGCTATGT GTTTTCCTG AATACCATGA TTTTAAACTN 240  
TTAAA 245

SEQ ID NO:3964  
SEQUENCE LENGTH:245  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04689

SEQUENCE DESCRIPTION:  
GATCGGTCAT GCTGGGGCCA AAAACATGGC AAGAAACGTC CCACTGTCAA CCTCCCGGGC 60  
AAGCGTGTGC ACCTGCAGCT CAGGGCCAGC CCACCACACT GCCTTAGTGA CACTGCAGCC 120  
GGGGGAGCCA CAGGCCGCCA GCAGGCTGAG GAACAATGCC GTGTGACCTT TCCNNCNNNN 180  
AAAAAACAAA AACTGCAATT TTTATTCAAA TAAAAAAGG GTAAAAATAA AAGTTAATAA 240  
GGAAA 245

SEQ ID NO:3965  
SEQUENCE LENGTH:244  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04690

SEQUENCE DESCRIPTION:  
GATCATGGAA AGTTTCAGTG AAAACCATCA TGCTGTCTTC CAGAACCACG TTCTCCTCTG 60  
AGGAGGATGA ATGAAGGTTG GGTTCAGTC ATCATGCCTG CCCTTTTTTT CTTTGTATTG 120  
TTTCTTAAGC ATCTCAGAGT CCTCTCATGG AATTGGTTT CTATTTCCCC TCCCAATCTC 180  
CACCTCACTC CATATCATAA GACATGTCTG CATTCTGGAA TATTAAACGT GGACATGGCT 240  
CAAA 244

SEQ ID NO:3966  
SEQUENCE LENGTH:244  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04691

SEQUENCE DESCRIPTION:  
GATCATGCTT TTCCCTACTA AACTTCTGTA ACTGCATGTA TGATACATTA TTGCAGAGGT 60  
AAGAGATAGT TTAATGGATT TTTAAAAACA AATTACTATA ATTNATCTGA TGTTCTCTAG 120  
TTGCATTTTG CTGAAATGTA GTGCTGTTCT AAATTCTGTA AATTGATTGC TGTTGAATTA 180  
TCTTTCTGTT GAGAAGAGTC TATTCATGCA TCCTGACCTT AATAAATACT ATGTTCAAGT 240  
TAAA 244

SEQ ID NO:3967  
SEQUENCE LENGTH:242  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS04692

SEQUENCE DESCRIPTION:

GATCCAAGCC CTTGTTCCAGA TTTGGTGCCT GATAAGACAG GGGTTTCTCT TTTTGTGACC 60  
 TTTATTATTA TTATTTTGTT AACTGTTGTA ACCAGTTAGC TGTGTGTTT TAAGATAGAA 120  
 AGGAACAAGA CTAAAATTGT AAATACTTTG TAAACATCAG CATTGTACT TGAATAGTAG 180  
 GATTTTAAAG GGCATTGATA GCATACCAA CAAAAGGCAA AATAAAGTGA CCTTTTATA 240  
 AA 242

SEQ ID NO:3968

SEQUENCE LENGTH:241

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04693

SEQUENCE DESCRIPTION:

GATCTTCCTC CCATGAAAGA AAAANCAAGA ACCAGAGGCG TAGACTNACT NAAGACACAA 60  
 CTCCTGGCTT TCTNAAGCTA TGGACTTGGA TTGGATTGCT GGGGGTTTTT AGAGAAAGGT 120  
 GACAAATTTT AGTACCTCTG GCATGCTGTC CCAGGAACT AGGGCTCCCA CTAACCTATG 180  
 AGGTTTTTAA ACACATTGAA AATGACATGA CACCTAAAT AAATTGGAT TTGCTCATAA 240  
 A 241

SEQ ID NO:3969

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04694

SEQUENCE DESCRIPTION:

GATCAAGGGT AAGAATAAGT ATCCACCTCT TTCCTTTTAA AAATTTTCCC TCAGAGTCCC 60  
 TATGTTGCAT ATTTNATTCT GTTCAGAATC TAACCTTTCC CTAAGGCTTA TCTTTCTAAC 120  
 AGATACTAAT TATGAATGGG CATCAACAAC TCTAATTAAA CCATTCTTTA AAACCTCTCT 180  
 GGGTGTTTTT CAAAAAGAAA TTCTCCCATG TTATGATGTG TGTGGTTGCT AAAAAGTAAA 240

SEQ ID NO:3970

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04695

SEQUENCE DESCRIPTION:

GATCCAGACT GGCCAGATTT GAACTCCAGC ACTATTCCTT GATACCTCTG AAACCTGGGA 60  
 CAAGTAACTT AGTCACTATG TATGAAAAGA GATAATAATA CTAGTACCTT CCTCATACTA 120  
 CAAGACTACA AGATGTGGTC AAGACCAGAA ATATATAAGC ACTGTAAAAA CAATGTAAAA 180  
 CCAATGNAA ATTCTTCATT TGTATCTNCC AAAAATAAAA AAATAGCTAT TTGGGAAA 238

SEQ ID NO:3971

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04696

SEQUENCE DESCRIPTION:

5 GATCAACCAG AAAAAAAAAA TATNATGAAA TGGATACACA CAGTGGACAC CTGTGAAGTT 60  
ATCTTAGCTC CCCCAAACT GAGANGTACA AATTAGTCTC CAAACCTAAT TACCAGTTTA 120  
CAGGAAACAT NGGGAATAAA AGANCAANTT AACAACACAA AGAAGCAAAC ANCCAANTGC 180  
ACAGTTTGGG AAATTCTGCA GAGGTAATGG CCTAGTTTTT TANCCAGTAC ATGTCAA 238

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SEQ ID NO:3972

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS04697

SEQUENCE DESCRIPTION:

20 GATCATAAAT GACAGGTGTG TGGAGGTCAT TGCAAAGGAA GGACAAAACC TGAAAGAGCT 60  
ATATTNGGTG TCCTGTAAAA TCACAGATTA TGGTAGGTAA TGANCCATTT NCCTAATCCT 120  
TTCTAAGANT AAAANGTTAC AAAATCATTG AAAGTNCTTA AAAGGAAATC AAGANCTATA 180  
TCATAGAGAC TGTCTATCGT CACTTATGCT CATNGTGACC NTACCAAANA NTAAAN 237

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SEQ ID NO:3973

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04698

SEQUENCE DESCRIPTION:

30 GATCGTAGAA GCCAAATGAA ATGTGACATA TCTACTGACT GATGACAAGG GAATTTTCATT 60  
AGGAAGAAGG TAAAGAAACA TCGTTGAGTA GCCTACCTTG ATTTCTGTCA AGTTCATAAC 120  
CAGCTTCATN CTTTAAAGG CTTCAGGTTT GAAATTAAGT CAACTGCATG CAGCTTTGCT 180  
GATAAATGAA TAATTCTCTT TGATGCCATT TATGAGAAAA GACTTCAATA TCTGTN 236

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SEQ ID NO:3974

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04699

SEQUENCE DESCRIPTION:

GATCTTCCAG TTTAGGAGCA ATTTGGTGAA AGGAGTCGGG TGACCAGAGC TGGAATAACC 60  
GTCTGCATGG CTGCACTCTG GTANCAGAGT GGNGACAGAN GTAAGGATAG TGTGGAGGGC 120  
ACAGTTGCAA GTTGAGTCTT TCCATGAGAC AATGTGCCAA AGTTAAAAA AAN 173

SEQ ID NO:3975

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04700

SEQUENCE DESCRIPTION:

GATCCCTAAA TAAGTAGTTA TTCTGTTTTT CCTGATTTTN AACTTTTACT AATAGAATGA 60  
GAGTAAATAT TTTTGGGTAT GTGGCTTCTT TTGTTCAACA TTGTTTTAAG ATTCATCCGT 120  
GTTGCTTG TG TAGCTGTAAT TTGTTTTAAT CTTTATAGTA CATTCAAGTT TGTNAATGCT 180  
TATTGTAGGA CTGTACCATA ATACAGGCAG CATGCTGCTG ATAAACTG GAAA 234

SEQ ID NO:3976

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04701

SEQUENCE DESCRIPTION:

GATCCTCCTG CCTCGGTCTC CCAAAGTNCT GGGATTGCAG GTCTTGGTCT TGATNCCAAG 60  
TTTGGGAAAG NAGTAAGAA GACATCCCAC TAGGAAGAGA GAGACTACCT CCACATCAAA 120  
AATATTTAAG TNATTATCTC AAACAGTGAC ATCTCTTGGG AAAATGGACT TAATAGGAAT 180  
ATGGGACTGA GTTCCAGTCT TTTTNAATAA AATAAAATCA AGCAANATCA TAAA 234

SEQ ID NO:3977

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04702

SEQUENCE DESCRIPTION:

GATCAACCCC GTGAAGGTGG CCAACCTGGT GAAGGCGTAC GTGGACAAGT ACAGGCACAT 60  
ANCNCAGGCA CANGAAACCA GAGGCCGGGG AGGAGCCGCC CACGCAGGGG GCCGAGGGCT 120  
GAGGCCAGGC AATCACGGGC TATGCCNGGG AGCTGTGCGG AGTGGCGGGA ATCGGGGCCA 180  
TGCCCGGGGA GCTGTGCGGA GTNGCGGGAA TNGGGGCCAT GCCCGGNGGA GCTN 234

SEQ ID NO:3978



SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04703

SEQUENCE DESCRIPTION:

GATCATCGCA TTGAAATGGT TTTGGGAAGT ATGGAAAATT AAATGGATTT TTGAGACACT 60  
 AGTTTATTGG CTATGCAAGT GACAGTTTGG AAAAAGGCTG AATCTTATTG TTGGAGCCTA 120  
 ATGTAAATGC ATATATAAAT TCTGACTGTA TTTCAGTCAG TGTTTTCTTG GAAAAATTCC 180  
 CAGATTGGAA GCAGAAAGTA CAGACCAAAT AAAGATTATT CACCCACCAA A 231

SEQ ID NO:3979

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04704

SEQUENCE DESCRIPTION:

GATCGTCTC ACTGGCCTGC TGCAGATNAG CCAGGGGGAG CCTAGGCCCA GCTCCTCCGC 60  
 GGTGCCCCC CCAGACCATA CCTCTGACCC ACCCAGCCCC CNNTGGTAGC CCCAGCAGTT 120  
 CTCAGGTGC TGACCTCTCT CTCCACAGA CCCCAGACAC CCATTGTCCA TAGCCTTCTN 180  
 AGGGCAGAGT GGGCTGGTTG TGTGACAAT AAAACAGTGT TGGTTTGCAA A 231

SEQ ID NO:3980

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04705

SEQUENCE DESCRIPTION:

GATCAAGTCT TGTCAGTTCG TGCCCTCTTT CCCCATGTTC CCTGGGAAGA CGGGTGGTGG 60  
 CAGAGTGAGA AGGCCACTGG TTCTGTGCCG CAGCACGCAA AATTTAGAAT TCTACAGACT 120  
 AGCTCTATAC GTAGTGAGGA CCCAGATTTA GAGAACTGA CCAATATTTA TCTCCGCATT 180  
 TGTGTGTGTG TCCAACCTCTG TAGGNCAATA AACCANCAAG ACAAATGAAC TGTGCTTCCA 240  
 AA 242

SEQ ID NO:3981

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04706

SEQUENCE DESCRIPTION:

GATCCACCTC TACACCAGCC CAGGAAGCCC CATCTGTGCC TGCCCTCAGG TGGTCCACCA 60  
 GTCTCCCCCT TTGGTTCCT TCCAGTCTNT TCCCCCTTC TATCCCAATN ACCAATAGAA 120  
 ATGCTAACAT CCCTGCCTGG TAGCCAGACT AGCCCACTAA AGCTCCCTG TAAATGGGGG 180  
 CTCCATTAGT TCTGCTGCCG AGACTAATAA ACGATTGGT TGGCTCTAAA 230

SEQ ID NO:3982

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04707

SEQUENCE DESCRIPTION:

GATCTATTCC CACATGANGT GCGCCACCGA CACGNAGAAC GTCAAATTTT TTTTCGACGC 60  
TGTCACCGAC ATCATCATCA AGGAGAACCT CAAAGACTGT GGCCTCTTNT NAGGCAGGGC 120  
CTGTNCTGCA GTCGGGGACA AGGAGCTTCC NTTTGGCAAG GCCGGGGCAC AATTTGCACT 180  
CCCTCAGCT AGACGCACAG ACTCAGCAAT AAACCTTTGC ATCAGGAAA 229

SEQ ID NO:3983

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04708

SEQUENCE DESCRIPTION:

GATCCTCCCT GCCCAAGTCT TACTTCGTGA GCTGGCCTTG CTCCCCATCC CCCAAGTGCC 60  
TCACCACTCC CCCAGACTGG GTGAAGGTAC AGCTGGCTCC TTTCGGGGGT GCAGCTTCAA 120  
CTCTCTCGGC GGTAGGGCGG TGCCATCCCC ACCCATAGGG CTGGCTCACA TCCAGTCACT 180  
CCCAACAGCG TCCANCACAC AAATAAAAGA CCCTTTGGCC CTGAAA 226

SEQ ID NO:3984

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04709

SEQUENCE DESCRIPTION:

GATCACTTGN GGTCAAGTCT NCGAGACCAN TCTGGTCAAC ATGGCAAAAC CCCGTCTCTG 60  
CTAAAAATGC AAAAATCAGC TGGGTGTAGT GGTGCGTNCC TGTAATCCCA GCTACTGGGA 120  
GCTGAGGCGA AAGAATTGCT TGAACCTGGA AGGTGGTAGG CTGCAGTNAG CCAGGATTGT 180  
GCCACTTCAC TCCAGCCCGG GCAACAGNGC AAGACTCTGT GTCAAA 226

SEQ ID NO:3985

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04710

SEQUENCE DESCRIPTION:

GATCCTGGGC CAAACTGATT TACTATTTTA AATTNAGTT TTAATGNGAC AGGGCCTTGC 60  
TATGTTGCAG GGTGGTGTG AACTCCTGGC CTCAAGCAAT CCTCTTGCCT CAGCTTGCCA 120  
AAATGCTGGC ATTACAGGCC TGAGCCACTG CCCCTGGTCT GATTTACAAT TTTNAATTGA 180  
GGGTAGGGA GTCATAATAC CANCAAAGAT GGTAAGGA ATTTN 225

SEQ ID NO:3986

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04711

5 SEQUENCE DESCRIPTION:

GATCATCCTC TAAACATTTT ATCATTTATT AATCCTCCCT GCCTGTGTCT ATTATTATAT 60  
TCATATCTCT ACGCTGCAAA ATTTGGGTCT CAATTTTAC TGTGCCTTG TTTTACTAG 120  
TGTCTGCTGT TGCAAAAAGA AGAAAACATT CTCTGCCTGA GTTTTAATTT TTGTCCAAAG 180  
10 TTAATTTTAA TCTATACAAT TAAAACCTTT TGCCTATCAA A 221

SEQ ID NO:3987

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS04712

SEQUENCE DESCRIPTION:

GATCATCATC TGTGAAGCAT CATGGTAGCT TCCAAGCATT TGCGGCCAC TGGCCAGNTG 60  
20 CATCCAAAAC ACATTCAGGA AACCCGAGAG TTGTAAGTTG CACATGTGTG GCCTACAGTG 120  
ACTTCCATGT AGTAACAGGG NTGNGCAAGG CANGNTCTCC ACCAGACTTA AAGCATTCAA 180  
CCACTCTGCC CCCAGGGCGA CACTGGNCAT GTGGTTCAAT N 221

SEQ ID NO:3988

25 SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04713

30 SEQUENCE DESCRIPTION:

GATCTTTTAA AGATNNNAAT AAAGAGCTTT CCTAAATAAA ATAAGCAATA TTAACTTTA 60  
GAAACTGTAC TCTATGAAAC GTGTTTTATG AAANCATCTN TTACAAAAAG TGCTTACTTA 120  
ACTCAGCAAG AAAGGTTTAA TGTACACATT TNACANCTAA ANTCAAAACC TACAAGAAAC 180  
35 TGCACTGCCT TCACTATTTA CAAATCGGCC TACAAGGAAA 220

SEQ ID NO:3989

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS04714

SEQUENCE DESCRIPTION:

GATCTGGCTA TCTCATTGAT TATATTTTTC TTCCCTTATA CTGCAAAGTA CATCATAGGT 60  
45 ATAATTTTAT TTTGAGAAAG AACTATATTC CAATTTTACC TATATATTCC TACTGTAATA 120  
ACCAAGAGGA CATTTCAAAA ATGTATATGC TACTATTTTC AGAAGGNTAT AGATACTAAA 180  
TCTTTTAAAG CCTTATTTAA CTATGTTTTA TATTGAAA 218

SEQ ID NO:3990

50 SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS04715

SEQUENCE DESCRIPTION:

GATCTGTTAA ATTGGATTTT ACATGTACAT TTGAATGCCA GAATTTCTAA ATAAATCCCC 60  
 TGGTTAGGAA ATTTAAAAG TCAAAGCTG TTTTCTTCAA CCACTACCTT CTACATTGGT 120  
 TGACTTAGAC CGTAAGCTTT TTAAGTTTCT CATTGTAATT TACCTTCTCA TGCAGATTGC 180  
 TGATGTTTTA TTAAACCTTA TTTTACAAA AATGAAA 217

SEQ ID NO:3991

SEQUENCE LENGTH:281

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04716

SEQUENCE DESCRIPTION:

GATCTTATTA GACTCATACA TCTAATTATA GAAATACATA GACTTGATAG AATTTNATTT 60  
 TCAGGCNTGA AGAAATATTC TTTGGAAGG CTAAATTTTT GGTGATTGAC ATAAAGATTT 120  
 ACTNGCTCAT ATTANCTNGG GGGGNTAGTA CTCTCCAAGA ATTAATGTGC CCTAAAAATT 180  
 TTCCTCCAAA ANCTTATCCT TATCATGTGA TAATGANGAN CATTGATTT CTTGAAAGGA 240  
 GACTGCTGTA GGCAGCATCT GGAATGCAA NTNNGGGGNN N 281

SEQ ID NO:3992

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04717

SEQUENCE DESCRIPTION:

GATCAGCCTG GGCAACATAG CCATAGTGAG ACACCAACTC TCTACAACAG CAAAACAAAA 60  
 CAAAACAAAA AAACATGCAG CTGGGCATGG TGGTNACACC TGTGGTCCTA GCTACTCAGG 120  
 AGGCTGAGGT GGGAGGATTG CTGGAGCTAG GATGTCAAGN TTAGTGANCG TATTGACCA 180  
 CTNACTCAGC TGGNAACAGA NGAGACCTGT CTAGAAA 217

SEQ ID NO:3993

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04718

SEQUENCE DESCRIPTION:

GATCATTTTT TGAGGCAGGA GCATAACACC TTCTCTAGGA TTTGTCAGCT TCTAAAAAGA 60  
 GCCTTTTGTA AGGACTTGTA TGAGCTTGGG TTTCACCATC ATTACTGGGG AGGCACTAAG 120  
 ACTGCACATA TCTCTGGGTG AAGTAATGTC TACACANCAC CTTTCATAGC AATAGTTCCC 180  
 AGCTAGCATA CCTGCTTCTG CCAGTCCAGG GCCAAA 216

SEQ ID NO:3994

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04719

SEQUENCE DESCRIPTION:

5 GATCCAGACT ATAATCCTGC TGACCCAGAG AGTGACTCAG CTGACTAATG GACTGTCCCC 60  
 ATCTGCAGAG AGGCTTGACT GCCACAGCAT CTGTGGCTAT GCTCAGAGGG TTATGATTTT 120  
 CCTTTCTTTT NNNTAAGAAA AAATTATTTT CAGGAGAATA TTCTTCTGAT AGCTTTCATC 180  
 ATTGAACCTA ATAAACTGAC CTTAAATTTT CAAATATAAA 220

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SEQ ID NO:3995

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS04720

SEQUENCE DESCRIPTION:

20 GATCTAAGGA AGAACTTGCT GCTGCAGTAT TGAAACTGTG AAGAACTGAC ATTTGAAGAA 60  
 AAATAGATTA CCGTTGCGGG ACTAGAATGG GCGACTGCTT GGAGCCAGTG CTGTGTTTTTA 120  
 TCTAGGACAC TTACTGTCCT GTGAAGTAGA ATACATTTAT CTGCATTTAG TTTGTAAATG 180  
 TCTGAAATGA ATAAAAAGAG GAAATTGCGA TTAAA 215

SEQ ID NO:3996

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25

CLONE:HUMGS04721

SEQUENCE DESCRIPTION:

30 GATCCAGAGA CAGAGGCAGC CTGTCTTTTC AGTTGGTTTC TGCTTTTAAT TTACTTGTAC 60  
 AATTCATTGT TACTGTTCTG TTTTTCCTAT TAATCTTTTG TCAACTTCCT GATTATGTAA 120  
 CAAAGTATGT ACAGTCTACT TTTGACCTAT TTTTATCACA GTATNATTNA TTNCTTCTTT 180  
 CAATAAAGTA CTNGNGCATA TTTCCACTGC CAAA 214

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SEQ ID NO:3997

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS04722

SEQUENCE DESCRIPTION:

45 GATCCGNAGT TCAAGGGAAG AGGAAGTTGC CTCTNAGCTC CATCTCTCTG CGCTGCTAGA 60  
 CATGGTGGAC ATTTGAGCAG CCTGACCTGT GGGGAGGGGG TCTCTCCCGA AGAGTTTCTG 120  
 TTTTACTCA AAATAATGTT ATTCTCAGAT GCTTGATGCA CTGTTGGAAA NGGGGATTAA 180  
 TTAAATCATG CAGATAAACC ATTTAAATGT CAAA 214

SEQ ID NO:3998

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

CLONE:HUMGS04723

SEQUENCE DESCRIPTION:

GATCGAAACC AGCCTGGTCA ACATGGTAAA ACACTGTCCC TACTAAAAAT ACAGAAATNA 60  
GCCAGCAATA CAAAAATTGG CAGCTGTAGT CCCAACTACT TGGNAGGCTG AAGCACAAGA 120  
ATCGCTTGAN CCCAGGAGGT GGGAGGTTGC AGTGAGCTGA GATTGCGCCA CTGCACTCCA 180  
GCCTGGGCGA CAAAGCGAGA CTCTGTCTCA AA 212

SEQ ID NO:3999

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04724

SEQUENCE DESCRIPTION:

GATCTCAGNA ATTGGAAAAA TTGTCCTGTC TGTCACCTTGT TTTGTTGCCT TAATAAGCAT 60  
CTGAATGTTT GGTGTGGGG CGGGTTCTGA AGCGATGAGA GAAATGCCCG TATTAGGAGG 120  
ATTACTTGAG CCTGGAGGT CAAAGCTGAG GTGAGCCATG ATTACTCCAC TGCACTCCAG 180  
CCTGGGCAAC AGAGCCAGGC CCTGTATCAA A 211

SEQ ID NO:4000

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04725

SEQUENCE DESCRIPTION:

GATCAAGGCT ATGAACATCT TGTGAAGTAG GATGTTAAGT CTGCAAATAT CAGAGTGAAT 60  
CCAAACTTAT CAATTCAACA CTGGATTGTA AAACAGCTCA AAAAAAGACT AAAACACAG 120  
CTCTACACTT TAGGAGGTTG GGGCAGGCAG ATTGCTCGAG CTCAGGAGTG GGAGACAAGT 180  
TTAGGAAACA TGAAAAAACC CTGTCTCAA 210

SEQ ID NO:4001

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04728

SEQUENCE DESCRIPTION:

GATCAGCATT CATACCATAG TAACTGATGT TGAAAACAGC ACAAATAAAC CAGAAGTTGA 60  
AAATGGCAAT AACATGCTAA AAATTTGCAA GTCAATTTGA NNACACTTGT CCAAATCTTG 120  
ATTTTTTTTC CTTCTCTATC GTTCCCCCCC CACCACCAGC TTTATGGAGG TATAATTAGC 180  
AAATAAAAAG TATACATATT TAAGGTAAA 209

SEQ ID NO:4002

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04729

## SEQUENCE DESCRIPTION:

GATCCTATGA ATTAATTCAG AAAGCAACTA AAATAACAAT GGCCTGCCAA ATGTCATTTT 60  
 GTAAATATAC GTCTATGACT TTAGGAGCTG TCCTGGTTTG AAAACATGAG GACAGTTTAT 120  
 CCATTGGATG CCATCTATNT AGTCCCAATT AAGAAAGTTG TTTTTTTGTG AGAATGACCA 180  
 AGGTAAATTT AAATATACCA TTCAAACAN 209

SEQ ID NO:4003

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04730

## SEQUENCE DESCRIPTION:

GATCGATGAA GCACTTTTTT ATTAATATTT TCCTTTGTGA AAGGAGGAAC CGTAACTCTC 60  
 CATAGCTGTA CATATAACCC TTTTCTCCTA AAGAGGAGTC AGTCAGTGCT CCTATATTTT 120  
 TCATTTTTTG TCAAAGCAAG AAGTAAATAC TTTAGAATTG TTAAATATAT AAATAAAGCA 180  
 AATAAAGTTG AGTGTCCAC ATGGTAAA 208

SEQ ID NO:4004

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04732

## SEQUENCE DESCRIPTION:

GATCTTTCCA CATACTACT ATTGTATTGT TCAAAATTCA TAGAAATNAC TTGCAATATA 60  
 TTGATTTAAG CCTTATGTAG TGA CTGTTGC TATATTTAAA GTAGCATTTT NAGTTTGCTG 120  
 TTTTTCCTCA CTGCTTAATC CTACAAAAAC CAGCCATCTG CCTAAAAAAT AAAAGAGCAA 180  
 AANTGNATCA GTGCAACCGG TATACGN 207

SEQ ID NO:4005

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04733

## SEQUENCE DESCRIPTION:

GATCCACATC TCAAAGAAGT GGGACTTCAC CAAGGTNCAA TGCTGATGAA TTTGAACNCA 60  
 TGGTGGCTGA AAAGGGGCTC ATCCCANGAT GGCTGTGGGG CAAGTCATCC CAGTCGTGGC 120  
 CTATGGCAAG TNNNGGCCT NACTCATGAG GGCTTCAATG TGCTGCCCCC TCTTAATACT 180  
 CACCAATAAA TTCTACTTCT GTCCAAA 207

SEQ ID NO:4006

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04734

## SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTACATT ATTACAGCAGC CTCGAAAATG TTAAGCCTGG ATTTAAAACA CAGCCGTCTG 60  
GCCAGCTGCC TCGAATATCT GACAGCTTAG CAAAAGGGC CANAGCTTTC CATAGGCGTG 120  
CTGCACTTGC TTGGTAAATT AAGCAGCTTT TGTATCTTCC CCTTTGACTT TAGGTAATAA 180  
AGCATCCAAA CTTGTAAATC TGAAA 205

SEQ ID NO:4007

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04735

SEQUENCE DESCRIPTION:

GATCTGGGAT AAAACCAGAC TGAAAGGAAT ACCTCAGAAG AGATGCTTCA TTGAGTGTTT 60  
ATTAAACCAC ACATGTATTT TGTATTTATT TTACATTTAA ATTCCCACAG CAAATAGAAA 120  
ATAATTTATC ATACTTGTAC AATTAAGTGA AGAATTGATA ATAAGTGAAT GTGAAACATC 180  
AATAAGACC ACTTAATGCA CAAA 204

SEQ ID NO:4008

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04736

SEQUENCE DESCRIPTION:

GATCTNCTTT TTATCACTAT AGTTTGTATT CCTAGAATTG TATATAAATG GAATCCAACG 60  
GGCACAGTGA CACATGCCTG TAGTTCCAGC TACTTGAGAG GCTGAGGTGG GAGGATTCCT 120  
TCAGCCCAGT TCAAGGCTGC AATGAGCTAT GACCACGCCT ATGCACTNCA GCCTGGGCAA 180  
TATAACAAGA CCCTATATCT AAA 203

SEQ ID NO:4009

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04737

SEQUENCE DESCRIPTION:

GATCTGAAAA GAATTTNTAT TTAAATTGGG TTGAGGGAGA GTAGATACAA TGAAACCTTA 60  
AATTTAGCT TTNATTCTAA ACCCTTTAAT TTTTATGGG TTATGTTTTA CTTGGCAAAA 120  
CTATCTGTGT TTCTNTCTTA GTGATATAGC ACCCTTAAAG TAACTTGAGT GGTAAAGGAA 180  
ATAAAATACA CCAGTTTTCA AA 202

SEQ ID NO:4010

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04738

SEQUENCE DESCRIPTION:

GATCCTCTTC CTGCTCCAGT TGCTGGCCGA CCACGTCCCT GGCCTTGGCC TGGTCACAAG 60



5 GCGGCTCATG GATTACTTGC CCACCTGGCA GAAAATCTAC TTCTACAGTT GGGGCTGACA 120  
GACCTCCCGG AAGGAGGGTG TGGGGAGGGG TGGGGCAGGG AGCCCTCTT CCCTAATAAA 180  
ACTGACTCCG GCAGCGTCAA A 201

SEQ ID NO:4011

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

10 TOPOLOGY:linear

CLONE:HUMGS04739

SEQUENCE DESCRIPTION:

15 GATCCTATTT GTACAAAAA ATGTAAACT TAAAATTGCA CAAAATTTGT NACCTGTACC 60  
AGCTTTTAGA ACTGTTTATC TTATCCTCCT CAGTGATACA TCATGAAGTT GTGTGCTTTG 120  
CCTAAATGC CCAGTTACCT GAAATTGTAT AAATNCTTGC CAAAAGTGT TGAACCTAAT 180  
ACAAACTTCC CATCTCTTAA A 201

SEQ ID NO:4012

20 SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04740

25 SEQUENCE DESCRIPTION:

GATCTCATTT TATTAGCAT CAGCTCAAGA AACTNAAGTC TTAGTGCACA GTATCACAAC 60  
AAAGAAAAAG CTTGTTTTT ATAAGTGGTA AAAACAAGAA AAGATTCTCA TCAAAATGAA 120  
AATATAAAT TAATCATTTT TCACCAAAGA GTATGCCTGG GAGCCTCCAG CTGTAAAAAG 180  
NCAATGCTAT TACTACTTCT N 201

30 SEQ ID NO:4013

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS04741

SEQUENCE DESCRIPTION:

40 GATCCAAGTT GCCCTTGGGG TATAAACTT GACAGCAGAG GCGGTCAGG GTCCCTCAGC 60  
TGCAGTGTGA AGTGGGACAC ACAGGTGAGA CTCCATCTGC CCTGGGCAGG TTCCTGAGCC 120  
TTNGGGGACC AGTTCACCCT ACATCCCAGG CTTCTGTTGT CCCTGCCTG CCTGTAAGGA 180  
ATAAAGTTGC TTTGCTTAAA 200

45 SEQ ID NO:4014

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04742

50 SEQUENCE DESCRIPTION:

GATCTGACCT TTTCTTCAGA TACATAAGCA TTATTTTCTC TGTTTAGGTC CAAGGAAAAA 60  
CAAAAGGTAA AGGNAATAAA GGAATATAC ATAAGGCAAA CATTTCTCTT TTTTTTTTGC 120

ATTATATCTT ACCAATTAAT TAAATTGTGG CCTTTGTTAT TATAAATGTA ATGATTCATT 180  
AAACTATATT ATGTAATAAA 200

5 SEQ ID NO:4015  
SEQUENCE LENGTH:200  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS04743  
SEQUENCE DESCRIPTION:  
GATCCTATGA CTGACATCAA CTAAAATTTA AAAGAAGAGG AAGACTCAGT TGGGAAATTT 60  
TNCCATGAGG AAAATGTGCT TTGGTGCAAG GTACAAGGCC CACACCCTCT CTGAGAGATA 120  
CTATGATTAA AAAAGCTTTA TATCTTGGGA TTTTNCACAA CTGATAATGT GCAAAGNTAT 180  
15 AAACNGATTA ACTTGTCAAA 200

SEQ ID NO:4016  
SEQUENCE LENGTH:200  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04744

SEQUENCE DESCRIPTION:  
25 GATCTTTCAA GAATGAACCA AGGNTTTTTA AAAGAATTAT AGGAAACACT TCATTCTTTA 60  
TAAAACTTTC TATAATGCCT TATTTGAATG TTAATCTTAT GTGCTTTCTA AAAAATGTTG 120  
TGAAATACCA AACTTATGGA TTATCACTAG GTTATCAAGC ATATATNAGT CTTTATCAGA 180  
NTAAAATGAA ATTNCATAAA 200

30 SEQ ID NO:4017  
SEQUENCE LENGTH:199  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04745

SEQUENCE DESCRIPTION:  
35 GATCTGAGAG GCAGTAAAGC AGTGATGAAG ACAGTGCAGC AGAACATTGA AGTCCTGATT 60  
GCAGCAGTGA CTCTGCAACC TTGGATAAAT TATTTCAATC TTTATTTTGT AAAACGGAGA 120  
TAACGGCCTA TAGGATTNTN AAGACTGANT ATTTTAAAAG NGCTTAGAAT GGTGCCTGAC 180  
40 AAATGAGNNN CANTAAATN 199

SEQ ID NO:4018  
SEQUENCE LENGTH:199  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04746

SEQUENCE DESCRIPTION:  
45 GATCATGTGA TTTCTATTTT TNCCCCACAG GGTAAGGGAC GAGTCTTCTG GAAGGCTCTG 60  
CCATGGACAT TTGTCCTCGG GCTCAGAGGC CCCACCCTGC CCCACACCTG CCCCTAATCA 120  
50 CTGCAGTGTC CAGCCCAGTG TTGAACAGAT TGTAGCGTTC TGTCTCATTG CGAGCAAATA 180

55

AATAGACTTT CATTGGAAA

199

SEQ ID NO:4019

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04747

SEQUENCE DESCRIPTION:

GATCACGCGG CATGTATTGA GGTGTGGCAT GCAGCATTTT GGAAGGAAAA TTGAAGACGT 60  
GTTCAAGAAA ACATGAACAG AAGCAAATNA TGAAAATGAG CATTTTACTT GATGTTGATA 120  
ACATCACAAT AAATTATGGA GAAAAATACA TATTTGGCTA ACTTTTAATT GCTGANCAAT 180  
AAAGTGTTTT CTTTTAAA 198

SEQ ID NO:4020

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04748

SEQUENCE DESCRIPTION:

GATCCCTACC GCCAGCTGCG AGAGAAGGAC CCCAAGTACA GTGCTCTCCG CCAGAATTTT 60  
TTCCGCTACC ATGGGCTGTC CTCTCTTTC AATCTGGGCT GCGTCCTGAG CAATGGGCTC 120  
TGTCTCNCCT GCCTTGCCCT GGAAATAAGG AGCCTCTAGC ATGGGCCCTG CATGCTAATA 180  
AATGCTTCTT CAGAAA 196

SEQ ID NO:4021

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04750

SEQUENCE DESCRIPTION:

GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTNAATC TTGCTCATTC TGAAATTTAA 60  
GCATTTTCT TTTAAAGAC AAGTGTAATA GACATCTAAA ATTCCACTCC TCATAGAGCT 120  
TTTAAATGG TTTCATTGGA TATAGGCCTT AAGAAATCAC TATAAATGC AAATAAAGTT 180  
ACTCAAATCT GTGAAA 196

SEQ ID NO:4022

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04751

SEQUENCE DESCRIPTION:

GATCTGGTTC CAGGGGAAAA AAATAGCTGG TTGGTGTCTA GCCCCCAAC ACTTTTGTCT 60  
GTTGTGTATA AAAGAAGAAA GACTGGCATG TACCTTCATT TGCTTAGCTA TTTGAGTATC 120  
TAGAGAAAAA TTAATGCA ATGAGTTAGC AGTATACCCT GGCACACTTA ATAAATTAAT 180  
CATTTGTGGA GCAAA 195

SEQ ID NO:4023

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04752

SEQUENCE DESCRIPTION:

GATCTAGAAG CTGGTAAAAA TGACAATATC AATCACATTA GGGGAACCAT TGTGTCTTC 60  
 ACTTAATCCA TTTAGCACTA TTAAAAATAA GCACACCAAG TTATATGACT AATATAACTT 120  
 GAAAATTTT TATACTGAGG GGTGGTGAT AACTCTTGAG GATGTAATGC ATTANTAAAA 180  
 ATCAACTCAT CAAA 194

SEQ ID NO:4024

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04753

SEQUENCE DESCRIPTION:

GATCCAACAG CAACACCATT TTAAATTAT TGTGAAAAGA TTAAGTGGCA ATGTACAGAG 60  
 TTTACTCAAA GCCCTTCTTA AGGGAAAACA CTACAAAAAG TCACAAGGAT ACCAAATGGA 120  
 AACACATGAT GATGCCTCTG GGTCTGTATG AGACCGTGAT GAAGTAGAAA TAAAGCCCTT 180  
 CTGAGATGGC AAA 193

SEQ ID NO:4025

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04754

SEQUENCE DESCRIPTION:

GATCCACGGT GGGCTCCAGC TGCCAAGNCA CCCAAGGGAG TCTGGGCCCT AGGCCTAGCC 60  
 CCATCCCTCC CCATGAGGGG CCAAGACACT GCCTAAGGTG TGGGAGGGAC TGGCTGAGAT 120  
 TGCAGCCCAT GGTAGGAGCT GGACCAACTG TATATAGTTT TCAATAAACT TTTTCCTTTT 180  
 CTGTTCTCAA A 191

SEQ ID NO:4026

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04755

SEQUENCE DESCRIPTION:

GATCCAGGAA GTTGGTGAAC CATCTAAAGA AGAGAAGGCT GTGGCCAAGT ATCTTCGATT 60  
 CAACTGTCCA ACAAAGTCCA CCAATATNAT GGGTCACCGG GTTGATTATT TNATTGCTTC 120  
 AAAAGCAGTG GACTGTCTNT TGGATTCAAA GTGGGCAAAG GCCAAGAAAAG GNGAGGAAAGC 180  
 TTTATTTACA NCCAGGGAGT CTNTGGTTGA CTACTGCAAC CAGGCTTTTA AAGTAGCAGT 240  
 TTNTTTCACC GAGCCCTAAA GGTN 264

SEQ ID NO:4027

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04756

SEQUENCE DESCRIPTION:

GATCTTCACA TATTTTATAT GNATATATAT ATCAAGAAGT TATATATATA TAACTCAAGA 60  
 AACTCAAGTT ATATATATAT GTCAAGAAAT GTATGATTAT TTTGGAGAGA ATGGGCCCAA 120  
 ATGTGAAAAA GATATAAAAA AAACAAAAAA AACNNAAAAA AAACCNCTNT TTNCCCCTNC 180  
 GNANTN 186

SEQ ID NO:4028

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04757

SEQUENCE DESCRIPTION:

GATCTGGAAG TCACCTCCT CTGGCCACG GAAAATTTTG GTAATCTTCT AGGTTCTAAA 60  
 ATGAAGATGT ATGGGTACTC TGGCAGACTG CATGTTGTAT AATTGAAAA ATACTAAAAG 120  
 TGGAAAATAA AATTGAATTA AACTTTGAAA 150

SEQ ID NO:4029

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04758

SEQUENCE DESCRIPTION:

GATCAACAAG TTCAAAACAC TGCTAAGTCT AAATCTAAAA CAGACCAAGA GTACCTTCAT 60  
 TTAANTTTAG CTTGCACAGA GCTTGATGCC TATCCTNCAT TCTTNCAGA AGTAAAGATA 120  
 ATTATGGCAC TTATGCCAAA NTTCATTATT TAATAANGTT TTAATTGAGG TAACATTACT 180  
 GATTTN 186

SEQ ID NO:4030

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04759

SEQUENCE DESCRIPTION:

GATCCAACAC AGAGACAATA GAAACATTGG GATTGAAGAG ATTCTTGGGA CTGTAAAAAT 60  
 CCCAAGAATA TGGGATTGTA AAAACCTGT CATCTTACTG CTATGATAGA TGAAGATTTT 120  
 GCTTGCCTAT ACCTTGTCG TATTCCTCTC TTCCTTTCCT CCAAATATAC TTGTAGGTAT 180  
 AAA 183

SEQ ID NO:4031

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04760

SEQUENCE DESCRIPTION:

GATCTAGCAT TTAAATTTCT AGCATTGCTA TTCACGGGCT TCCTTATTTT ATATGTAAAA 60  
ATTAAGATTT TATATTTAAT CTTCTTGTTT CTCATAGATA TTTTGTGAGC ATTTTNTTGT 120  
TTATTTTGAA GAAATGTGGA TAAGATACTT GGTAGTATAA AACAGNCTCT CTGAGAGTAT 180  
TTN 183

SEQ ID NO:4032

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04761

SEQUENCE DESCRIPTION:

GATCAAGGTC TGTATATTAT CCCAAACTTT ATTAAGAATT GTTTTCTAAT TNGTTATAAC 60  
ATTTTNAAT TAATAGTTTC AAAACAAATT GTTAATACAA CTGTATAAAA TGAACATAAT 120  
TTTCCTCACT TGTATTTTGG TTATTGAGCA AGTTTATCAA AATAAATNGT CTAATAAAGA 180  
AA 182

SEQ ID NO:4033

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04762

SEQUENCE DESCRIPTION:

GATCTCTTAT CAATTAGCAC TCACTAATGT ACTACTAATT GAGCAACCTA CGCACTCAGT 60  
TGACTACGTA AATCTGTCAG GTCTTTTGTG ATTTCTCTG ATGCAGGAGA GGAAAAATTG 120  
TAATTGATGA AAATAATGAA TGAAAAATCAA CAGATGAATA AATGGTTCTT TATAAGTGAA 180  
A 181

SEQ ID NO:4034

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04763

SEQUENCE DESCRIPTION:

GATCTGGAGT CCCACGTTCC CCAAGGCCAG CGGGATGTGT GCCCCCCTC CTCCCAACTC 60  
ATCTTTCAGG AACACGAGGA TTCTTGCTTT CTGGAAAAGT GTCCCAGCTT AGGGATAAGT 120  
GTCTAGCACA GAATGGGGCA CACATTAGGT GCTTAATAAA TGCTGGATGG ATGCAGGAAA 180

SEQ ID NO:4035

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04764

SEQUENCE DESCRIPTION:

5 GATCCTGTTT GTACAAAGTC TTGCTTTTAT AAGGTTTCAA TAATATCTAA AACAACACAT 60  
TAAAAAGCTG AGACCATTTT ATGAAGATAA TTGTTTGTA TCATAGGTGT TGAAAGTAAA 120  
AAGGTGCCAT CTTGTGGTAT TGACTTGTAT TTATAACAAA TAAACTGCTC AAGAGACAAA 180

10 SEQ ID NO:4036

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04765

15 SEQUENCE DESCRIPTION:

GATCCTGGTT ACAGCCATTT TGTGTGATTC ACTTCGGGGG TTAAGTAATG CAGGATTCTG 60  
CAAACAAGGT GTCGCCGTCC AAATGTACTG TCCTGGCATA GAGAGCACTG CTTTGTTTTC 120  
CACTGTTGTA GAGAAAACTA GGGAGAACTT TATTTTTC AA TAAACTTTTC TTGTGTGAAA 180

20 SEQ ID NO:4037

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS04766

SEQUENCE DESCRIPTION:

GATCATGTAT AAAAAGAAAA AAAAGAAGTC ATGCTNTGTG GCCAATTATA ATTNTTNCA 60  
AAGACTTTGT CACAAAAC TG TCTATATTAG ACATTTTGGA GGGACCAGGA AATGTAAGAC 120  
30 ACCAAATCCT CCATCTNTNC AGTGTGCCTG ATGTCACCTN ATGATTTGCT GTTACTNN 178

SEQ ID NO:4038

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS04767

SEQUENCE DESCRIPTION:

GATCAGGATT TGGGAAAATT GTGGTCAATA TTTGATTTTC CTTTCTGTT TGATAGCCTT 60  
40 ATCTAAATTC CCCTAGCTTG AATGTAGTAA ATATGAGTGT GTAAAAATGT GTATCTAATT 120  
CACCTCTTNG GGGAGGTTTA ATGTAACAT AAATAAAAAAT TCTTCCCCA GGTTAAA 177

SEQ ID NO:4039

45 SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04768

SEQUENCE DESCRIPTION:

50 GATCTTACCT CCTAACCAAC TCCATACATC ATGACCAATG GCTCAGTCCA AGCNGTCATC 60  
TCTTGCTTGG TCACTGCAGG TACTTGCTAA CTTTCTTCCC AATAATCCAA CCCCCACAGA 120

55

GCAGCCAGAG TAGCCTTTTT TTGTTTTGTT TTGTTTTGTT TTGTTTTGTT TTGTN 175

SEQ ID NO:4040

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04769

SEQUENCE DESCRIPTION:

GATCTTAATA GCTAAAATAT GAAAAATATT TGGNAAGTCT GAAATNAGGT CTCCTGGCCC 60

TGGTGTGCCC TTAATGCCTG TNACAGTTGG CCTCTGTGAA TATTGGTATA ATTNTAAATA 120

ATGTCAAACCT CCATTTTNTA GCAAGTATTA ATAATTAAGG GAAGTATGTC TGAAA 175

SEQ ID NO:4041

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04770

SEQUENCE DESCRIPTION:

GATCCTCAGG ATATGCAGGG CTCAAGAGAA ATGAAATATC TTGGGGATAT GGTACTTAA 60

GACGTGATAC TGTCACAGTG AATTCACAG AAGATGGTGC TGCCCTAACT GAGGTTCAAT 120

CCATGTATAA GCCAGACCAA TCTGAAGACA AATAAAGTAT TTCACAGCCA CAAA 174

SEQ ID NO:4042

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04771

SEQUENCE DESCRIPTION:

GATCTTCAAA CATTAACCTA AGCAGACCAA AAATTCTGAT GACCGCATCT AGATTATTTT 60

TTTATAAAAA TGATTTTCAC TATAGCTATG TTACGCTAAG CTAAGTGTCCA ATCTCTTGTTG 120

ATGTGTAACCT TTTACATGTG AATATTAAAG TAGATTTCTC TGTCTTGTA A 171

SEQ ID NO:4043

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04772

SEQUENCE DESCRIPTION:

GATCTTTAAA GATGTGCTAA ATGACTTTTT TGGCCAAAGG CTTAGTTGTG AAAAATATAA 60

TTTTTAAATT ATACATTCAA GGTAGTGGCC AAATGTAACA CATCAATCAT GGAATGATTN 120

CTCTGCTAAC AGCCGCTGT ATGTTTCAAT NAATTTGTCC AAAGCTCAAA 170

SEQ ID NO:4044

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid



TOPOLOGY:linear

CLONE:HUMGS04773

SEQUENCE DESCRIPTION:

5 GATCCTTCCC AGTGGACAGA TGAAGAATTA GGTATCCCTC CTGATGATGA AGACTGAAGN 60  
 TGTAGACTCA GCCTCACTCT GTACAAGAGC CAGGTGAGAA TTTCAAGGAT TATCGACTTC 120  
 ATATTGCACA TTAAAGTTAC AAATTAAAGT GGCTTGGTCA AGAATGAAA 169

10 SEQ ID NO:4045

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04774

15 SEQUENCE DESCRIPTION:  
 GATCTAGTGT GTAGTGAGCT CAGTATAGAG GACAGAGCTT TCATCATGTA AATTNATATG 60  
 CAAAGCCAAA TNAACGTGG TGTGTACTTC CTA CTACTGATGC GTCAGGGTAT AGGCCTCTTT 120  
 TTCTGCCATT CAAATAATGG AAGTTAATTA AATTTTAAAC AAATGTAAA 169

20 SEQ ID NO:4046

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS04775

SEQUENCE DESCRIPTION:

30 GATCCATACT GAAAAAATNC TGAGCCAGCC ATCTTTGGCA AAGNNCCCTG AGCTCTTGCT 60  
 ATCTCTCAAG AGTGCTGAGA NCCACGGTGA AAGTNCTGCT CTAGGCCAC AAGTGTA ACT 120  
 ATGCTGT TAA CAGCTGTCAA TAGATAATTA AAATTCATAC TGTATGAAA 169

35 SEQ ID NO:4047

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04776

SEQUENCE DESCRIPTION:

40 GATCTCTGTT CTNGNTTGAA TGTATTTAAT TTCCAGCAGA ATGAGCCCCA TTCCTTATTT 60  
 TGATTGGCCA TTTATCATGT ACATATGGTG AAATGCCTAT TCGTGA CTTA GCCAATGTTG 120  
 TTTCTTTTTC TTA CTGATTA CTACAGTACA TTTTATATG AAAGCAAA 168

45 SEQ ID NO:4048

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04777

50 SEQUENCE DESCRIPTION:

GATCTGCTGA AGCATCTGTC CAGCTGGTAT CCTGTGAAAG TTTGTAATTT NCTGAGTAGA 60  
 CATTCTTATA GAGTATTGTC TTTAAAATCA GATTGTCTCT NCTATATTGA AAGCATTTNN 120

55

ATGTTTNCNA ATTTAAAAAT TAATATTTCC TTATAGATAT TGTGCAATAA AGCTGAAGTA 180  
 GAATGTGTGG TTTTGGCAA TNCTTTAGCG GN 212

5

SEQ ID NO:4049  
 SEQUENCE LENGTH:167  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

10

CLONE:HUMGS04778

SEQUENCE DESCRIPTION:

GATCTTGTCT CACAAAATAA ATTAATAAGA TTTTAAATA GCAGGTTTCT AAAACAATGA 60  
 GAAAGACAGC ATTACATATC AGTGTCTACA ATTTAAACAA AGCTATACTT AGAAGTAAAT 120  
 TCATTGTCTT AACTGCTTTT GTTCCAATAA AACAAAATAG CAGGAAA 167

15

SEQ ID NO:4050

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear

CLONE:HUMGS04779

SEQUENCE DESCRIPTION:

GATCGTACT ATGTGTCAA GGGTTTGAG AACATTGATT AAGGAAGCAT NTTCTGATT 60  
 GATGAAAAA ATAACCTAGT TATGGCCATC TACCCCTGCT AGAAGGTTAC AGTGTATTAT 120  
 GTAGCATGCA ATGTGTTATG TAGTGCTTAA TAAAAATAA ATGAAAAAA TGCAA 176

25

SEQ ID NO:4051

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear

CLONE:HUMGS04780

SEQUENCE DESCRIPTION:

GATCTATAAC TGTACTTTGC CTGGCGCTGT GCGAAGGTCA GAAAACTTAC TGCTAGTACC 60  
 TAGAAACACA CAAGGCTGCC CAGCCAAATC TTAATGTAA GTAGCTAGAG CCATGGAAGT 120  
 ACAGTATGAA TAAAAAGAA AAANGTATTG ANCTTCAAAT TCTAAA 166

35

SEQ ID NO:4052

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

40

TOPOLOGY:linear

CLONE:HUMGS04781

SEQUENCE DESCRIPTION:

GATCTTGTA GTAGGAAAGC TGTAACAAA AATTGTATTG TTTGCTTATT AGCCATGTAT 60  
 CTCTAAAAT TTTGTTATGT TTACAACGAT GTACCTTATT GGCAACAAGT TATTAGTTTG 120  
 ATGTTAACA ATAGTGCCTT TAGTAAATNA TTTTACAACT AAA 163

45

50

SEQ ID NO:4053

SEQUENCE LENGTH:162

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04782

SEQUENCE DESCRIPTION:

GATCCAAAAG CTGGCTNTCT AACCACCAGC CAAGGGCTCT CTTACCACC AAGCCAACTC 60  
TCAGGGCAGC AGCAATGTGT ACCTTATTAA CCTCTGCACC CNAGGTCCTA GCACAGGGCT 120  
NGTCCATAAC AGGCGNCCAA TAAACATGTG TCATAATCTA AA 162

SEQ ID NO:4054

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04783

SEQUENCE DESCRIPTION:

GATCCCTGGT CCTGCCGACA CGCAGCTACT GAGAAGACCA AAAGAGGTGT GTGTNTGTCT 60  
ATGTGTGTGT TTCAGCACTT TGTAATAGC AAGAAGCTGT ACAGATTCTA GTTAATGTTG 120  
TGAATAACAT CAATTAATGT AACTAGTTAA TTACTATGAA A 161

SEQ ID NO:4055

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04784

SEQUENCE DESCRIPTION:

GATCGGCACC ACACCAGACA TAATCCTGGA CGACTTGCTG GAGACGGACC GCGTCACCGC 60  
CCACTTCTAG CCCCGTGGAT GCCGTCACCA CCAGCACACG GAACTACCTC CCACCCCTT 120  
TTTGTACAAA ACACAAGGAA AAACATTTTT TGCTTGAAA 159

SEQ ID NO:4056

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04785

SEQUENCE DESCRIPTION:

GATCTAATTC TTTTGATAAA GTTCTAGCTC TAAAAGTGAT AGTGGGACTG TATGTTTTCT 60  
GATACTGGTG GCTTATGTTA TTAANCCTTT TTTAAAAAAG GTCCACTCTA AAGGCTGANN 120  
NCCACCCTAN GTTCCAGCC TCCTGGCCTC NACCNGGGN 159

SEQ ID NO:4057

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04786

SEQUENCE DESCRIPTION:

GATCTTGTGT TCTTTGTGCC AATATGAAAA GGAGAGGGTT GGTTCTTTCC TTTATTGTTG 60

AATGCTCCCA TTTAATGCTT TATGGCTTTT ACTGTATTAC TTTTITAGAC TCCCGTCTGC 120  
 AAAAAATGCA ATAAAAATAA TTTTATTATA CCCTTAAA 158

5 SEQ ID NO:4058  
 SEQUENCE LENGTH:158  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04787

10 SEQUENCE DESCRIPTION:  
 GATCACACTG GGGAAAAGTG ACAGAACCAA ATTTCAAACCT CCAGTCTTTC TGCTTCTAGA 60  
 GATTGAACTA CTAACATCTG CATTATATAA AATTAAGTNT CTCAAGGTAG TTTGTGAACG 120  
 TAACATACAA ATAAGTGATT AAAATTTTNG GTGATAAA 158

15 SEQ ID NO:4059  
 SEQUENCE LENGTH:308  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04788

20 SEQUENCE DESCRIPTION:  
 GATCCCAAGT GATTAAAATA GGGTTTCTGA ATGGATGTTG AATGGCGTGG ACTCGCTACT 60  
 CCGTTCTTCA CAGCTGCCTT CCAGAATGTG TTCAAAAGAA AGACAAGAAG GAGTGTATGG 120  
 25 CTTATAAAGT GAATCTAATA CAGTATTTGT TGCATTTAAA CAAACTAGAC ATTTTCTTAC 180  
 GGAAAANTTA TGAAATACAG CATATTTNAT GTNCTCCCAT TGAATCAATC ATGACAATAT 240  
 TTCTGCTTTA ACACCATCTT TCATGATTAG NAATGTTTGT NATTGGAAT GTTACACCAT 300  
 GTAAATAN 308

30 SEQ ID NO:4060  
 SEQUENCE LENGTH:155  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04789

35 SEQUENCE DESCRIPTION:  
 GATCAGCCCC AGATTTGACG TGAATCAAA GACCTGGAAA AATGGCAGAA TAATCTGCTT 60  
 CCATCCCGCC AGTTTGTTT CATTGTACCT GACCACCCTC ACNGGCAANC ATGGACCCAT 120  
 40 GAAGNAGCAA NNCGGAAACN CACNAGAGGG AAAAN 155

45 SEQ ID NO:4061  
 SEQUENCE LENGTH:155  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04790

50 SEQUENCE DESCRIPTION:  
 GATCTCATTG GTATGTTTTT TAATGTGTAG AATTAACACT TAAAAATAAA CAGGTGTGAA 60  
 AATTATAAAG GAATATATAT GACAATTATT TNCTGTACAT TAATGTCTAA ACATTATACT 120  
 TACTTTTCCA TAATAAAGGA AATTTTGGAA CCAAA 155

SEQ ID NO:4062

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04791

SEQUENCE DESCRIPTION:

GATCTTAAAA CCCAAGACAT TATATTTGAA GGGGCACAGC AAACAGTGCA AGAAAATCTG 60  
CTGATGGAAG ATNATTTTNA TCAGTCCTCA GANCCAGAAA CTATAAACT GGAAGGAAA 120  
GTTTAAATAA AGANTTTATT TCCAAATTCA GCAAA 155

SEQ ID NO:4063

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04792

SEQUENCE DESCRIPTION:

GATCTAAGNA GGATTCAACA CCTTTNTTGT GTTGCTCAGT GTGTAATGAC TGAGATTTGT 60  
AAATCTTTGT GAACATTCTG TACTGGTCC CAAGAGCTAT TCATTCCCTG CTACCTGATT 120  
TCAGCACAAAT AAATATACTT CTGCTGTGGG AAA 153

SEQ ID NO:4064

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04793

SEQUENCE DESCRIPTION:

GATCTTAGCT GTATGGAGTA ACTATTTTCTAG AAAACCCTAT AAGAAGTTCA TTTTCTTTCA 60  
AAAGTAACAG TATATTATTT GTACAGTGTA GTATACAAAC CATTATGATT TATGCTACTT 120  
AAAAATATTA AAATAGAGTG GTCTGTGTGA AA 152

SEQ ID NO:4065

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04794

SEQUENCE DESCRIPTION:

GATCAGAGAA GGCTGAAGAA GGTGGAGAAA CTNAGGCACA AAAAGAGGGC AGTGAAGATG 60  
CGGGCAACCT CCCTGAAGCC CAGGAGAAGA ATGAAGAAGA AGGAGAGACA GCCACAGAAG 120  
AGACGGAAGA AATAGCCATG GAGGGTGCN 149

SEQ ID NO:4066

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04795

SEQUENCE DESCRIPTION:

5 GATCAACTAT GGGTTTATAT AAATNCCAAA TTTAGTACAA CAAATTTAGG TCATCAGGTG 60  
 AATACAAGTA TTTTTTTAA CAGGNAACAT TTTATTATAN NAAAAATATT AATGATAAAC 120  
 GCATATTGGT TGA AAAATAT TTTTAAACN 149

SEQ ID NO:4067

10 SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04796

SEQUENCE DESCRIPTION:

15 GATCTCTGTG ACCCATACCC TATTTNTACA CTCCTCCCC TTTTGAAAAT CACTAATAAA 60  
 AAATTTNCTG GTTTTATGGC TCAGGGGGCA TCACAGAACC TGCCAACATG TGATGTCTGC 120  
 CCTGGACACC CAGCTTTAAA ATTTCAAA 148

20 SEQ ID NO:4068

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04797

SEQUENCE DESCRIPTION:

25 GATCATTTTC TTGGGACCTT GAACTGTGAA TGTTTTGTCC TAACCATTTA ATATTTTCTA 60  
 GGTACTTGCT GCAAGTNCTT GAACTATTTT ACCAGCTTTA ACTTTGGGGC TCTTAGNTTC 120  
 TNTNCTCCAG ATTCTTGTTA TNNNATN 147

30 SEQ ID NO:4069

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04798

SEQUENCE DESCRIPTION:

35 GATCAGAGAA GCAGATATTG ATTGAGACGG ACAAGTCAAC TATGAAGAAT TCGNACAGAT 60  
 GATGACTGCA AAATGGAAGA CCTACTTTCA ACTCCTTTT CCCCCTCTA GAAGAATCAA 120  
 40 ATTGAATCTT TTA CTNACCT CTTGCAAA 148

SEQ ID NO:4070

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04799

SEQUENCE DESCRIPTION:

50 GATCTTTTAC AACTGGTGA CCCTGAGAGA GGAGGGAGGA GGGAACCTGG CGGGGGTGTC 60  
 TGAGGCCGCA-CTGTCAGCTG GCCGGTCCAA GCCTGTGGCT GGAGCTGGGG TCTGTTTACC 120  
 TAATAAAGTC CCACAGGTGC CTCATTAAT 149

EP 0 679 716 A1

SEQ ID NO:4071

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04800

SEQUENCE DESCRIPTION:

GATCCCTTC AAGTCTCTCT GACCTTTCTT CTGCCCTCCA GCCTGGGTGA CAGAGCTAGA 60  
GTCTGTCTCA AATAATAATA ATAATACAAT AAATAAATAA ATAAATAAAT AAATAAATAA 120  
ATAAATAAAG TACGCTTTCC ATTAAA 146

SEQ ID NO:4072

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04801

SEQUENCE DESCRIPTION:

GATCTCATAG AGCCCAGTTC TTAGAGTCAA CTAAAGAGTT GATAGGAATT TACTAGGTCC 60  
AGGGAGAAAA GGCAGTGGTT GGGGTACTG GAAATTTTGC TCATTTTCTC TAATGACTGT 120  
ATGAATAAAA GTGAACTTAC TTGAAA 146

SEQ ID NO:4073

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04802

SEQUENCE DESCRIPTION:

GATCTGAACT TACAGACAGT TGCCAAATTT CTCTAGATAA GAAAATAAAG AATAGAGGGA 60  
ACCTAACTGG ATAACAAAA AAAAGGAGAG AGAAAAATGC CATTGCAGTT AAAGGTTATT 120  
AAATAAAGCT TAGTGCAAT GTCAAA 146

SEQ ID NO:4074

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04803

SEQUENCE DESCRIPTION:

GATCAGGAGG GACCACAAGG ACAGGAGAAT TAGCAACGAG AGACTGGCTG GCACCAGTNT 60  
TGGGAAAACT TCAGAGTGAG CTCCATTCAT GGTCTATTAA AAGGCCTTN TTGTCATTCA 120  
GTGATATGTG NCTGGCCCCT GAGAAA 146

SEQ ID NO:4075

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04804

SEQUENCE DESCRIPTION:

5 GATCAAAAAA TTATTTTAT TTATCCTAGC TTTACGTGCA TCTCACGGAA ACAGGATACA 60  
CGGTGTATAT ATTATNATGC AGTTCGTTGG AACTAGAATT TCAAAAAATT TTAATAAATA 120  
TGTTTAATCT GTTGCCTCTG GAAA 144

SEQ ID NO:4076

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04805

SEQUENCE DESCRIPTION:

15 GATCACTGGG CCTACCTGCA CTGTGGGGCC AAGCCCTGTC TTTTCCCAA GCCCTCAAGC 60  
ACACGCATGA ATGTTTCATCC CGACTTGGTA GGGGGCTTTT CACCCTTACA AGATGGCAAA 120  
AGATTCACAT TGCTTTTTTT AAA 143

SEQ ID NO:4077

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04806

SEQUENCE DESCRIPTION:

25 GATCTGTCTAT NNTTTAGCAG TCAAGTGGGA TGGGCATTAT ATAAACAACG TTACAATGTA 60  
AGGAAAATCT NTAAGNGAT GGGGAGAGAA AAAGGCAGCT GGTATAATCG GTTACTGCTG 120  
CTTAGTTCTA CTTAATTTN NNN 143

SEQ ID NO:4078

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04808

SEQUENCE DESCRIPTION:

35 GATCTGCCTC TCAGGAAAAA GTACTAACTT GTTCTTTTGG TTCCTGGCTT TCATCAGTTT 60  
GTGAGATTTC TCTATTTT TTAATATAA TTTTATTCTT TTCAACAAAT ATAAATAAAA 120  
AAACAACTTT GGNNCANTGA AA 142

SEQ ID NO:4079

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04809

SEQUENCE DESCRIPTION:

50 GATCCTGGCT AACCCTNGCC TATTTAGATT CCTTCCTCTC ACCTGGACCT TCCCATTTCA 60  
ATCATGCAGA TGGTTTCTTT TTGTAAAGAG TTCCGTTTGC CTTTCAATTT TTAGAGAAAA 120  
TAAAGACTGC ATTCATCTCA AA 142



SEQ ID NO:4080

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04810

SEQUENCE DESCRIPTION:

GATCTTCTTC TCTCTTGTC ACCTATTAAT TGTTTACAAT ATTTGTTACA TCTTATGCAA 60  
 AATACTTGAN TGGGCCATGG TGCCTTTTTT CCTTGTNAGT ATTTAATTAA AAATGAATTG 120  
 TTGTGCATTT GCAATGTAA A 141

SEQ ID NO:4081

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04811

SEQUENCE DESCRIPTION:

GATCCCGTTT TCCCCATGAC AATGTTGTAG TGTCCCCAC CCCCACCCC CAGGCCTTGG 60  
 TGCCTCTTGT ATCCCTAGTG CTCCATAGTT TGGCATTGTC ACGGTTTCGA AGTCATTAAA 120  
 CTGGTTAGAC GTGTCTCAA 140

SEQ ID NO:4082

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04812

SEQUENCE DESCRIPTION:

GATCTGTGCA GCAAACCACC ATGGCACAGG TTTATCTATG GAACAAACCT GCACATCCTG 60  
 CACGTGTACC CCTGAAATTA AAGTAAAAAT TGGAAATAAA ACATTTAAAA AGAAAAGAAA 120  
 ACAACAACA ACAACAAA 138

SEQ ID NO:4083

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04813

SEQUENCE DESCRIPTION:

GATCTATCAA AGGAAAAGGA AACTGAGACC GAAAACTTAG GGTCTAAGTT GTTCTAAACC 60  
 CAGGGTTCTC AAATGTGTTG TACAAAAAGT TTCATGTAAT AAAATTAAGC AAATAAAACA 120  
 AATGAATAGA GGTCCAAA 138

SEQ ID NO:4084

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04814

SEQUENCE DESCRIPTION:

GATCACAATG TCATTTCCTA ATACAAGGCA GGATATGTGG GAAGAATATG TACAATTATT 60  
 5 TGATTAAAAT TATTCCAC TGACCTAAAC TTTAGTGAT TTGTGGGAAA AATAAATAAA 120  
 TGTCTACAC CAAGAAA 137

SEQ ID NO:4085

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04815

SEQUENCE DESCRIPTION:

GATCCACTGC CTCAGCCTCC CAAAGTGCTG GGATTATAGA CATTATGAT GAATTCTTAT 60  
 15 TTTANNNNTA ATATAAGCA AATACAATTA TTGTAGATA ACAATGCACA AAATAAAATT 120  
 CAAGGGTGAA AAATAAA 137

SEQ ID NO:4086

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04816

SEQUENCE DESCRIPTION:

GATCCATGCC TGTAAGTCAA GCTACTCAGG AGTCCGAGGC ACAAGAATTG CTTGAACCTG 60  
 25 GGAGGCAGAG GTCACAGTGA ACCATGTTCT GTCAGTGCAC TACATCCTGG GTGACAGAGC 120  
 GAGACTCCAT CTCAA 136

SEQ ID NO:4087

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04817

SEQUENCE DESCRIPTION:

GATCTGGTCC CTGTAGCACA GAGGTCCGAA GAACCGCCTT CAGAAAGAGG AGGCATATTT 60  
 35 GGAAAGTATG GGAAAGACTT TNTGGACAAG GATGGAGAAC ACTTTGGAAA ATTGCATTGT 120  
 40 GCCAAGAGAC AACAAN 136

SEQ ID NO:4088

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04818

SEQUENCE DESCRIPTION:

GATCTACAAC ACCTGCCAGT GACCCCTGCC CAAGGCCTAC CCCAGTTCCT AGCACTGCCC 60  
 50 CACATGCATG TCTGCCTATG CACTGAAGAG CTCTGGCCC GGCAGGCCAC CAATAAACCA 120  
 GTGTGAACCC CCAAA 135

SEQ ID NO:4089

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04819

SEQUENCE DESCRIPTION:

GATCTGCTGA CAGTGAGTAG TATTTTGTTC TAGGATGTTG TGACTTAGCA AAAATAATAC 60  
AGATGTCTTC CCCCTTTTG TAGCTTTGAC AATTGAATT AGATTTCAAA TAAATCTGA 120  
ACAGAAACT AAA 133

SEQ ID NO:4090

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04820

SEQUENCE DESCRIPTION:

GATCCTTACA TATGCCATCC TTCTGTGTCA TTTGTGGCT GTTCTGTGTT TTTCTTCTA 60  
GTTATTATT ATTGTTAATA ACTTACTTTT TCTTACATTC TGTTGTAAAT AAAATACAAA 120  
GCAATCTTCA AA 132

SEQ ID NO:4091

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04821

SEQUENCE DESCRIPTION:

GATCAACAG AGGCATGCTA AGATATATTG GGGCTTGAAG CAAAGGGAAA ACTATTGTGTT 60  
GCTATATGTT TGTAGGGATT TTTTGCCAGT TTTAAAAATA CATGTATCAT AAAGTTTACT 120  
ATCTCAGCCA AA 132

SEQ ID NO:4092

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04822

SEQUENCE DESCRIPTION:

GATCAGTGGG GGAGGGCACC TCAGCAACCT CTGAGTGTGG ACAATAGCTG CTTTCTTCTC 60  
TATCCAAGAG CACCAGGCTG TGCTTGNTC CTTGCTCTCA GAGTCTATAA ATAAAAGAAT 120  
ATAATGATTA AA 132

SEQ ID NO:4093

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04823

SEQUENCE DESCRIPTION:

5 GATCGGGGGT GGGATGGGAT GGAGTGAGCC CCATCCAGTT AGTTGGACTA GTTTTAAATA 60  
AAGGTTTTTC GGTGTGTGTT TTTTGAACC ATACTGTTTA GTAAAATAAA TACAATGAAT 120  
GTTGAGTAAA 130

SEQ ID NO:4094

10 SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04824

SEQUENCE DESCRIPTION:

15 GATCACAGAG GGAGGAGCTC TGAGAACAGT CTCCTTCAAC AGCTCGGCCA AGCAGAACTG 60  
CTGTACCTCT GACCACTTGT GTTAGGAAAA CTATCGGCTC CCTGTATAAT AAATCAAGCC 120  
AGGTCAAA 128

20 SEQ ID NO:4095

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04826

SEQUENCE DESCRIPTION:

25 GATCTTTGCC TTAAGCTTG AATATTTGGC TTAAANTTTG TNCATATGAA TACTGTAAAA 60  
GGTATATTTN ACTACATTTT GAAAGGAAAA AGGTAGTCCT GCTAAAATTG ACATTAGGG 120  
ATANN 126

30 SEQ ID NO:4096

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04827

SEQUENCE DESCRIPTION:

35 GATCTGAAAT TCTGAGATAT CAATCTAGGA ATTTCAAAAG AAACAGATTA TAGAATTTAA 60  
AACTTAACAC CNGTCTTGTA TTAAGAGAAG TCAACATTTT AAATAAAACC TTGTTCTTAC 120  
40 CAAA 124

SEQ ID NO:4097

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04828

SEQUENCE DESCRIPTION:

50 GATCTCAGAA CTGTGCCAAG CAGACACTGG GACAAAGGGA GAATATCTTG CTCCCTCCT 60  
GAGTCAGCCT GGTGTTGCCC TTTATTCCCC TTATGTGCAT ATGATTAAAG AGTTATTTT 120  
AAA 123

EP 0 679 716 A1

SEQ ID NO:4098

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04829

SEQUENCE DESCRIPTION:

GATCCTACAA ACAGACATTT TCCACTCGTG TTTCCATAGT TGTAAAGTGT ATCAGATGTG 60  
TTGGGCATGT GAATCTCCAA GTGCCTGTNT AATAAATAAA GTATCTTTAT TTCATTGATA 120  
AA 122

SEQ ID NO:4099

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04830

SEQUENCE DESCRIPTION:

GATCTTCTCG CCTCAGCCTC CTGAGTAGCT GGAGCTACAG GTGTGAGCTA CCCAGCATGG 60  
CTCATTTGAG ATTTCTGAGT AGAGAAAGTAA CATGATTAAA CTTGGGTATT GAGATTATAA 120  
A 121

SEQ ID NO:4100

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04831

SEQUENCE DESCRIPTION:

GATCAATCTC TCCCTCAGCT TTCTTTCCTA CTTTTCGAGC TTTGCTGGCT TTAACTGCT 60  
TCATTCTTCT GCTTCATTGG TATCCTTTTT TCTTTTGAAA TAAAAACATG AAATACTTAA 120  
A 121

SEQ ID NO:4101

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04832

SEQUENCE DESCRIPTION:

GATCGACTGA GTCCAGAAAG TCAAGGCTGC AGAGAGCCAC ATTCACTGCA CTCCAGCATN 60  
GNTGNCAGAG GNAGACCCTG TCTCAAAAAA AAAAGAAAAA AGAAAAAGTG ACAATGNCAA 120  
A 121

SEQ ID NO:4102

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS04833

SEQUENCE DESCRIPTION:

5 GATCGGTAGG GGGCCTGCTC CTCGGACTCT GGTACCTCT AAGGCTGGGA AAGGCCTGGT 60  
TGCCCACTGC NTCNTCCCT GCCCTCCTT TNATGTCCAT AAAGTGGCGT GAAGTGAAA 119

SEQ ID NO:4103

SEQUENCE LENGTH:116

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04834

SEQUENCE DESCRIPTION:

15 GATCACCCTT AAATCNGNGT TGGGAAAATA TCAATTAAC TGGACTCTCTG GTTTGAATTC 60  
TCAATATGTA TCTTAATATG AAATAGCTCA TTAATACTTC ATGTGTAAT ATTAATA 116

SEQ ID NO:4104

SEQUENCE LENGTH:115

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04835

SEQUENCE DESCRIPTION:

25 GATCTGGGTG GTAGTTACTG GGTGTGTTCT CTTGTGATA CTCTCTCGAG ATGTACACTT 60  
AGGATTGCA ATCTTTTCTG TAAAATATT CAATAAAGA CATTTATTTT TTAAA 115

SEQ ID NO:4105

SEQUENCE LENGTH:115

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04836

SEQUENCE DESCRIPTION:

35 GATCTTAGCT AAATCTCGGT AGATGTCATT ACAACCTNGA AAATAAATCA CCCTAAGTGA 60  
CACAAATTGA AGCATGTACA AATTATACAT AATAAAGTGT TTTAATAAT TGAAA 115

SEQ ID NO:4106

SEQUENCE LENGTH:115

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04837

SEQUENCE DESCRIPTION:

45 GATCCTNCAC CTCTGGNAA TTAAATGTG TGGTCACTGG GGAAAGCCTG AGTTTGCAAC 60  
CAGTTGTAGG GTTCTGTTG TGTTTTTTT TTTTAAATA AAAAAANTN NAATN 115

SEQ ID NO:4107

SEQUENCE LENGTH:115

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS04838

SEQUENCE DESCRIPTION:

5 GATCAGACAA GGAATGAAGC AATGNCTGTG GGCTGGGAAA CTGTACCTAC CTCTCTNCCC 60  
ACTGCAAAATN NCTGGGATAG ACCAAAAGTG AATTTAATTA TGTNTTGGCT GAAGN 115

SEQ ID NO:4108

SEQUENCE LENGTH:115

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04839

SEQUENCE DESCRIPTION:

15 GATCCCAACT TGAAACAACA GCCAGTGCCT GTGGTAACTT AANNTNTTGT CAAATACTTT 60  
TATTGATTGG TTTATATGCC ATTNTTGTTA TAGAAGAATA TGCCTTTTAA AAANN 115

SEQ ID NO:4109

SEQUENCE LENGTH:112

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04840

SEQUENCE DESCRIPTION:

25 GATCAGCTCC GTGGGACTGA TATTGGTCCA CANCANAACA GGCAGTGCCT CCTTCCCTCT 60  
GGGGAATGCA AAAGAAANCA TGGATTAAGN GAGAAGGGAG ACTCTCAGCN TN 112

SEQ ID NO:4110

SEQUENCE LENGTH:111

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04841

SEQUENCE DESCRIPTION:

35 GATCGCCCAA TAAACATTCC CTTGGATGTA GTCTGAGGCC CCTTAACTCA TCTGTTATCC 60  
TGCTAGCTGT AGAAATGTAT CCTGATAAAC ATTAAACACT GTAATCTTAA A 111

SEQ ID NO:4111

SEQUENCE LENGTH:111

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04842

SEQUENCE DESCRIPTION:

45 GATCGGCATA TGCATATCAA AAACAGCTCC CAGCTCTGTA AGGCATTAGA GTGAAAGCAN 60  
ANAATTTTTT AATGAAACAT TTATTTGCCT TCTTTTACTG CAGTGCTNNN N 111

SEQ ID NO:4112

SEQUENCE LENGTH:111

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS04843

SEQUENCE DESCRIPTION:

5 GATCATACTN CTTTATCTAG AGNTTGTCT CAGCTTGAG AGNTTGAGGA GAAGATAGAC 60  
CAGTTACATC AAGAACAAGC TTTCTCTGAC TTTAATATGT TTNCNGAACT N 111

SEQ ID NO:4113

SEQUENCE LENGTH:110

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04844

SEQUENCE DESCRIPTION:

15 GATCACAGTG CAGATAATTA CCTCACACCT GTTAGGATGG CTTTCACCAA AAAGACAAAA 60  
GATACGTGTA GGCAAGGATG TGGAGGAAAG AGAACTCTTG TATACGTAAA 110

SEQ ID NO:4114

SEQUENCE LENGTH:110

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04845

SEQUENCE DESCRIPTION:

25 GATCTTAGTC CGTTTTTTTT TTATATATTG TAACGTAAA TGAAAAAGA ACCCCCCTNN 60  
TGTATTATAG TCATGCGGTC TTATGTATGA TAAACAGTTG AATAATTAAA 110

SEQ ID NO:4115

SEQUENCE LENGTH:110

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04846

SEQUENCE DESCRIPTION:

35 GATCTGGGAC TTCCAGAAAA CAGAACTNTN AAAANACAAG TTTCTTTTGT TTAAACCACC 60  
CAATCTNAAG TATTTTTTNA TGGCAGTCCT GGCAGACTA ATACAATATN 110

SEQ ID NO:4116

SEQUENCE LENGTH:109

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04847

SEQUENCE DESCRIPTION:

45 GATCTATCAT AAAAAGCAAT GTCTTCTCTG GAATGGGGCT TCAGTTTCCA CATTACAAT 60  
TAGTACATAT TACAATTAGT GATATGAATA AAGGCTGTTA TCCTACAAA 109

SEQ ID NO:4117

SEQUENCE LENGTH:109

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS04848

SEQUENCE DESCRIPTION:

5 GATCAAAACA GGTGACAGTG AAGTGGTTTC GGCCCTGCCA ATCTGATATC GTGTATGTAT 60  
GAGAGTGGTC AGCATTTTAC CACTGGTAAC AAGTTCCTN CTGTNCAAA 109

SEQ ID NO:4118

SEQUENCE LENGTH:109

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04850

SEQUENCE DESCRIPTION:

15 GATCTATATA ATTTATGTAT CACCTTCATT GTAAATTTAG CAGGAAATGC ATCACAATTA 60  
TNATTTTTTT TTTTGNACC AGTGAAACAA TAAAGATGCT ATTACCAA 109

SEQ ID NO:4119

SEQUENCE LENGTH:107

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04851

SEQUENCE DESCRIPTION:

25 GATCATGTTG CTGGCTTTTA TAAACTCTAA GCGAAGGAGG AGCACTGCCT CAGCCTTTGC 60  
ACATGGTAAT GAAGCACTGT TTTTAAATAA AAGAGAGAAA CACCAAA 107

SEQ ID NO:4120

SEQUENCE LENGTH:118

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04852

SEQUENCE DESCRIPTION:

35 GATCCGTGAG GCGGTGANTT GGA CTGGTACC CACTGCTGAT TCCCTGCACC TAGCACAGTG 60  
CTTGCCACAA AGTGGGCTCT CAATAAATAT TATTTGTCCA AGGAAGGAAT GAATGAAA 118

SEQ ID NO:4121

SEQUENCE LENGTH:108

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04853

SEQUENCE DESCRIPTION:

45 GATCGTCTGA GCCCCNCGGG CACTGGGTGG GGCAGAGCAC GAGTTATTTA AAACAGTTAC 60  
ACTGCAGGT TTCGCCAAT AAAGGTGGAC TGACATTCCC TCTTCAA 108

SEQ ID NO:4122

SEQUENCE LENGTH:107

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS04854

SEQUENCE DESCRIPTION:

5 GATCTTTTAT ACTCAGNTTN AAACACTTTA CTTGGGTTTA CCAAGCCTCA ACTGGCATAC 60  
CATAAACANG CCACANGGAC CGTTCCTGCA GGCCCAACCC ACAGGGN 107

SEQ ID NO:4123

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04855

SEQUENCE DESCRIPTION:

10 GATCCGGAAC CCACTTTTTT ATTCCTCCC CATCGTCGTT TGGCCNTTCC ATCNNTCTTT 60  
15 NTCTTTCCT CTGCCATCCG TGACACTGAT AGTTNGTCAT ATAAATN 107

SEQ ID NO:4124

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04856

SEQUENCE DESCRIPTION:

20 GATCTCCAAT CTCCTCGGTT GCAACACCTG AATAAAGCCT TCTTCCCTCA CAATACTTGN 60  
25 NNNCTCAGTG ATTGGCTTAC TGTGCAGTGA GCAACCTAGA CCAANN 106

SEQ ID NO:4125

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04859

SEQUENCE DESCRIPTION:

30 GATCAAAATC ACGTTTGTAG TATCATATCA AAAATTCTAA CCTGTTTACA TTGTTTTNAT 60  
35 GTTCATGTTT CTATGTTATT AAAATATTAT TTTGTACTTA AA 102

SEQ ID NO:4126

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04860

SEQUENCE DESCRIPTION:

40 GATCTACGGC AATGTGAATC ATTCAGATGT TTACAATAAA AAACACCACA TGAGTAAATG 60  
45 AATTCATAA TGTTAATGTT AAACCTCATG GAAAGNNNNN N 101

SEQ ID NO:4127

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS04861

SEQUENCE DESCRIPTION:

5 GATCCCCCT CAGGACAAAT CTACTCCAGC CACGATGAGA AGTGGGTGAG CCAGGGTCTG 60  
AGTTTCACAT TTGAACCAA TAAATGCTG TCAAGAGAAA 100

SEQ ID NO:4128

SEQUENCE LENGTH:97

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04862

SEQUENCE DESCRIPTION:

15 GATCATGCCA TTGCACTGCA CCTGGGCAAC AAGAGTGAAA CTCCTCTTA AAAAATATAA 60  
GAAATAAAAA AATAAAACC TGTCCCAGA CTGAAA 97

SEQ ID NO:4129

SEQUENCE LENGTH:97

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04863

SEQUENCE DESCRIPTION:

25 GATCCTGAGC TAGGAGAGTA CATTTTGCAG ACCTTTGGTT TCCATATTAA GAAATTCAGA 60  
TTTTNATGTA CAATAAGAA GTTCTGGAAT TCTCAA 97

SEQ ID NO:4130

SEQUENCE LENGTH:96

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04864

SEQUENCE DESCRIPTION:

35 GATCTCTNTN CAGCCCTAAA GCTCCTTGGT TCTGTAATTC CACCAATAGC CCATTTCAAA 60  
AATAATTCTA CAGTAATCAG TGGGACTCCT GTTTNN 96

SEQ ID NO:4131

SEQUENCE LENGTH:95

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04865

SEQUENCE DESCRIPTION:

45 GATCACACCA CTGCACTCAA GCCTTGGCAT CAGAGTGAGA CTCTGTCTCA GTAAAAAAA 60  
AATAAATAAA TAAAAATGTT TAATTAACCA TGAAA 95

SEQ ID NO:4132

SEQUENCE LENGTH:95

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

EP 0 679 716 A1

CLONE:HUMGS04866

SEQUENCE DESCRIPTION:

GATCGTAGGG CATCAGAAAA AAAAAAGAA ATAGAGAGAG TAAAAGAGAA GCAACAGAAA 60  
GAACTCAATA AACAAAAACA GATTGAAAAG GTAAA 95

SEQ ID NO:4133

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04867

SEQUENCE DESCRIPTION:

GATCTTTATT GTTCCTCACC CCATTTTCCT CCTTGTGTAT GTACTTCCCC CACCCCCTT 60  
TTTTTAAGTA AAATGTAAAT TCAATCTGCT CTAAGAAA 98

SEQ ID NO:4134

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04868

SEQUENCE DESCRIPTION:

GATCTAATAA GTATTGGAAT GCTTCCTATT TGCTGATAGA AGTACCAAAT AGTATTATTG 60  
AAGTCTAACA AAGACTTTTT GTTGAGAACA CAAA 94

SEQ ID NO:4135

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04869

SEQUENCE DESCRIPTION:

GATCGAGGTA AGAGGGACTT TNTTAAAGGC CTAGTCTATG GGATGGGGCG GCGGAGGGAA 60  
TTTTTTGAGA AATAAAATGA AGCTGCAGTG TAAA 94

SEQ ID NO:4136

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04870

SEQUENCE DESCRIPTION:

GATCACACCG CAGACATTTA GATTTTTATA CCCAAGGCAC TTAAAAAAA TGTTTTATAA 60  
ATAGAGAATA AATTGAATTC TTGTTCCATA AA 92

SEQ ID NO:4137

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS04872

SEQUENCE DESCRIPTION:

5 GATCTTACT GATGCACTCA TGACAAGTAC CCAATGTATT TTAGCTATTT TAGTAGTATT 60  
TGTTCATAAA ATACGCAAGC TGTAAGGTAA A 91

SEQ ID NO:4138

SEQUENCE LENGTH:91

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04873

SEQUENCE DESCRIPTION:

15 GATCTGCTTT TCTGCATGTT TGTCTGTGTG TCTGCGTTGT GTGTGATTTT CATGGAAAAA 60  
TAAAATGCAA ATGCACTCAT CACAACTAA A 91

SEQ ID NO:4139

SEQUENCE LENGTH:90

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04874

SEQUENCE DESCRIPTION:

25 GATCAAAAAA AATAAATCAC AATGGTATTT AGAAAATATT TTTCAGTAA GGCTAACAAA 60  
AACTACATA TTAATAATTAT AAAATGCAAA 90

SEQ ID NO:4140

SEQUENCE LENGTH:90

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04875

SEQUENCE DESCRIPTION:

35 GATCTTTTGA TGTGCACTAA TGCCATTATT GGTAATGCCG GTTATTGGTG AATACAGCAT 60  
AGTTAAATAA ACTGTTACAG TAAATCTAAA 90

SEQ ID NO:4141

SEQUENCE LENGTH:89

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04877

SEQUENCE DESCRIPTION:

45 GATCTAGGGC AAACCTGTCC AACTGTTGGC CCATGGAACA GCTTTGAATG CAGCCCAACA 60  
CAAATCTATA AATTTNCTTA AACATTAAA 89

SEQ ID NO:4142

SEQUENCE LENGTH:88

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS04878

SEQUENCE DESCRIPTION:

GATCAGTCTC ATGGGCCATC TCTTCCTCAG ATGTAAATAA TATCTGGTTA AGTGTTATAT 60  
GGAATAAAGT GGACATTTTA AACTAAA 88

SEQ ID NO:4143

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04879

SEQUENCE DESCRIPTION:

GATCTCAGTG ATGTTTGAAC CTTCTGTGTA ACTTTTATT AAGTCTTTGT ATCTCTCGAC 60  
TGATTAATAA AGAAGAGAAA CACGTAAA 88

SEQ ID NO:4144

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04881

SEQUENCE DESCRIPTION:

GATCTTTATT GGTGACCTTT TGTAAGACAT TAGTTTGAGG TACTACCTAT GTACTTGAAA 60  
ATAATAAAGT GGCATTTCTT TATGAAA 87

SEQ ID NO:4145

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04882

SEQUENCE DESCRIPTION:

GATCCACTTT GTACTCCTAC CAGTAGGAAC GGTCTTCTAA CAGAGAAGAT TATAGCAAAA 60  
AATAAAATCT CTTCTTAATT CCCAAA 86

SEQ ID NO:4146

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04883

SEQUENCE DESCRIPTION:

GATCCAAAGT CCAGCTCTCT CACTGAAGCC TTATCTTTCG GAAAGCTTCC AACAGTAACT 60  
CAGGAATTNA GCTTACTTGC TTAAAA 86

SEQ ID NO:4147

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS04884

SEQUENCE DESCRIPTION:

5 GATCTAAAGA AGAAGGTTCA GTTTTCAAAC AGAATTTAGA GAAAATATAA AGAAATAATT 60  
TCTTGCTCTCA AAAGGCCAAA GTAAA 85

SEQ ID NO:4148

SEQUENCE LENGTH:84

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04885

SEQUENCE DESCRIPTION:

15 GATCCAGCTG TGCCTAAAGC CTGCCCTACC TCCGGACTTT AAAGTTTGT GAGCCAATAA 60  
AGTCCCTTTC TTGTTTAAGA TAAA 84

SEQ ID NO:4149

SEQUENCE LENGTH:84

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04886

SEQUENCE DESCRIPTION:

25 GATCTGAAAA GGCATTAATT TATGTACTAA TTCTATAAAC ATGTATTAAT AATTGCAGTA 60  
TTATTAAATA CAGATGGACT CAAA 84

SEQ ID NO:4150

SEQUENCE LENGTH:83

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04887

SEQUENCE DESCRIPTION:

35 GATCAGGCCC CCCAACTCTC CAGAACAGGC TACAAACATG CAAATTAGAA TTCTTTTAAT 60  
ATAAAAAAAAA GTACTAAAAT AAA 83

SEQ ID NO:4151

SEQUENCE LENGTH:83

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04888

SEQUENCE DESCRIPTION:

45 GATCAGAGGG NAGTACAGAA NCCCTGAACT AAAGCNTTAA GTACATACCA TACAGCAAAT 60  
AAATGGTAGC AAAACATTCT AAA 83

SEQ ID NO:4152

SEQUENCE LENGTH:83

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS04889

SEQUENCE DESCRIPTION:

5 GATCTAAAT TTGTAATATT TTTGTCATGA ACTGTACTAC TCCTAATTAT TGTAATGTAA 60  
TAAAAATAGT TACAGTNACT AAA 83

SEQ ID NO:4153

SEQUENCE LENGTH:81

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04890

SEQUENCE DESCRIPTION:

15 GATCAGATGG TTCCTACCA AATNACCCTC AAATAAGCCA GATGAAAATT TGAAGAAAAA 60  
GGTCACCCAG TTCTCTGGAA A 81

SEQ ID NO:4154

SEQUENCE LENGTH:81

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04891

SEQUENCE DESCRIPTION:

25 GATCAGAGCG TAGTTTTAAN TGTATTTTGT ATACACTTGT GAAATATTTT ATAGAAATAA 60  
AAATTTTAC TTAGGAGCAA A 81

SEQ ID NO:4155

SEQUENCE LENGTH:81

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04892

SEQUENCE DESCRIPTION:

35 GATCCTTCCT CCCACCCTAN GCCTTCCTTT CCTCTTCCT CCTCACTCTC CCCGTCATGC 60  
TCCCTCTGCC CNGNCCTCAA A 81

SEQ ID NO:4156

SEQUENCE LENGTH:80

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04893

SEQUENCE DESCRIPTION:

45 GATCCAAANT AGTAACNTT TNTNATGAAC TGTACTACTC CTAATTATTG TAATGTAATA 60  
AAAATAGTTA CAGTGACAAA 80

SEQ ID NO:4157

SEQUENCE LENGTH:79

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS04894

SEQUENCE DESCRIPTION:

GATCATTAGT CAATTGCTTT AATTATAAGC CCTGTTTTTT TTAAATCTA AAAACTAATA 60  
AACATCTATA AGAATTAAA 79

SEQ ID NO:4158

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04895

SEQUENCE DESCRIPTION:

GATCNACTGT CAAAAAGAAG GGTTCAGTA AAATAAATG AGAGCAATTA TATATATAAA 60  
TATATATCAT ACACAGAAA 79

SEQ ID NO:4159

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04897

SEQUENCE DESCRIPTION:

GATCACCTGA ATTCTGGAGG TTGAGGCTGC ACCACTACAT TCCAGCCTGG GAGATAGAGT 60  
GAGAGCCTGT CTAAA 76

SEQ ID NO:4160

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04898

SEQUENCE DESCRIPTION:

GATCCCAAAT NTTCCACAA GCTTTATTCC AAAAATAATT TTATTTAATA GGTATTAAAT 60  
AATGTATAGA AGGAAA 76

SEQ ID NO:4161

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04900

SEQUENCE DESCRIPTION:

GATCTTCCTG TTTCAGTCCC CAAGGTGTTG GGATTATGGG CATGAACTGC TGCACCCAGC 60  
CCTTTATACT CAAA 74

SEQ ID NO:4162

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS04902

SEQUENCE DESCRIPTION:

GATCACTGGT ATGTAGATAA TAAAATGTGA AAATAAAAAAT TTAAAAATAA AACAAAAATT 60  
ATGTGATAAT AAA 73

SEQ ID NO:4163

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04903

SEQUENCE DESCRIPTION:

GATCGTGCAA CTGCACTCCG GCTTGGGCTA CAGAGTGAGA CTCCATCAGA AAGAAAAGAA 60  
GAGAGAGATG AAA 73

SEQ ID NO:4164

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04904

SEQUENCE DESCRIPTION:

GATCAGCATG TAAAGTGTCT GCGTGAGT AGGCTCTTAA TAAACTCTGG CTGAATATGA 60  
ATTGGAATGA TAAA 74

SEQ ID NO:4165

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04905

SEQUENCE DESCRIPTION:

GATCTCAACT CGTGGCACTA ACTTGGAAAA GGGTTGATTT AAAATAAAAG GGAAGACTAT 60  
TTTACAAGCA AA 72

SEQ ID NO:4166

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04907

SEQUENCE DESCRIPTION:

GATCCTAAAC AGATGCATTG TTGCTTTTCT GTGCTGTCTC TGCAGATTAA AACATAATGA 60  
TTACTACTAA 70

SEQ ID NO:4167

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS04908

SEQUENCE DESCRIPTION:

5 GATCTATTAT GCCTTTTAC AAAAAAATG GCTGTAAATN ATTGTAAATA TTAAAGGAAC 60  
TTTCCTTACT TCCTTCCCTT TCTCAGGCTT TTTTGTACTG TTCCTTTCCC TACCAACTCA 120  
GGCCTTCTTA TTAAC 135

SEQ ID NO:4168

10 SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04909

SEQUENCE DESCRIPTION:

15 GATCCTCCTG GAGGTTTCAT AGCAAGGTTT GACTTGATGA ATTAATTAAT AAAGCTAAAT 60  
ATCCTGAAA 69

SEQ ID NO:4169

20 SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04910

SEQUENCE DESCRIPTION:

25 GATCACCCAC GGGGAGGAGA AGGAGGAGTG AGACCCAGCC GGGTCAATAA ACCTGGACGC 60  
TTGAAAA 67

SEQ ID NO:4170

30 SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04912

SEQUENCE DESCRIPTION:

35 GATCTGCTTA TAAATAAACT TAACAAATAC ACTATGGAGA TTAAAAACAA AATACCACCC 60  
ACAAA 65

SEQ ID NO:4171

40 SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04913

SEQUENCE DESCRIPTION:

45 GATCTGTTTC TCTAGAAAAA AAGTCCATCT CTGGCTTTAA TAAAATTATG CATCAGAAAT 60  
CAAA 64

SEQ ID NO:4172

50 SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

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EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS04914

SEQUENCE DESCRIPTION:

5 GATCTCATGC TNAGCAGAGC AAAAATTGTA AAATATTTTG ATTAAAAATC TAGGGACCTT 60  
TATGTCCTAT TTGAAA 76

SEQ ID NO:4173

10 SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04915

SEQUENCE DESCRIPTION:

15 GATCAGGAAG TGGCTTTGTG TCTTCCCACA TGTATGTATA AATAAAGTGT TCTTTTAAGC 60  
AAA 63

SEQ ID NO:4174

20 SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04916

SEQUENCE DESCRIPTION:

25 GATCCTCATT TTTTCCCATT GTAAAATTGG GCTAATAAAA GATGCTACCT ACTGACTATT 60  
AAA 63

SEQ ID NO:4175

30 SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04917

SEQUENCE DESCRIPTION:

35 GATCACGCTA CTGCACTCCA GCACTCCAGC GCAGGCAACA GAGGGAGACT CTTTGTCTCA 60  
AA 62

SEQ ID NO:4176

40 SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04918

SEQUENCE DESCRIPTION:

45 GATCCTGAAT TTCCCAGCCA ACAGAACCAA GTGCTAAATA AAACCTCTTT TAATAAGTTA 60  
AA 62

SEQ ID NO:4177

50 SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

55

5 TOPOLOGY:linear  
CLONE:HUMGS04919  
SEQUENCE DESCRIPTION:  
GATCAAAACT CTGTTCTCAA AAATAAATAA AAAATAAAAA ACAAACAAC AACAACAACA 60  
AA 62

10 SEQ ID NO:4178  
SEQUENCE LENGTH:61  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04920  
SEQUENCE DESCRIPTION:  
15 GATCACGCCA CTGCATTCCA GCCTGGGAGA CAGAGTGAGA AATAAATAAC TGTAATGTAA 60  
A 61

20 SEQ ID NO:4179  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04921  
SEQUENCE DESCRIPTION:  
25 GATCCAAGCA AACTACTTTA AGCAAATATT TGTAATAATTA AAAACGGAGG ACCGCTCAAA 60

30 SEQ ID NO:4180  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04922  
SEQUENCE DESCRIPTION:  
35 GATCTAACAG TTCTCCAATA AAATAGTTCT CATTCCAGAG AGCAGATGAA TATATTTAAA 60

40 SEQ ID NO:4181  
SEQUENCE LENGTH:59  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04923  
SEQUENCE DESCRIPTION:  
45 GATCTATGAC TGTACTACAC TCCAGCCTGG TCAACAAAGC AAGACCATAT CTCTTTAAA 59

50 SEQ ID NO:4182  
SEQUENCE LENGTH:59  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS04924  
SEQUENCE DESCRIPTION:

55

GATCCAAGTA TTTNATCTGT GTTGTCTCTC TAAACCCAAA TAAATGTGTA AATGTGAAA 59

SEQ ID NO:4183

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04925

SEQUENCE DESCRIPTION:

GATCCAATAC ACACATANCT TACAACTATC ACAAATTCCT ATTAAATATT AAAAGTAAA 59

SEQ ID NO:4184

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04926

SEQUENCE DESCRIPTION:

GATCTCAAAN NGAAATCTTA TACCAGTGAC AACTGTATTA GAATATATCT GTTCTTAAA 59

SEQ ID NO:4185

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04927

SEQUENCE DESCRIPTION:

GATCTCATAT TAATATTTTA ATATTTCTTT TCAAAATAAA ACAGAAAAGC AAGTAAA 57

SEQ ID NO:4186

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04928

SEQUENCE DESCRIPTION:

GATCTGTGTG TTCTTTCAAA GAGAAGTTAT GTCTAATTAA AATGTGTAAC GGACAAA 57

SEQ ID NO:4187

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04929

SEQUENCE DESCRIPTION:

GATCCGNGAG AGAACGACCA CAATTTAAAC ACATCAATAA ATACTTTAAC TTCCAAA 57

SEQ ID NO:4188

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

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5  
 TOPOLOGY:linear  
 CLONE:HUMGS04930  
 SEQUENCE DESCRIPTION:  
 GATCAAGAAG GACTACCTGT CATGTGAGAC CATCACTAAG AAACCATTTG CTGAAA 56

10  
 SEQ ID NO:4189  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04940  
 SEQUENCE DESCRIPTION:  
 15 GATCCCACTT CGGTCTGTAA ATTCCCTCAA TAAATCACCC AATATTGACA AA 52

20  
 SEQ ID NO:4190  
 SEQUENCE LENGTH:51  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04945  
 SEQUENCE DESCRIPTION:  
 25 GATCCCCAAA GCTTAAAATA TCGACTATTT AGAGTGAGAC TCCATCACAA A 51

30  
 SEQ ID NO:4191  
 SEQUENCE LENGTH:51  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04947  
 SEQUENCE DESCRIPTION:  
 35 GATCAGCCAN GCATTCCAGC CTGGTGACAG AGCGAGACTC TGTCTCNGAA A 51

40  
 SEQ ID NO:4192  
 SEQUENCE LENGTH:56  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04948  
 SEQUENCE DESCRIPTION:  
 45 GATCTTGTTT GTTGAGGGAG ATGGGACTAT AATAAAATTG AATGCTGAAG TTGAAA 56

50  
 SEQ ID NO:4193  
 SEQUENCE LENGTH:50  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS04950  
 SEQUENCE DESCRIPTION:  
 55 GATCGCGCCA CTGCGTTACA GCCTGGCGAT AATGCAGGAC TCAGTCCAAA 50

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SEQ ID NO:4194

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04965

SEQUENCE DESCRIPTION:

GATCTGTCTT GTAAACCACA TTCTTGACAA CTATTTGCTT TTGAGTAGTT TGTATTTTAA 60

TATGTGACTT TNGTCTTGAA AAGTAGTAAA GCCATAGACT TGTGCAAAAC AAA 113

SEQ ID NO:4195

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04985

SEQUENCE DESCRIPTION:

GATCATTATG CAATAAAGCT GCTAAAGTNA CATTTGTGGT TGATACTCAA GCCTTGTACA 60

AGCACATATN ATGTAGACAT TTTNAAATGT NAAGCTTTAA CAGGAATAGG ATAGCTGTTT 120

CAAACCTTGT GCAATTGTAA ATAAATTGTT TAGCTGTGTT TCTTTCATT TNAATAAAAA 180

ATTAAAAAGA AA 192

SEQ ID NO:4196

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04986

SEQUENCE DESCRIPTION:

GATCAATTG TAATTGCTTA CATTTTTACA ATAAATAATC TGTACGTAAA 50

SEQ ID NO:4197

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04987

SEQUENCE DESCRIPTION:

GATCTTTCTT TGGCAACCAC TTTTACTGT CGCCATAGTT CTTCTTTTC TAGAATGTCA 60

TATTGGAATC ATATAGTATG TAGCCTTTTC AGACTGGCTT CTTTCACTTA ATAATATGCA 120

ATTAAGGTTT CTCCATGTCA TTTTATGGCT TAATAGTGCA TTTATTTTGA GCACTGAATA 180

ATACTCCATT GTCTAGATGA ATAGTTTATC CATTCACCTA TTGAAAGACT TCTTGGTGGT 240

TTCCAAGTTT TGGCAATTAT GAATAAAGCT GTTGTAACA AA 282

SEQ ID NO:4198

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04988



## SEQUENCE DESCRIPTION:

GATCTTTTCA GTCAAAAATC TAAGATGATT TATTTTGTAT CACTTTGTGA AAAGCTGAAT 60  
 ATTGTTAACT ACAGTTAATA TTAACACTGT ATTTATACTT TCTCAAATA CATCCGCCCC 120  
 ACCACTTCTG GTTGCCCTCTG TTGACTATTA ATCCAGATGT AAACAACCAG ATGTTTTTTT 180  
 CTAACCTGTA CAAACTGACG TGTGTCAACT ATCATGGAAG GAAAAAATG TACAGATTAA 240  
 AATTATTCAG NGTTAAA 257

SEQ ID NO:4199

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04989

## SEQUENCE DESCRIPTION:

GATCCAGGNG TTGACTATAA CCAGATTTAC TCTTTGCTTA CTAGGNTTTC CATNNTCACC 60  
 ATTGGATGAA CCNCTGGTTT AGCCACAGTT GTGAAAATAA ATGGAAGTTG GTTGATTGTC 120  
 TAGAAAGTGA AA 132

SEQ ID NO:4200

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04990

## SEQUENCE DESCRIPTION:

GATCCGCATC CAAGCTTAAC CAAGGCTCCA ATAAACGTGC TAGGAAGCAA A 51

SEQ ID NO:4201

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04991

## SEQUENCE DESCRIPTION:

GATCAGTCGC TGACTCATTA GATGAACCAG GAGCCTGCAT GCTACAGCCC ACCTGCCAAA 60  
 TCTTGCCCCC ACCTGCTTTT TAAAATAAAG TTTTATTGGA ACATGAAA 108

SEQ ID NO:4202

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04992

## SEQUENCE DESCRIPTION:

GATCTTTGCT CTGTTTCCAG TGGGGTTTGA AGCAGAGTTC AGGGAACCCT GCCCAAGGTC 60  
 CTCCTGTTC A GACATTCTA TGTTGAATAA AGTATGTTTG ACTTCCCCGG AAA 113

SEQ ID NO:4203

SEQUENCE LENGTH:471

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04993

SEQUENCE DESCRIPTION:

GATCCACCT CAAATTAGCT TGATTGCAAA ACAGATATTG GAACATGGAG CTGAGAAGAA 60  
GATGGTCTGG GCTTCAGGCA CAGCTGGGTC CAGGGACTCA GACNNNTTG TCTCCATCTA 120  
TCTNCTGTGT TTTNCTGTAG GAGGTGGCCT CACTTTCCCC TAGTTCAAAA GGGCTTACTC 180  
CATATGATGG GGAAGGGAA GACAGGNCCA TGAACAGCCC TAGACTTCCA TCAGCCCACC 240  
TGGGAAGCCC TCACAGGAAA ATNAGTCTCA TTCCTAGTAC ATGAAATCTC AGGGGAGGGA 300  
ACTCCGATTG GGCCACCTTC AGTNATGTGC CCNGTCCCTN GGGGCCAAAT CCNCTTTTGG 360  
GTTGGTGGGG GCGGGTTTCA AGTGATTGGG NAAATNGCCA ACCNAAAGTT CANGTTNGAA 420  
GTTGGAGNAA NGGGGAANTT TTNCCCAAAA AGAAANGGNA AGGTTTGNTA N 471

SEQ ID NO:4204

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04994

SEQUENCE DESCRIPTION:

GATCAGGAAT GGGTGATTGG AGATTATTAG ATTCTAGGTT AACTTCTACC ACTTTACCCT 60  
AATACATAAA ACTTTTTCCT AAATAAATGA TGGAAGGAAT AATACTTGGT TACCTGGCAT 120  
TATTTTTCAG TAAGAAAAAA GCTTTACTAA CCACTACATT TATGGAAATT TGTAGGGGTA 180  
AGTATTTTAT AGGTCATAAA AAACACCATA ATATAACGAA TCTCATTTNC TTTAAATGTG 240  
AATTAAATCC TAACAGTCAT CTTTATAAAA TGACCATAGG CTAAANTCTT ACGTGTAAAGT 300  
NCTACTACAN TAAATANTTT CTGGAAACCT TTTATAAA 338

SEQ ID NO:4205

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04997

SEQUENCE DESCRIPTION:

GATCACCTTC CAGACCACAG CAGATGTGGG ACACACAGCC TCCTGACTCC AGGAAGAGCC 60  
AGANCTGTGC AGGGAGGAAG GGGTGAGAGG GGGGCCCCCA CACCTAGACT CAGTAAGGAA 120  
GTCGGGTING ACCTTAACAT CTNCATTGGA CAACTCCACC CNTNCCTTGG CTTGCCCCCT 180  
GCCCCGNNTAC ACTCCTACGT NTCCANGGGC TTNGGCCGTG ACTTAGGNAG AGGAGTN 237

SEQ ID NO:4206

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04998

SEQUENCE DESCRIPTION:

GATCATCCGC AGNCTCATGT TAAAAGGATT TTAGCTCACT AAAAGTGTA TAATGGAAAT 60  
GTGGAAAATA TCGTAGGTAA AAGAACTAC CTCATGCTCT GAAGGTTTTG TAGAAGCACA 120

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ATTAACATC TAAATGGCT TTGTTACACC AGAGCCATCT GGTGTGANGA ACTCTATATT 180  
TGTATGTTGA GAGGGCATGG ANTAATTGTA TTTNGCTGGC AGTAGACACA TTCTTTATTA 240  
TTTGCAGATT CCTCATCAAA TCTGTANTTA TGCACAGTTT CTGTTATCAT TAAACAAAG 300  
GAATCCNGTT AAA 313

SEQ ID NO:4207

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS04999

SEQUENCE DESCRIPTION:

GATCACATCT NTNTGAAGCC AAAGCCCCGT GGTGCCCCAT GAGAAGTGTC CTTTTTCATT 60  
TTCACCCAAA TGAAGTGTGA ACGTGATGTT TTCGGATGCA AACTCAGCTC AGGNATTCAT 120  
TTTGTNTCTT AGTTTTATAT GCATCCTTAT TTNTAATACA CCTGCTTCAC GTCCCTATGT 180  
TNGGAAGTCC ATATTTGTNT GCTTTTNTTG CAGCATCATT GCCTNTACAA TACTGNCCGG 240  
TGGACAAANT GACAATNGAT ATGTNTTGCT N 271

SEQ ID NO:4208

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05001

SEQUENCE DESCRIPTION:

GATCGCACTG TGGGCCGGGG CCCTGGAGGG CTGCTCTGTG TTAATAAGAT TGTAAGGTTT 60  
GCCCTCCTCA CCTGTTGCCG GCATGCGGGT AGTATTAGCC ACCCCCTCC ATCTGTTCCC 120  
AGCACCAGGAG AAGGGGGTGC TCAGGTGGAG GTGTGGGGTA TGCACCTGAG CTCCTGCTTC 180  
GCGCCTGCTG CTCTGCCCCA ACGCGACCGC TGCCCGGCTG CCCAGAGGCT GGATGCCTGC 240  
CGGTCCCCGA GCAAGCCTGG GAACTCAGGA AAATTCACAG GACTTGGGAG ATTCTAAATC 300  
TTAAGTGCAA TTATTTTAA TAAAAGGGGT ATTTGGAATC AGAAA 345

SEQ ID NO:4209

SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05002

SEQUENCE DESCRIPTION:

GATCTTACTT TCATAATTCT TTGATTCTAG CTTGCAGAGT CAAGACGNAA AGNTAACTCA 60  
TGGGATGGAC AAAGTGAAG ATGTAAATA AGTAAGGCTT TNTGGGCCAA AAAGCCTCTT 120  
CTTACAGAAA ATCAAATTTT AAAAGAACAT TGACCTCAA ACAATAAAC TGTCCTGGTT 180  
ATGCAATAGA AATAGCTATA TAAATGGAAT CATATCCTTA ATGAACACCT CCTGTGGCTA 240  
CCCAACTTTT CACACATCTT ACTGATTATA GGCCTTGCTG TGAATGCTTT CTTGCTCTAT 300  
CTGAAGTATT CCCACCAGAG TTGTTTCCAA CNNTATTTC TATATTATGA AAAATGANGT 360  
TTTTTTAACA TTGTAACAAA GTATTTGNAA GGTAATGTAT ACTGTN 406

SEQ ID NO:4210

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05003

SEQUENCE DESCRIPTION:

GATCTAAAAA AANNATAATT ACATTAGTAA CACAACATAA GAAAAAGACA GGGACAAAAA 60  
CAAAAAAATAA TAAA 74

SEQ ID NO:4211

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05004

SEQUENCE DESCRIPTION:

GATCCTATGT GGAAGGGCTG TTTTAAAGA AAAAATTTT GGTAAACAGT ATTGTGTAAA 60  
ATTGCTTTT GTATACCAAT ATATGCATGT TTTGTGCATG AGTAGTACTT GTGTTGATAC 120  
TCCTGTTGAT GTTAAATTAC TATATAATAT AANCAGTATG TGTTTTTATA TATCATTGTG 180  
TAAATTTAAT ATAACATATG CNGTAATAAN CCATTNGTNT TACGGGCAAA 230

SEQ ID NO:4212

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05005

SEQUENCE DESCRIPTION:

GATCTCAATC AAGTTAGCAT GCTTNCTCCA GCTGCCCTAT NACCTGCCAG CTCATCACAA 60  
AGAACCACGG CCACCCAGGT CATGGCAAAC TCTGCTGGAC TTAAC TTCAT CAATGTAGTG 120  
GGCTCTNTTT GTGGGGCCCA GGCTTTGATG AGTNGGNNNN N 161

SEQ ID NO:4213

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05006

SEQUENCE DESCRIPTION:

GATCGAGACC ATCCTGGCCA ACATGGTGAA ACCCGTCTC TACTAAAGAT AAAAAATTA 60  
GCTGGACATG GTGGCGGGCG CCTGTNTTCC CAGCTACTGG GGAGGCTGAG GCAGGAGAAT 120  
GGCTTNGAGG CAGTAGAACT GCTTGAACCC TGGAGGCGGA GGTACAGTT ATCCGAGGTT 180  
GTGTCATTGC ACTCCAGCCT GGGGAACAGA GCGAGACTCC ATCTCAAAAA AAATAAAAAA 240  
CTTCAGCTTT TGCATGAAA 259

SEQ ID NO:4214

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS05007

SEQUENCE DESCRIPTION:

GATCATGCTT TAAGGTTTAT GTAAAGAAAG TGTACTGATG TTCTTACATT AAAGCTTTAC 60  
 AAAGATTTAA A 71

SEQ ID NO:4215

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05008

SEQUENCE DESCRIPTION:

GATCTTGGTG GTAGTAGCTG TCTATGATTC TNGCTCAGCA AAGTAAAATA AATGTTAAAT 60  
 ATGGAAA 67

SEQ ID NO:4216

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05009

SEQUENCE DESCRIPTION:

GATCAAATGA AATAATGTAC ATGAAAAGAC ATATATAAAA TGTATAATAC AGACAAAGGG 60  
 NCCTGTTACA CAGTTGGAAG TCATNCCCTC AGATTTTGGG CCTAGGAAGG TAGGTGATT 120  
 AAACCTACTG AAAGCANNGN NNN 143

SEQ ID NO:4217

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05010

SEQUENCE DESCRIPTION:

GATCACAGCC ACTGGTCCAT AACAAATTAGG AAAAATCATT GGACAATGGT TGTCAGGTTC 60  
 CTCCATTGGA GGGAATTGTG TTTCATGATT AGGCACTGTT TCTGCTCCTT AAAAATGACT 120  
 TTCCAGTCTA TCCTCCACAG CTCTTTGTTC TACACTCTAG GGAATCATT TTTTCCCTC 180  
 ATCTTCCTTA GTCACCTGCA AAGGACATTA GAGAATATGC CCTTTTGGT GGATAAATGG 240  
 GTTCTTCAAC CTGCTTCTG CCTGTAGAAA ATTAGAGGCC AATAATCTGT TTATATCTTG 300  
 TAGAATGTCT ATTTTAGCTG GTACCGGTAC TTTTGTCAAT AAAGTTCTTT TTAAACTTA 360  
 AA 362

SEQ ID NO:4218

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05011

SEQUENCE DESCRIPTION:

GATCTGNGAA GAGCACATAT GTGTCAGGGC ACAATTCCCN CTCATAAAAA CCACACAGCC 60

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TGGAAATTGG CCCTGGCCCT TCAAGATAGC CTTCTTTAGA ATATNATTTG GCTAGAAAGA 120  
TTCTTAAATA TGTGGANTAT GNTTATCCTT AGCTGGAATA TTNCTCTAC TTCCTGTCTG 180  
CATGCCCNAG GCTTCTGAAG CAGCCAATGT CGN 213

5

SEQ ID NO:4219  
SEQUENCE LENGTH:169  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS05013

SEQUENCE DESCRIPTION:

GATCACTACA ACANTTTNTT TGCCTCCAAG GTCCTCTGAG GCAGCAGGCT CTGGGGCTTC 60  
TNCTGTCCCT TGGAGGGTGT CTTCTGGGTA GAGGGATGGG AAGNAAGGGA CCCTTACCCC 120  
CGGNTCTTCT CCTGACCTGC CAATAAAAT TTATGGTCCA AGGGAGAAA 169

15

SEQ ID NO:4220  
SEQUENCE LENGTH:235  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS05014

SEQUENCE DESCRIPTION:

GATCGCGCAG GATTTCAAAA CCGACCTGAG GTTTCANAGC GCANCATCGG TGCCTGTCAG 60  
GAGGCTAGCG AAGNANCCTG GTGGGTCTGT TCGAAGATAC CAACCTGTGT GCCATCCACG 120  
CTAAGAGAGT CACCATCATG CCCAAAGACA TCCAGTTGGC TCGCCGGATA CGGGGAGAGA 180  
GAGCTTAAGT GAAGGCAGTT TTTATGGCGT TTTGTAGTAA ATTCTGTAAA ATAAA 235

25

SEQ ID NO:4221  
SEQUENCE LENGTH:196  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS05016

SEQUENCE DESCRIPTION:

GATCAAAGTC CTACAGTGGC TGTCACGCAG CCACNAGGTC ATCTCCTTTC ATCCCCACCC 60  
CAAGGCGCTG GCTGTGACTC TGCTTCCTGC ACTGACCCAG AGNCTCTGCC TGTGCATGGC 120  
CAGCTGCGTC TACTCAGGTC CCAAGGGGTT TCTGTTTCTA TTCTTTCCTC AGACTGCTCA 180  
AGAGAAGCAC ATGAAA 196

40

SEQ ID NO:4222  
SEQUENCE LENGTH:262  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

45

CLONE:HUMGS05018

SEQUENCE DESCRIPTION:

GATCTGCACC AGACTGTTAC CTTCTGGGGG AGATGGAGAT TTGACTGTTT AAAAAGTAA 60  
AACAGCGAGG AGTCTTTCTA GAACTTTTGA AACTAAAAG GATGAAAAAA ATTAGCAAAC 120  
CGAAGTTTCT TCAATGACCC CTCGAGAACT TTGGGACCAG TTTCTATGG GGGACTCAGT 180

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55

TTCAGAGAAC TGAGACAGAA GCTCTTCTGT CGTTATATTC TTCTTTCCTT TTTTGGATT 240  
TATTAAATAT TTTCTGTGGA AA 262

5 SEQ ID NO:4223  
SEQUENCE LENGTH:277  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS05019

## SEQUENCE DESCRIPTION:

GATCCTGCAG TGTCCTGTGG GTTCATCTCG GATGGGCGCT GCATAAACAG CCTGCAGGGA 60  
ACGTCTGGGA GAACCAGCTT CACAACAGAT ATAATAAGGA AGAAGTTTGA AATATTGCAA 120  
GANTTGCGAA AGTGTGACAC ACAGATACAA AGTGGGCACA TGCTCGTGGG AAAATGTTGC 180  
15 CAATAGACTT GCTTGACTCT GGAGTTACCC CGAACCTTCA ATTTGTTTAA AAAAAAAAAAN 240  
GGGCANTTTN TTGNNNGCA NTAAGGTGNC CTGCAAA 277

20 SEQ ID NO:4224  
SEQUENCE LENGTH:271  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05021

## SEQUENCE DESCRIPTION:

25 GATCGCGTCC ACCTTCATCG CTGTGGTGCA AGCCATCGTC CGCACGGCTG GTGGCTGGGC 60  
AGCTGCCTCG GACTCCAGGA AAGGCGGGGA GCCTGCCGGC TACTGAGTGC TCCAGGAGGA 120  
CAAGGCTGAC AAGCAATCCA GGGACAAGAT ACTCACCAGG ACCAGGAAGG GGACTCTGGG 180  
GGACCGGCTT CCCCTGTNAG CAGCAGAGCA GCACAATAAA TNAGGCCACT GTGCCAGGNT 240  
30 CCAGGTGGCC TNCCTGGNCT GTTCCCCAA A 271

35 SEQ ID NO:4225  
SEQUENCE LENGTH:138  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05023

## SEQUENCE DESCRIPTION:

GATCCACGGA AGACTGTCAG CAGACTTCAC CAGAAAATT TCACGCCAGA NGGCAGTCGT 60  
40 GATATATACA AAANGCTGAA AGGAAANCAC TGCCATCCAG GANTACTATC TCCAACNTC 120  
CTGTGTTTCA AAANTTAN 138

45 SEQ ID NO:4226  
SEQUENCE LENGTH:64  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05024

## SEQUENCE DESCRIPTION:

50 GATCTGCATT TAAAAATATG GTCTTTGTTT TATATGATTA AATGGTTTGT TTTCATAGAT 60  
GAAA 64

55

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SEQ ID NO:4227

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05025

SEQUENCE DESCRIPTION:

GATCCCGGCT GTTGGTGAGC AAAGAGCCCA GGCCCTAGA GTGCGCATGT NCAGGCTCCG 60  
 CTGTTAGANT CACAGCGGTT CAAATCCGGC ATCTGGTCGC TGAGTGGCCT CAGGCAGTGA 120  
 CCACGCTCCC GGACCCAACC TTCAGCTTGC CCAAAGCAAT AATCTTTCCT AAAGAAGTGC 180  
 TTGGNTGGGG ATGGTGGCTC ACGCTTGTA ATCCAGTAC TTTGGGAGGC CAAGGCAGTC 240  
 TGGGCAATAT AGTGAGGCTC CCATCTGTAC TAAAAATAAA AAAGTTAGGC GTGAAA 296

SEQ ID NO:4228

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05026

SEQUENCE DESCRIPTION:

GATCAGACCT CTCATGCTGT GGAGATGAAA AAGCCCTAAA GTTTATGTTT CTAATGTGTC 60  
 ACAGAATAGG ACGATATGAT TCTACAACAT AATCAACTCC CTATTAAATT CTTTAATGAA 120  
 GATTTTTTTT TTAAA 135

SEQ ID NO:4229

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05027

SEQUENCE DESCRIPTION:

GATCCTCTTT CTAGCATGAA TGAAGGATGC CAAGAATGAG AAAAAGCAAG GGGTTTGTCC 60  
 AGGTGGCCCC TGAATTCTGC GCAAGGNATG GGCCTGGGGG AACTCAAGGG AGGGCCTAAA 120  
 GCACTTGTA CTTTGAACCG TCTGTCTGGA GGTGAGAGCC TGTTGGAAAG CAGGGGTAGA 180  
 GGGGAGCCCT GGAAGCAGGG CTTTCCGGA TGCCTAGGGG TGGGCAGTGC CAGCCCCTCC 240  
 TCACCACTCT TCCCCTTGCA GTGGAGGAGA GAGCCAGAGT GGATACTATT TTNATTAAA 300  
 TATATTATTA TATGTTAATA AAAAANTCAT ATCCAAA 337

SEQ ID NO:4230

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05028

SEQUENCE DESCRIPTION:

GATCCTTCGC GAGCGAGTGA ACAAGAGGCG GGTGAAGGAG ATGGTGAAGG AGTTCACACT 60  
 GCTGTGCCGG GGTCTCCATG GCACAGGGTA CACAGCTGAC TACTGAGGGG TGCCCCCATC 120  
 CCATCCACCC CTTCTCTTCA TCCTTCCCTA TTCCCAAAGN GTAAACCTGG NCCCTNAAA 179



# EP 0 679 716 A1

SEQ ID NO:4231

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05029

SEQUENCE DESCRIPTION:

GATCGCTGGA CGCTATGAGA GGGCGTCCCA GGGCCCAGCC TCCCACAGCC GTTTCAGCAG 60  
GGACAGGGGC TGAACAGGCC CTATTCCAGC CCCCTTGCTT CACTCTACCG GACAGACGGC 120  
AGCAGTCCCA GCTCTGGTTT CCTTCTCGGT TTATTCTGTT AGAATGAAAT GGTTCCTATA 180  
AATAAGGGGC ATGAGCCCTT CCTCAA 207

SEQ ID NO:4232

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05030

SEQUENCE DESCRIPTION:

GATCTGAAAT AGTTTTCTTC CACTACATTG TTGAAATCAA TGAAGCAATT AGTTTCTCAT 60  
TCAGAAATGT GCACACTAAT ATTTAGTTTT GCTTCTCGT GGATAATATT AAGCNCTTAC 120  
TCTGCAGTTT CCTGGAAGTT GTGTCAACTG CAGTGATACT ATTCAGGATG GTGGGAAATC 180  
CCCAAAAATA TGTATGTGTG GGCTTGCTTA GATTACTATA TTTCATAGTT AATCTTTTGT 240  
CTCTTGCGGT GCTCATGATG TGTGGGGCAC ACGGAAGGCA TTGCTGTAGT CAGTCATTTT 300  
GGTTTTCTTC TATAGCCATT TTATTATTTT AGTGTATTAG TTATGAAGAT AATATTNNCT 360  
ATTTGTAAAT NGCTACTTTG TATTTN 386

SEQ ID NO:4233

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05031

SEQUENCE DESCRIPTION:

GATCTTCANA TTGCTGTGAT TAATGCATCC AGATTNTTTT CCTAGTATTT CCAGGTTAGA 60  
ACCTGTGGAT TGTTTCANTT GCATATAGCT TGGTTTCCAT AACATAGAGC ATTGGTTGAC 120  
TGTTTACAGA AGACTCACTC ACCAGGATAA ACATTGCNGT ATGTNACAGT AAAGCTATCT 180  
GGAGAGANCA CATAAATGAT TTTGGCATAC CATTAGAGAA ACCATTTGTA AAACCTAAAT 240  
GNCCACATAA NGCTTATCAG GGGGTCTAGA TTGGTNTTGT NNTATACCAT ATGGGATGAN 300  
GNAANTAGA AATGTCAGTA GAACTCATTG AGGGTGCTCT NGCCAGCTGC NGANAN 356

SEQ ID NO:4234

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05033

SEQUENCE DESCRIPTION:

## EP 0 679 716 A1

GATCTGCTTT TTTNAAATGT TAAGGACATA TTTTNAAGTT ACTGCTGAGT GAAGAAAGAA 60  
CATAGCTCCC CCTCATTCCC TGC GTAAGAA AGGAGCTTAA AGAAA 105

5 SEQ ID NO:4235

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10 CLONE:HUMGS05034

SEQUENCE DESCRIPTION:

5 GATCAGGGCC TTCCTGCCTC CCGCTGGGCA GGTCTGGCCT TGCNCTCTTG GCAGGGCCCC 60  
AGCCCTCTA ACCACTCTGC AGCTCACCAT GCAGCTGATG CCAAANTTGT GGTGTCCAGT 120  
15 GTGCAGCAGC CCTGGGAGCC ACTGCCACCT TCAGAGGGGT TCCTTGCTGA GACCCACATT 180  
GNTTCACCTG GCCCCACCAT GGCTGCTTGC CTGGCCCAAC CTAGCGTTCT GTGCCATGNT 240  
AGAGCTTGAG CTGTTGCTCT NCTTCAGGGG AGGAAATAGG GTNGAGAGNG GGAAGAGNNT 300  
TNGCTCCTAA GTGTTGCTGC TGTGGCTTTT TTTGCCTTCT GCN 343

20 SEQ ID NO:4236

SEQUENCE LENGTH:370

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS05035

SEQUENCE DESCRIPTION:

5 GATCATTTCA AAATCATTT CCTATGTAAC TGCATTGAGA ACTGCATATG ATTCGCTGAT 60  
ATATGTGTTT TTCACATTG CGAATGGTTC CATTCTCTCT CCTGTACTTT TTCCAGACAC 120  
TTTTTTGAGT GGATGATGTT TCGTGAAGTA TACTGTATTT TNACCTTNTT CCTTCCTTAT 180  
30 CACTGACACA AAAAGTAGAT TAAGAGATGG GTTTGACAAG GTTCTTCCCT TTTACATACT 240  
GCTGTCTATG TGGCTGTATC TNGTTNTTCC ACTACTGNTA CCACANCTAT ATTATCATGC 300  
AAATGCTGTA TTCTTCTGTT GGGTGGAGAN AAAGGATTC TTGNAGGTTT NGTTTTTAAA 360  
ATTNAAAGCN 370

35 SEQ ID NO:4237

SEQUENCE LENGTH:529

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS05037

SEQUENCE DESCRIPTION:

5 GATCTGTTTC GTGCATTGGA AGACCCACC CAAGCTTGGC AGNCGAGCNN ATTGTATCCT 60  
GGGGCTCCCT TCATCTCCAG GGAGTCCNNT CCCC GGCCCT ACCAGCGCCC GCTTGGCTGA 120  
45 GCCCCTACCC CACACCAGGC CGTCCTCCCG GGCCCTCCCT TGGAAACCTG CCCTGCCTGA 180  
GGGGCCCTCT GCCCAGCTTG GGCCAGCTG GGCTCTGCCA CCCTACCTGT TCAGTGTCCC 240  
GGGGCCGTTG AGGATGAGGC CGCTAGAGGC CTNAGGATGA GCTGGAAGGA GTGAGAGGGG 300  
ACAAAACCCA CTTGTTGGA GCCTGCAGGG TGGTGCTGGG ACTTAGGCCA GTCCCAGGGG 360  
CAATGTATTG GCCTGGAAGG TGGGGTTTGG GATTNNGGGG GCTTGGTGCC AAGCTTTCCT 420  
50 TTTNNANGNT GACCTTNTT TNGTNCCTNC CCCTTTGGGG NGGGNTNAAA AGNCCCAAGT 480  
TTGANANTGG GAAATAAANT TTTTTTGGGC CTCCGGNTTT CCCTNAAA 529

SEQ ID NO:4238

SEQUENCE LENGTH:365

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05039

SEQUENCE DESCRIPTION:

GATCGTTTTC TGATTTGTAT GCTTCACAAA CTTGGATTG ACAAAGAAAA TGTATTATGNN 60  
 10 NGAATTGCGA CAGTGTATTC GCAACTNTCC TCAGTTCAGA TTTGACTGGT TTCTTAAGTC 120  
 CAGAACTGCA ATGGAGCTCC AGNNGGAGATG TAATACCTTA ATTNCTTTGA TTGAAAGAGA 180  
 AAACATGGAA CTAGAAGAAA AGGAGAAGGC AGAGAAAAAG AAACGAGGAC CAAAGCCTTC 240  
 ANCACAGAAA CGTAAAATGG ATGGCGCACC TGATGGTCGA GGTAGAAAAA NGTGGCTGGA 300  
 15 ANCTATGNNT ATGGTTTTNT TTCATAAATC ACTNAGCTTT ANACCNAGTA GTTCCTNTNA 360  
 NTTTN 365

SEQ ID NO:4239

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05040

SEQUENCE DESCRIPTION:

GATCATTACA ACANTTGTNT GCCTCCAAGT CCTTGAGGCA GCAAGTCTGG GGCTTCTGTN 60  
 25 TCNTTTGAGG GTGTCTTCTG GGTAGAGCGA TGGGAAGGAA GGACCCTTAC CCNN 114

SEQ ID NO:4240

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05041

SEQUENCE DESCRIPTION:

GATCATCCGC GGCGGCCGGG CTCGTGGGGC GCCTGGAGTG AGGGTTCTGG TTCCCGCCGG 60  
 35 CGAGGATTGT TAAAATNAGT CTTGGGAAGN AGACCCCTAG TGAATTCTTA AAGCAAATCA 120  
 TCGGACGACC AGTTGTGGTA AAATTAAATT CTGGAGTGGA TTATCGAGGG GTCCTGGCTT 180  
 GCCTGGATGG CTACATGAAT ATAGCCCTGG AGCAGACAGA AGAATATGTA AATGGACAAC 240  
 TGAAGAATAA GTATGGGGAT GCATTATCC GAGGAAACAA TGTGTTGTAC ATCAGTACAC 300  
 40 AGNAGAGACG GN 312

SEQ ID NO:4241

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05042

SEQUENCE DESCRIPTION:

GATCGGAGTA CANAGTNACA NTTGGAGGGC AGGGGGACTN TAAGGCAAGG AGATTACAGT 60  
 50 TGGGAAGGAG GCAGTGGCAG AGGGGTGAGG GACAGGGGCC CTTAAGTCCA GCGAGGAAAG 120

EP 0 679 716 A1

CTCGGTGTGG GCCCGTCTAC GCTCCGTTTG GGGTGACCTG GAACGCCTCT TCTACAGCTC 180  
 CTNCAGCATC AGCAGCCTCT TGTCAAGTTT TGCCTCGCCC ANTCTATCCC AACCCAAATA 240  
 AGACACTTTC TTCACGNCAT ATTATCTTTG TCCTTTCTTT TTTAAGAACA TCACAAAACC 300  
 ATGAAA 306

SEQ ID NO:4242

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05043

SEQUENCE DESCRIPTION:

GATCTTAAAC CCAGTCTTGA CAGACTAGAA GTTAAGTTTA ATACAGAAAA TGTCCTGTTC 60  
 ACTTGAAAGA AAAGACCTAC TTTTAAATG GACACTATCT TGGTTCTTTT TTTTAAAGTC 120  
 ATCTTTTGT TATAAGTGAC CTTTGTCTGG AATGTCTGAA AAGTAGTTAA TGCTTTTNGG 180  
 TATTGAAGTA ATGGGTAACT AAAATGGACT TCCATAGTAT TGACTGTAGA AGGAGCCTCT 240  
 ACAATATTGA CTATATATNN NNATAAACTA CTGGCAAGGN ACTTAAA 287

SEQ ID NO:4243

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05044

SEQUENCE DESCRIPTION:

GATCTCCACT GTTGGGTGGG TGGGCCCTGC CGGGACCCTG CTTCACAGGC AGGCTTTTCC 60  
 TCCAACTGT GGCCTGCAG CAGGGCAGGA AGGGGAAACA CAGCTGATGA ACTGTGGTGC 120  
 CACATGACCC TTGTGGCACA GATGCCACG TATGTGAAAC ACACATGGAC ATGTGTCCCA 180  
 GCCACAGTGT TATGCTCTGT GGCNGGCTCA CCTTTGCTGA GTTCCGGGGT GCAATGGGGG 240  
 AGGGAGGGAG GGAAAGCTTC CTCCTAAATC AAGCATCTTT CTGTTACTTG ATGTTCAATA 300  
 AAAGAATAGT TGGCAAGGCT GAAA 324

SEQ ID NO:4244

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05045

SEQUENCE DESCRIPTION:

GATCATTCAT ATGTGTACAT AAAATTTTAA AAATAAAGGG AATTGACTGC TTTGTTAATG 60  
 AGAAA 65

SEQ ID NO:4245

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05046

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCCAGAGA ATGAATCCCT GACCGCATCA CCTAAACTGT CTTCCAAACA TGAGACAAAG 60  
 CTGACTGTTC AACTGATTG CCCAGCACAT ACCGTCTTGC CAGTTTCTTC TTTTCTCCCA 120  
 GTCTCCTGTT CATCCATTCT GTTCTCCCTT GGGGTGGGAA TCTATGATGG AGGTTACTGG 180  
 GGAAACAGCT CAGCAGATTT TTGGAGACCA AACCAAAGGT CTCACTAGGA AATTTATCTG 240  
 TTTTAAAACA TTGCTTCCTT CCTGGCTCTG CTAAATTGAA TGCTCATN 288

SEQ ID NO:4246  
 SEQUENCE LENGTH:333  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05047

## SEQUENCE DESCRIPTION:

GATCTCTGCT CTAACGATG AAGACTGGGC CTATTCACAG CAGCTCTCTG CCCTCAGTGG 60  
 TCAGGCGTGC AATTTTGGTC TGCGCCACAT AACCATTTCTG AAGCTTTTAG GCGTTGGAGA 120  
 GGAAGTTGGG GGAGTGTTAG AACTGTTCCC AATTAATGGG AGCTCTGTTG TTGAGCGAGA 180  
 AGACGTACCA GCCCATTTGG TGAAAGACAT TCGTAACTAT TTTCAAGTGA GCCCGGAGTA 240  
 CTTCTCCATG CTTCTAGTCG GAAAAGACGG AAATGTCAA TCCTGGTATC CTTCCCAAT 300  
 GTGGTCCATG GTGATTGTGT ACGATTTAAT TGN 333

SEQ ID NO:4247  
 SEQUENCE LENGTH:288  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05051

## SEQUENCE DESCRIPTION:

GATCCTCCAC AGAGAGGAGG GGACCAATTC TGGACAGACA GATGTTGGGA GGATACAGAG 60  
 GAGATGCCAC TTCTCACTCA CCACTACCAG CCAGCCTCAG AAGGCCCCAG AGAGACCCTG 120  
 CAAGACCACG GAGGGAGCGA CACTTGAATG TAGAATAGGC AGGGGGCCCT GCCCCACCCN 180  
 ATCCAGCCAG ACCCCACGNT GACCATGCGT CAGGGGNCTA GAGGTGGAGT TCTTAGCTAT 240  
 NCTTGGCTTT NAGAGCCAGC CTGGNTCTGN CCNCTCCNC CATGGGGN 288

SEQ ID NO:4248  
 SEQUENCE LENGTH:170  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05052

## SEQUENCE DESCRIPTION:

GATCTCTAAG TGACCACCAG GGGCTCTGAA CTGCAGCTGA TGTTATCAGC AGGCCATGCA 60  
 TCCTGCTGCC AAGGGTGGAC ACGGCTGCAG ACTTCTGGGG GAATTGTCGC CTCCTGCTCT 120  
 TTTGTTACTG AGTGAGATAA GGTGTTCAA TAAAGACTTT TATCCCCAAA 170

SEQ ID NO:4249  
 SEQUENCE LENGTH:136  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS05053

SEQUENCE DESCRIPTION:

GATCTACATA GATTTGGAAA CTGTTTTCCT CTGTTTGGT CTCTGGGCA ACATTTTGG 60  
 CCCAAGTTTGG GGCACATTT GGCCCAAGNT TGGGCATTTT GGCAGTAGCT GTATGGNAGA 120  
 AAAAGAGTAA GAGGAN 136

SEQ ID NO:4250

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05054

SEQUENCE DESCRIPTION:

GATCNTTTGC TTTAGNGTGT AAAGTNTGTC TCTGAACAGA ATTATTTGTA AAAGTTAGGA 60  
 GTTCTTTTTT AAATCATTAA AAGAGGCTTG NTGAAGGAAA 100

SEQ ID NO:4251

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05055

SEQUENCE DESCRIPTION:

GATCCTAGAG CCCTTCACTT CGGNTTACTC CCTCTTTTTT GCCTCTNTTT NTTAGTTGGA 60  
 AGAAATAAAC TCACAAATTA TGGTGCAGTA ATTNCCGGG GAAAGTAAAG CCTCAGGAAT 120  
 GCCCAGCCTT TTTTCCAAA GCCTTTNTCT CTGAGACCTC TTAAGTTCTA AGATTAAATG 180  
 CCCCTCGCTG TTTCTCCTCT GAAA 204

SEQ ID NO:4252

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05056

SEQUENCE DESCRIPTION:

GATCAAGGAG CAATTATGAA GGTCTACAAG CAAGANCAAG AGGAAGAATT ATNGAAAAAG 60  
 TTGGCAAATG NCCCCAGATG GAAGAGATAC AGGAGATGGA TGAAGAATGA AGGGCCTGGG 120  
 CGGTTAACAT TTGTGGATGA CTGANGATTG ATGGAATGCT ACTATGCCAA ACCTTAATTG 180  
 TGATATTATT TTCATAACTG ANTTATTTTA GAAATGTATC ANTNGACTGC TGCTCAGCAG 240  
 TAACTAAAAT TCCTCAAGTA TTTGATTAAA CAGATTAATG TCAAANTTTA AACCTTCCCT 300  
 TAAAACTTTN 310

SEQ ID NO:4253

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05058

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTAATTG CATTGGTTAA AAGCAGCTAA CCAGGTCTTT AGAATATGCT CTAGCCAAGT 60  
CTAACTTTAT TTAGACGCTG TAGATGGACA AGCTTGATTG TTGGAACCAA AATGGGAACA 120  
TTAAACAAAC ATCACAGCCC TACTAATAA CATTGCTGTC AAGTGTAGAT TCCCCCTTC 180  
AAAAAAGCT TGTGACCATT TTGTATGGCT TGTCTGGAAA CTTCTGTAAA TCTTATGTTT 240  
TAGTAAAATA TTTTTGTGA TTCTAAA 267

SEQ ID NO:4254  
SEQUENCE LENGTH:307  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05059

SEQUENCE DESCRIPTION:  
GATCANAAC CAAACGGGCC GGNNTTCTA AGGTGTNGGT ATGTGGGGAG TGGTACAAAA 60  
TGGTCTGATG CTCCTTCAAA AACATTCAC TTTTACAACG TCAAGGAATT AAGCATAAAA 120  
AAGATTGGTT AAAAGCTTTG GTTCTAGTA AAGGTTAGTG TGTGTGGTTT TTTAAGAAG 180  
CTGTNTTGCT AAATNATTTT TACTTGGAAT GTTTCAAACA GATTTAGGC TGCAAACTTG 240  
TTNATAATC GTNNGCTTCT CCAAGTGAAG CTTCAGGAAT ACCTGGAAAA TAGCTGTAAC 300  
GTTTCGN 307

SEQ ID NO:4255  
SEQUENCE LENGTH:297  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05060

SEQUENCE DESCRIPTION:  
GATCTAATAA AAATTGAAAT ATGCCTTTTA GAATGGCTTT CAAAGATAAC AAATGCTGGA 60  
GAGGATGTAG AACAACTGGA ACCTCTCGGT TATTGCTGGT GAGACAGCCG CTTTGA AAAA 120  
GTTTGAGTTT CTTACAAAAT TAAACTTACA CTTACACTTA CCATATGACC CAAAAATTCC 180  
ACTGCTTGCT CTTTACTCAA GTATAAGGAA AATCTATGTA CACACAAAAC TNGTACGTGA 240  
ATATTTATTA ATAGTCATTT TATGCCCCAA ACTAGNAATA GTCCAAATGT TCTGGGN 297

SEQ ID NO:4256  
SEQUENCE LENGTH:208  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05061

SEQUENCE DESCRIPTION:  
GATCTINTATT NTTTTNGCAA CAGACTTCAA GTGGTCCCTC TTTTTCCCT ACACACTCAG 60  
CTCTTCTCTA AAAGCAAGGA TTTGGAATGA NCAATTCAGT TTGACAGAAA AAGCTGAATA 120  
AAATGGCATC TGTAATTGAN TTGTTGGAAA TGCCTTTTTN GCTCCTAAAT NTTAAACATC 180  
ATTAATAAAA TANTGTTTCA CAAAGAAA 208

SEQ ID NO:4257  
SEQUENCE LENGTH:208  
SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS05062

SEQUENCE DESCRIPTION:

5 GATCACAGGA AGACTTTGTA AGGACAGTTT AAGTTCTCCT GCAAGGTTTA ATTTGTTATC 60  
ATGTAAATAT TCCAAAGCAG GNTGCCTTGT GGTTTTGGCC AGCCTTGTGC TATGTTGATA 120  
AGATTGATTT ACTGCTTAAA ATCACTTTAC TTTATCCAAT TTTTACTGAA CTTTTATGT 180  
AAAAAATAA AATCAATTAA AGAACAAA 208

10 SEQ ID NO:4258

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS05063

SEQUENCE DESCRIPTION:

15 GATCAGTTTT CTATTTTAAT GTGTAAAAA AATAACTTGT CGTATCCCAT TTAAAGGCCA 60  
ATTCTGTAT TCAGGCAGGC ATATGTACAT ACATGAATAA AGCCAACAAA AGTGTGCACA 120  
TGTA 126

20

SEQ ID NO:4259

SEQUENCE LENGTH:552

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS05064

SEQUENCE DESCRIPTION:

30 GATCGGGGTG CCCCTCAGCC TTCAGACACT CTGAGCCCCA GANGCAGCAA AGGGTGAGCC 60  
TCCTGCCTTG GTTCTACCA CCATCTGGTG GTCAATGGCG GGACTGCAGT CGGCCAGGGA 120  
CTGCGGTTGA CCTACACCTT CCTCCCTGA GACATCAGCT GGCATGCCTC CAAGCCCTCT 180  
GCGCATGCC TCATTCTCTC CTGCCCCCTG GCTGACTTTG CATGTTGACT TGAACCCCTC 240  
TGGGGAATCT NTGTGCATGT CCACAGCCCC TGGTTATGCT CTCACAGCCA CTGCCCTNT 300  
CTNTGTTGAG GCTGAGCTGG CTGACCGACC CAATCCCNCT AACC GGCCCTC TGCCCGNTGA 360  
35 NCCGGTGGTT GAGAAGCCCG AAGTCTNAGG GGGCCAGCAA GGCCCAACC NCAAGGNAGG 420  
CAATTGCTTG CNGGACCCCA AGGGGNCGGN TNGCCAATGG GGGTGNACTT TGCCGGGCCA 480  
AAGGGGNTNN GAATTTCCGG CNCTTAAGTN GTNACCCTTC AANANNAANG GGGCAAACGG 540  
GTTTNGNAAA AN 552

40

SEQ ID NO:4260

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS05065

SEQUENCE DESCRIPTION:

50 GATCAGACCT TCTTGGGGTC TTCTGGCCAG AGCTTGTCAC CAGCCCCATG GCCTCTCCAG 60  
GCGTGCTCAT GCCCACAACC CGCGGCCAGC CCCACGTGGT GCCGCTCAGC CTTCTCTGCC 120  
CCTCCTGGGA ATCTGTCATT CGTGGGTGCT TCAGAGTAAA ATCAATGAGT TTCTGAGAAA 180

55



# EP 0 679 716 A1

SEQ ID NO:4261

SEQUENCE LENGTH:553

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05066

SEQUENCE DESCRIPTION:

GATCAGCGTG CGGGGTGTGA AGATAGGCGT CAAGGCCGAT GACTCCCAGG AGGCCAAGGG 60  
 GAATAAATGT AGCCACTTTT TCCAGTTAAA AAACATCTCT TTCTGCGGAT ATCATCCAAA 120  
 GAACAACAAG TACTTTGGGT TCATCACCAA GCACCCCGCC GACCACCGGT TTGCCTGCCA 180  
 CGTCTTTGTG TCTGAAGACT CCACCAAAGC CCTGGCAGAG TCCGTGGGGA GAGCATTCCA 240  
 GCAGTTCTAC AAGCAGTTTG TGGAGTACAC CTGCCCCACA GAAGATATCT ACCTGGAGTA 300  
 GCTGTGCAGC CCCGNCCTTC TTGGGGTCCC CCCAGCCCCT NAGGGCCAAG TTGCCAGGGA 360  
 CAAGCTTGGC TTGCTGGACA AGGGATGTTG GCAACTTGNT TTNAGGGAGG GGGGCAACTT 420  
 GNCCAAACCG CCANNNGGGN CAAAGGGAAA GTTNGGGGGG NCCCGTTTGG NCCAANGGGT 480  
 TAGGGGGAAG GGGTTGGGGG GNAATTNGGG GGNGGNGGGG AAATTTCNA GTTTTANTTG 540  
 TTAATTTTTT AAA 553

SEQ ID NO:4262

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05068

SEQUENCE DESCRIPTION:

GATCTCCCGG ACCCCTGAGG TCANATGCGT GGTGGTGGAC GTGAGCCACG AAGACCCTGA 60  
 GGTCAGTTT AACTGGTACG TGGACGGCGT GGAGGTGCAT AATGCCAAGA CAAAGCCGCG 120  
 GGAGGAGCAG TACAACAGCA CGTACCGTGN GGTCAGCGTC CTCACCGTCC TGCACCAGGA 180  
 CTGGCTGAAT NGCAAGGAGT ACAAGTGNA GGTCTCCAAC ANAGCCCTCC CAGCCCCCAT 240  
 CGNGAAAACC ATCTCCAAAG CCAAAGGGCA GCCCGAGAA CCACAGGTGT ACACCCTGCC 300  
 CNCATCCCGN GACN 314

SEQ ID NO:4263

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05069

SEQUENCE DESCRIPTION:

GATCCAGGGA ACAATGACTA TAGGTGAGCA GATGCTTTAA ATTAAGGAAA GATGGAGAAG 60  
 AAGCCAACTA GGAAATTAGA GAACACAGCA AGCAAAGAGA AGCAAGCGAG TCCCCTTGAG 120  
 TGATGCCAAT ACTTTTTTTT TTTTTTTT NGANANATTT TNTNNCCANT NTGGTN 176

SEQ ID NO:4264

SEQUENCE LENGTH:389

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05070

## SEQUENCE DESCRIPTION:

GATCTTTNAG GAAAGACGGA TTGCNTTAGA AATAGACAGT ATATTTTNG TCACAAGAGC 60  
CCAGCAGGGC CTCAAAGTTG GGGCAGGCTG GCTGGCCCGT NATGTTCCCTC AAAAGCACCC 120  
TTGACGTCAA GTNTCCTTCC CCTTTCCCA CTCCCTGGCT CTCAGAAGGT ATTCCTTTNG 180  
TNTACAGTGT GTAAAGTGTA AATCCTTTTC NTTTATAAAC TTTAGAGTAG CATGAGAGAA 240  
TTGTATCATT TGAACAATA GGCTTCAGCA TATTNTAGC AATCCATGTT AGTTTTGNAC 300  
TTTCTGTTG CCACAACCCC TGTTTTAACT ACTGTACCTT TANTTAAATT TCNNGGTTNN 360  
TAGTTTTTTG CAACAGGTTT TTTCCCAAA 389

SEQ ID NO:4265

SEQUENCE LENGTH:436

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05071

## SEQUENCE DESCRIPTION:

GATCACCATG AAAGAAGAAT AGTTTTTGT CCCAGAGAC ATTCATTTAG TTGATATAAT 60  
CCTACCAGAA GGAAAGCACT AAGAAACACT CGTTTGTGT TTTAAAGGC AACAGACTTA 120  
AAGTTGTCCT CAGCCAAGGA AAAATGATAC TGCAACTTTA AAATTTAAAG TATCTTGAC 180  
TGATAAATAT ATTTAANANT TGTATGTTA TAAAGTTATT AATTTGTNNN GNCNGTGTTA 240  
CAAAATGTTT AGTTTATATT GTTTTAGATT GTTTTGTAAT TTTAAAGGT GTAAAATAAC 300  
ATATTNTCC TTTATGGNNA TCTATAAAC TTTCTGGTAG TAAAATGTTT TCATTTTAC 360  
TGGGTATATT ATTTGCTTCC ATGNTTTTGT TNCCNTCCA TAAGNTTTN NTGCCAGNTT 420  
TTTTTTTTNN CAGGNN 436

SEQ ID NO:4266

SEQUENCE LENGTH:533

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05073

## SEQUENCE DESCRIPTION:

GATCTGTCCC CATCCGAAGA GGCTTTGTGA ACTGCCTGCT GAATGGAAGG AAAGCAACTT 60  
TAAACATTT AGAGTTTTGC TGAGTAGC CAAATGCCTG TNCTGAACT TATAGGAAAT 120  
TGGAATTTG TTTAAATTT TACACTTAA GGTAGCAAAT GTCAATTATT NGNCCGAGCA 180  
TATTGTGAAG AATTAACTA AAATTAATAC GTACAGTTT CTCTAATTAG GTGACTGTTT 240  
ATAATGGGTA TATTGGAAT TTAGAAGAAA TAATTTGTG GNACTTGTGG CCCTTATGTT 300  
TAACAGATTA ATTCAGCATT GCGTATTTN CTTTGTCCA ATACAAGGAT GCCAAAGGAG 360  
GGAAACAGGA AAAATTGCCG TCCCATTTT AAAAATTTA GGGGTTTGGN TGGTTTTAA 420  
CCCNTAAATT TGTTTCCCAN GGANCNTTT TTTGGGGACC TTNCTAAATT TTTGGGGGN 480  
CATTTTNAAN TTAAAGGNAT TGNNGGNNC NAAGGNNGTN TTTGANTTN TGN 533

SEQ ID NO:4267

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05074

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCAAGGAA GAGATGGAGG CTTTCCCCGA AAAGTTCTAG CTGAGTGGCA GAAGTGAGAA 60  
 TTTGTAAACT TATGTACAAT GTACGTGTAA ATAAATGGAT TGAATTCAG TTTGTCATCA 120  
 GAAA 124

SEQ ID NO:4268

SEQUENCE LENGTH:451

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05075

SEQUENCE DESCRIPTION:

GATCTGGGAC AGATTCTACT CTCACCATCA CCAACCTGCA GCCTGAAGAT TTTCCAACTN 60  
 ATTACTGCCA ACAGTATGAT AGTTACCCGC TCACTTTCGG CGGAGGGACC AAGGTGGAGG 120  
 TCAATCGANC TGTGGCTGCA CCATCTNTNT TCATCTTCCC GCCATCTGAT GAGCAGTTGA 180  
 AATCTGGAAC TGCCTCTNTT GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG 240  
 TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT NTCACAGAGC 300  
 AGGACAGCAA GGACAGCACC TACAGNCTCA GCAGCACCCT TGACGNTNAG CAAAGCAGNC 360  
 TACGNGAAAC ACANAGTNTA CGGCTGCGAA GTTNACCCCN TCAAGGGCCT TGAGCTTNGN 420  
 CCNGTCACAA AGGNGNTTNN AAACAGGNGG N 451

SEQ ID NO:4269

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05076

SEQUENCE DESCRIPTION:

GATCTAGAAA CTGAGTTGTG GAGCTGACTC TAATCAAATG TGATGATTGG AATTAGACCA 60  
 TTTGGCCTTT GANCTTTCAT AGGAAAAATG ACCCAACANT TCTNAGCATG AGCTACCTCA 120  
 TCTCTAGAAG CTGGGATGGA CTTACTATTC TNGTNTATAT NGNAGATACT GAAAGGTGCT 180  
 ATGCTTCTNT NATTATN 197

SEQ ID NO:4270

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05077

SEQUENCE DESCRIPTION:

GATCCCATCC CCTTGTCTGA ACTGGAGCCA TGGGCACAAA GGGCCCAGAT TAAAGTCTTT 60  
 ATCCTCAAA 69

SEQ ID NO:4271

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05079

## SEQUENCE DESCRIPTION:

GATCTTGCCT CCCATCAGCC ATCTTTCTCC CAATAAATTT TTGTTTTGTG CAAA

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SEQ ID NO:4272

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS05080

SEQUENCE DESCRIPTION:

GATCTAACCA ATTNAAATAT GANTTCATAC TCNAAAGTAT CAACAAAAAA ATGAAAAGAA 60

ATAGCTGGTT TGGNTGTAAG AAATGGTGTA ATTAATGGNT TTN 103

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SEQ ID NO:4273

SEQUENCE LENGTH:449

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS05081

SEQUENCE DESCRIPTION:

GATCACTGCT GGCCTACTCT GGTACGGGG AACTGACGC CCGGGTCACC GCTGCCATAG 60

CCAGTAACAT CTGGGCCGCC TACGACCGGA ACGGGAACCA AGCGTTTAAT GAAGACAATC 120

25

TCAAATTCAT CCTCATGGAC TGCATGGAGG GCCGTGTAGC CATCACCCGA GTGGCCAACC 180

TTCTGCTGTG TATGTATGCC AAGGAGACCG TGGGCTTTNN NNTNCTCAAG GCCAAGGCC 240

AGGCTTTGGT GCAGTACCTG GAGGAGCCCC TNACCCAAGT GCGGGCATCT TAACGGCATT 300

GGTGGAAGCT GGGGGTCAGA AAAGAGAAAT GACCCATTG NGAGGGGCTG GGGGNCCTCC 360

TAGGAAGAAC CTTTNTTAGG ACAATGGGGG GNAAGGGATG GGACTTTTNN TTTTTTCCC 420

30

AAGNATTAAA ACTTNAACT CCCTGTAAA 449

SEQ ID NO:4274

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS05082

SEQUENCE DESCRIPTION:

GATCTNCATA ANCAGGGTTC CTGAGCTCAC TGAAAAGACT ATTGTCCCTT AGGAAAAGCA 60

TTTCCTGTGT NTCGTNAGCA TCTGGCTCCA GGACAGACCT TCAACTTCCA AATTGGATAC 120

40

TGCTGCCAAG AAGTTGCTCT GAAGTNAGTT TCTATCATNC TNCTCTTGA TTCAAAGCAC 180

TGTTTCTCTC ACTGGGCCTC CAACCATGTC CCCTTCTCCT NAGCACCACA AATAATCAAA 240

ACCCAAA 247

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SEQ ID NO:4275

SEQUENCE LENGTH:424

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS05083

SEQUENCE DESCRIPTION:

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GATCATTTC CAAGATTGGT TTCCCTTGAG TTTTGGCTAA AACAAATCTT AGTAGTTTGG 60  
CCCGTTTAAA ACAACTCACA ATCGTAAATG CTACTATTCC TAAGATATCT NACCTTTTNA 120  
TTTCAGTTTA GCCATGTATT GTATGAGTGT ATTAGTCTAA GCAGTGAGAA TCTTTNCTAT 180  
GCCTCTATT CAGCAAAAAG TAGAAGTATC AAATAAAANG GGCAACTTTT AAAATATTAA 240  
GCCTGAAGAC TTCTAAAANG ACANGANACA TGGCCTAANT ANCCAACATA GGATTTACAT 300  
AGTANGTTTC ACACTACCTT ATTACCAAAA GCAAACCACC TCTTACTTTT NNNCTACATT 360  
TATCCATGTA TATCTNTNGT ATGCTGGTCT TTNCTTTTT NGCCAAANTC NANCATTTTT 420  
TGNN 424

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SEQ ID NO:4276  
SEQUENCE LENGTH:308  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05085

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SEQUENCE DESCRIPTION:  
GATCTAAAC TTCTGTTGCT TTTGCCATT CAAAACTTTG TCTTTGCCAG AAAAGTGTGG 60  
GTAACATAA AGAAAATTAT ATATGANCAC GGCAGTTTGC ACTGTGTTTG AGTAGAACGT 120  
GTAAATGAAT TGTNCCCACC TTTGGTTTGC CAGTAAGTGA CTGGATTCTT GGCACATTAA 180  
TGTTACCAA AGTAGAACAA GAAGATATTA TTNCTATTTA TCAAGCAAAA GGAATTTTAA 240  
GATTTTNTTT TTNCNTTAAA ACCAANTTGG GATTTTNNNN TTNNTTTTN TTTGGGGGAA 300  
AAGGNTTN 308

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SEQ ID NO:4277  
SEQUENCE LENGTH:374  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05086

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SEQUENCE DESCRIPTION:  
GATCGAGTCC GCCATGGAGA GGGACCGCTA CATGAGCCCC ATGGAGGCCC AGGAGTTTGG 60  
CATCTTAGAC AAGGTTCTGG TCCACCCTCC CCAGGACGGT GAGGATGAGC CCACGCTGGT 120  
GCAGAAGGAG CCTGTAGAAG CAGCGCCGGC AGCAGAACCT GTCCCAGCTA GCACCTGAGA 180  
GCTGGGCCTC CTCTCCAGAN TCATGTGGAG GGGCCAGAGG CTGCCAGACC CCCAGCTGGG 240  
CCCTGCTCAC CCCTGTGTGC TGGGCTTGGG GGGGCCNTT GAGGAACTTT TAATTTGCAG 300  
GGGTGCCCGN TATGGACGGG GCATTNCAGC TGAGACACTG TGGATTTTAA ATTAAATCTT 360  
TTGTGGTCTT TAAA 374

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SEQ ID NO:4278  
SEQUENCE LENGTH:510  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05087

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SEQUENCE DESCRIPTION:  
GATCTGTGCT TTCCAGCTCA CCCCCACAC TCACTCCTGA GACCCCTGGC CTCCGGCGTC 60  
ACNTCCAGCN TCTGTTCCCC TAGTAAGTGC CTTCCATGTC GGCCTCTAAC CCCAGGCCCC 120  
GAGGACCCAG ACCCAGTGGG GAGGCGGACG TTCCAGCCGG CATGGNTGGG AACTGCAGAC 180

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CTGTCTCCT GGTGGGTCCA GGGGCCCCCTC CAGCTTGTGG AGCCCCACAN TGGGGTGCCG 240  
 CCTGCCCGTT TTTTCCCAT GGAGCCCCAG CCCCCTTTGG GCCCAGGGAC ACCAGCCAGG 300  
 CTCTGTGCTG ACCCTCCTGT TGCACCCAGN CCTGGTNTCA GCAGCGACCA CCCCTTGCNT 360  
 TCACCCTTTG GAGCTTTTGC AATGTTTCCA NTAAANCCCN GGGNTGGGT NGGNAAGGTT 420  
 GGGAGGTTGT TAAGGTTGTT TNGGTGNNCT TTTTGAAAGG GGNAGGATNA ATTAACCTTG 480  
 ANCCNNTGGG GCGGNGNGNC TTTTGNGGTN 510

SEQ ID NO:4279

SEQUENCE LENGTH:466

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05088

SEQUENCE DESCRIPTION:

GATCTAGCTT GGAGAGCTTG TGAATCTTAG GAGAGCTAGG CATAGAATGA CTAAAGTTTG 60  
 TCACCGCATG AGATAAAATA AATGAAAAGC CACTTCTGGA GGAATGAGG CAGTCTGCCT 120  
 TTNTTGGAGA GATACATATT GTTGAACAGC TCTGGGCAGT TGATTGTTG CCTGGGAGAG 180  
 CTAACCATGT TTAATCTACA CTTGACCTGT GATGGTCTGT ATTGATTGTN TCACACGCTT 240  
 AGCTTTCTAA GGCTAACCAG GTCATCGTCC TCAGTCCCTG CCTGCAACTA GGTGGCAAC 300  
 TGGCCCTTGA TTTCCACCC AACTTGTTC GTTTGCCCTC AATCCTGGGG CCTCACTNAT 360  
 TTCCCAAAA NGATATGGTT TGGTACCACC TGTAGTTTNC CTGTTGCATG GTTAAACCTG 420  
 ACTTTTGGG GAAACTNAAA ATANAACANT TTTTCAAAAC GGGAAA 466

SEQ ID NO:4280

SEQUENCE LENGTH:470

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05089

SEQUENCE DESCRIPTION:

GATCGAGCCA CTGCTGAAGA ATGTCTAAAG CACCCCTGGT TGACACAGAG CAGTATTCAA 60  
 GAGCCTTCTT TCAGGATGGA AAAGGCACTA GANGAAGCAA ATGCCCTCCA AGAAGGTCAT 120  
 TCTNTGCCTG ANATTAATTC GGATACCGAC AAATCAGAAA CCGAGGAATC CATTGTAACC 180  
 GAAGAGTTAA TTGTAGTTAC TTCATATACT CTAGGACAAT GCAGACAGTC TGAAAANGAG 240  
 AAAATGGNGC AAAAGGCCAT TTCCAAACGA TTAAATTTG AGGAACCTTT GCTACANGAN 300  
 ATTCCAGNG ATTTTATCTA CTGAGCAATA TTTCCCTTN GAACTTCAAG ATTTCTNCAC 360  
 TGNANAATTN TTAATNTTN TTTTTTGGG GCCCTCTGGG CCAAATTGGN GNCATGTTCC 420  
 TTTGNAGGTG GGTAAACCCA GTTNTCACTT TNCACAGTC CANNTNTTN 470

SEQ ID NO:4281

SEQUENCE LENGTH:476

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05090

SEQUENCE DESCRIPTION:

GATCTACAGT CACCATATAT ATCAGCAGGA CCTAAGGNAA AAGATTTTGG ATGTTGGGAA 60  
 AAGGTTAGAT GTGACTGGAT TTTGCATGAC AGGNAAGCCT GGTATAATCT GTGTGGAGGG 120

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TTTCAAAGAG CACTGTGAGG NGTTCTGGCA CACAATTAGG TACCCCAATT GGAAGCACAT 180  
 TTCCTGTAAG CATGCTGAAA GCGTGGAGAC AGAAGGAAAT GGTGAGGACC TCGCCTTTN 240  
 CCATTCTTTT GAAGAGTTAC TCCTTGAGGC TCATGGTGAC TATGGATTAN GGAATGACTA 300  
 TCACATGANT CTGGGCCAAT TCTTAGAATT TNTCAAGNTG CACAAAATTT NAGGCATGTT 360  
 TTTTCCNGT TACTATTTTG GGTNTTNTNA AGCAAAAANT TTCAGNCTTC NTAAAAAGCG 420  
 GNTTAAAGGG GGNCTATTG NCCTGTNAAT TTTCCACTNA GGNCAAGTNT TTCTTN 476

SEQ ID NO:4282  
 SEQUENCE LENGTH:277  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05092

SEQUENCE DESCRIPTION:  
 GATCTGAATT GTNCGAAAAG CAGCCAGTGC CTAANTTGTA GCTCCACTTA TGCCAACGTG 60  
 ATATATACCT CTCGTGAGCA TAGCAAGTNA TTTANTATTT TNAAGAGATG GCTAAATCC 120  
 TTTTAATGAA CAGCACTAAA GTTATATGTA TTAGAGGAGA ATTATTGANT GANATGGAGA 180  
 AAGAGTTCTG AAATTANTAT TTNCATTTGG GCTTTTTTAC AGATAATATT ATATNNCTAA 240  
 GTGACCAGAC GAAAGAGAAG GGNGTAGAAA AGGNTGN 277

SEQ ID NO:4283  
 SEQUENCE LENGTH:314  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05094

SEQUENCE DESCRIPTION:  
 GATCCCAGA CCTCACTTGC CTCTGCCTCC ATCTTGGCCC TGATTCAACC CTAAGATAAT 60  
 AGCACAAACA AATTCTNCAT AAAGATATTT TAATTCACCT GTNCCGTGCT ATATGGAGGA 120  
 GGCCAAGTCC ATTTAGTGAC ATTNCTNCCC ATAATGTGAG TGGGGAGGAT TGTGGGGAGG 180  
 AGGGGGTTTG GGTTCTGTG TTTGTGCATA TGAAGGGAGA TGGGGGTTAG GTGGAGGAGG 240  
 AGAGCAGCGT GGTTAGCTAA GGTTATTGCT TTTTGTGGCA AATCTAATTA AATGACAGGA 300  
 ATCTCTTCAC GAAA 314

SEQ ID NO:4284  
 SEQUENCE LENGTH:489  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05095

SEQUENCE DESCRIPTION:  
 GATCTTCATG GAGCTGAATG ACGCCTGGTC GGAGTTTGAG AACCAGGGCT CNCGGCCCTT 60  
 CTTCTGAGGC CGCAGTGGTG GTGGCTGCGC ACACAGCTCC ACAGGTTGGG AGCCGTCGTG 120  
 GGACCTGGGT CCCACCGTN AGGACCCCGT GGGCGACAGA GGTGTGGCCA GGGTGGGGCT 180  
 CCGAGCCCGG GGTACCGCC CGCCAGCGT TCCAGGCACA TGAAGAGAAA GCATTCCAAA 240  
 GCCTCTNATT GTTGTTCCT TTTNTCCTC CCGAAGAACA GCTGATTCAT GCTCCTCCCG 300  
 CAATTNTNAC GTCTGTAATT TATTTGGTGT TTCGGGCGTN GTCTCTTGGA GCCCCGGCAC 360  
 GTTNGTGGGG CCCACGGTTG CTTGGCGGTT CAATGGGGCC CTTGGTGTTT TGCACCGGAA 420

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CTTTGTAAA TCAAGTNCCG TGGGTTGGTN TTGTTACAAG AATTNAAAAC TAATTTTCC 480  
CGNTTGAAA 489

5 SEQ ID NO:4285  
SEQUENCE LENGTH:292  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS05096

SEQUENCE DESCRIPTION:

GATCATATTT CCCCTTGGAC ACTTGGTTAG ACGCCTTCCA GGTCAGGATG CACATTTCTG 60  
GATTGTGGTT CCATGCAGCC TTGGGGCATT ATGGGTTCTT CCCCCACTTC CCCTCCAAGA 120  
15 CCCTGTGTTC ATTTGGTGTT CCTGGAAGCA GGTGCTACAA CATGTNAGGC ATTCGGGGAA 180  
GCTGCACATG TGCCACACAG TGACTTGGCC CCAGACGCAT AGACTGAGGT ATAAAGACAA 240  
GTATGAATAT TACTCTCAAA ATCTTTGTAT AAATAAATAT TTTTGGGGCA AA 292

20 SEQ ID NO:4286  
SEQUENCE LENGTH:173  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05099

25 SEQUENCE DESCRIPTION:

GATCCCAAGTG GAGGCTGTAA CCCACCTGCC CCCGCACCAC CCCCNTGAC CCCTGTTACC 60  
GCATTGTGT GTATTAATGC TGAAGAATTA AATGTTTAAA GAGTTTAAAT TTTGAAGGCG 120  
TTTGCTATAT ACAGTTGTCC TGCATTATTA TAAAGAGTTT TCAGGAAGTT AAA 173

30 SEQ ID NO:4287  
SEQUENCE LENGTH:307  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

35 CLONE:HUMGS05100

SEQUENCE DESCRIPTION:

GATCAGAAAT GTGAAGCACA AATGCTGCTT CTCCCCCTCC TGTTCCCATG TCAGAGATGG 60  
AGAAGAAAGC ACAGTGAGCT GTTCACCAGT CCAGCGGTGA CCTCGGAGTC CTTTGTAACA 120  
40 GTGTTTCCAA TANCTTCTGC CAATAAAACA GAATTNNGT TAGAACCTAT CTGCTGTCCC 180  
TCAACTAGTG TCTGATAGCT GAGAATGTAA TTCGTTNTN TGTCTATTAG AAAATTAGGC 240  
AGGCACCACA GACAGTAGCA ACATAAAGGA ACCTGCTTAG AAGNGGTTTT NATGGGNNNN 300  
NNCNCNN 307

45 SEQ ID NO:4288  
SEQUENCE LENGTH:244  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS05102

50 SEQUENCE DESCRIPTION:

GATCCTTAAA TCTCCATTCT GTTTGTGGTT GCCCCCTCAA CCTCCCCTAC ACCCTTCCTA 60

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TTCTTTTNC A TTCTTCTTGC AGTTCTGGGA GTAAAGCTCC CAGCATATTT AGATAATAGG 120  
GCAGGGGAAG CACCCTCTTT CTTTCTAGAC TGGATTATGC TCACATGCTC CCTTGCCCTG 180  
ACATTTTGT AAATNCTGTG CCCTTTGCTG TAGCTACACT TCAGATTAAA GTAGGAGAAA 240  
GAAA 244

SEQ ID NO:4289

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05103

SEQUENCE DESCRIPTION:

GATCAAAGTT GCGGGGGGCT TGGCTGTGCC CTCAGATTCC GCACCAATAA AGCCTTCAAA 60  
CTCCCTAAA 69

SEQ ID NO:4290

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05104

SEQUENCE DESCRIPTION:

GATCTTTNAT CCTTTGTTGC AAAAGTGTGG AACTTTTNA NAGCTTGGCA GATTTNAACT 60  
CCAGAAGCAC TTTATGAAAT GGTACACTGA CTAATCCAGA AGACATTTCC AACAGTTTGC 120  
CAGTGGTTCC TCACTACACT GGTACTGAAA GTNTAATTNN TTAGAGCCAA AAAACTGGAG 180  
AAACAAATAT CCTGCCACCT CTAACAAGTA CATGAGTACT TGATTTTAAT GGTATAAGGC 240  
AGAGCCTTTN NTTCTCTTC TTGATAGATG AGGCCATGGT GTAAATGGAA GTTTCAGAGA 300  
GGACAAAATA AAACGGAATT CCATTTTTTT NTCAGTGTAA A 341

SEQ ID NO:4291

SEQUENCE LENGTH:395

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05105

SEQUENCE DESCRIPTION:

GATCTTAGAG TCACTTTGGA ATAAGNTCTT ACATAAATAC CCCCAGCCTT TTGAGAACGG 60  
GGCTTGTTAA AGGACGCGTA TGTAGGGCCC GTACCTACTG GCAGTTGGGT TCAGGGAAAT 120  
GGGATTGACT TGGCCTTCAG GTCCTTTGG TCATAATTTT AAAATATGGG AGTAGAAAAC 180  
AACANAGNNT GGAATGGACT CTTAAAACAA TGAAAGNGCA TTTATCGTTT GTCCCTTGAA 240  
TGTAGAATTT TTTTTTGATT TCATAATTCT NCTGGTAAAT NTGNCAGTTA AAATGGTGCA 300  
TTATGTATAT ATTANTATAA TTTAGANATT CCATTTTATA NTTNTCCTA TTCCAGGGTN 360  
GCATAANGCA TTTTNNANTT TNGGGGTTTT GGNTN 395

SEQ ID NO:4292

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05106

SEQUENCE DESCRIPTION:

5 GATCATATTT TGCAGTTTTA GTAAAAGGGA AATATTGTTA TACATTTNTT AAATATACTT 60  
 CCCCATGAN GTGAAAAGGT TAATTTTNC TANTGTTTTA AGTTGAAGTT ACTTCATGGA 120  
 TGTACATACC ATGANGTGCA TTTGGNTGAG ATAGCNGAAA TTTTTTTTAA AAAAGTTTAA 180  
 GTACCAAAGG TAGTCTAGTC TAGAACGATA AGTTAATACG TTTTGGCTTT NNTAATTTGT 240  
 ACTGTAACAT CCTTATACTT TCTATTTNAA GTATATCTGT TTCTTAAGTA AACAACTTAG 300  
 10 ATATTTTCCA CACCTTTTTT TTTTTTNCC CNTGNNGGGT CCNGGGTNN 349

SEQ ID NO:4293

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05107

SEQUENCE DESCRIPTION:

20 GATCTGCCAT TTATTAGCTG TGGGATTTTG GGCAAATTTN TTGACTTTCT GTGCTTCANT 60  
 TTTCTTAGCT GTAAAATTGG AAGAGTTGTT ATGAAAATNC ACTGAAAGTA TATTTGTATA 120  
 CATCATAGGA TAGTGTAAGA ATATAGTATG GCTTTGAGAA ATGTTTATNA TTATNACTCC 180  
 CAGAGGAGTT TTAGGTATTA AGTGATGCCA AATATAATTT NTNAATTGTA TAATAAAAAT 240  
 CTATATNCTT ACTGAAA 257

SEQ ID NO:4294

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05108

SEQUENCE DESCRIPTION:

30 GATCACCATC CCAGTAACCT TCNAGTCGCG GGCCAGCTT GGGGGCCCAG AAGCTGCAAA 60  
 ATCCGATGAG ACTGCCGCCA AGTAAAGCCT TAGCCCGGAT GCCCACCCT GCTGCCGCCA 120  
 35 CTGGCTGTGC CTCNCCCGTN ACCTGTGTGT TCTTTTNATA CATTTATCTT CTGTTTTTNT 180  
 CAAATAAAGT TCAAAGCAAC CACCTGNANA AA 212

SEQ ID NO:4295

SEQUENCE LENGTH:559

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05109

SEQUENCE DESCRIPTION:

45 GATCCAGTGG GGATGTTGTN ATGACTCAGT CTCCACTCTC CCTGCCCCGN ACCCTTGGAC 60  
 AGCCGGCCTC CATCTCCTGC AGGTCTAGNC AAAGCCTCCT ATACAGGGAT GGAAACACGT 120  
 ACTTGANTTG GTATCAGCAG AGGCCAGGCC AACCTCCAAG GCGCCTCATT TATGAGGTTT 180  
 CTAAGCGGGA CTCTGGCGCC CCAGACAGAT TCAGCGGCAG TGGGTCAGCC ACTGATTTCA 240  
 CACTGACANT TAGCAGGGTG GAGGTTTGAC GATGTTGGGA TTTACTATTT GCATGCAAGG 300  
 50 AACACACTGG NCTCAGACGT TCGGCCAAGG GGACCAAAGG TGGNAAATTC GAACGAACCT 360  
 GTGGCCTTGC ACCNATCTTT TTTTCATCTT TNCCGNCATC TTGGTTGNGC AAGTTTGNA 420

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ATNTTGGGAA CCTNGCCTCC TTTTGGGTGN TGCCTTGNCT TGAAATAACT TNNTTATTCC 480  
CAAGAGGAGG GNCAAANTTC AAGTTGGGAA GGTGGGTTTA ACCGGCNTTC CAATTCNGGG 540  
GNAANTCCCN TGGNGGGNN 559

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SEQ ID NO:4296  
SEQUENCE LENGTH:50  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05110  
SEQUENCE DESCRIPTION:  
GATCTCTATG TATGTGTGTA TATAAATATA GTTTTTTATC TATATATAAA 50

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SEQ ID NO:4297  
SEQUENCE LENGTH:548  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05111  
SEQUENCE DESCRIPTION:  
GATCAAACGA ACTGTGGCTG CACCATCTTT NTTCATCTTC CCGCCATCTG ATGAGCAGTT 60  
GANATNTGGA ACTGCCTCTT TTGTNTGCCT GCTGAATAAN TTCTATCCCA GAGAGGCCAA 120  
AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCAQAGA 180  
GCAGGACAGC AAGGACAGCA CCTACAGCNT NAGCAGCACC CTGACGCTGA GCAAAGCAGA 240  
CTACGAGANA CACAAAGTNT ACGNCTGCNA AGTCACCCAT CAGGGCCTGA GCTCGCCCGT 300  
CACAAAGAGC TTCAACAGGG GAGAGTTTTA AGANGGGAGA AGTGCCCCCN ANCTGGNTCC 360  
TCAGTTCCAG CNTGACCCTC TCCNATCCTT TGGCCTGTGA CCCTTTTTTT TCCACAGGGG 420  
GNCCTACCCN TTTTGGNGGT CCTCCAGCTC ATTTTTTTAA CCTTAACCCC GNTTNNTTCT 480  
TCCTTTGGGG TTAAATTAT TGNTTAATT TTGGGGGNGG ATTGNTTTAA ATTAAAGGGA 540  
ATNTTTTN 548

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SEQ ID NO:4298  
SEQUENCE LENGTH:415  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05112  
SEQUENCE DESCRIPTION:  
GATCAGCGCC TGAGAAGTCG TCGGGCGATG TCCCCGCGCC GTGTCCCTCT CCAAGCNCCG 60  
CCCCTGGGTG GGCTCGGTGG AGCAGACCCC GCGCAAGAGG CTGCGGTGAG CCAATTTAGA 120  
GCCCCAAGAG CCCCAGGGA ACCTGCCGGG GCAGCGGACG TTGGAAGGGC GCTGGGCCTC 180  
GGNTGGNACC GTTCATGTAG CAGCAACCGG CGGCGNNTGC CCAGNAGCAG CGTTCGGTTT 240  
TTTTTTTAAA TTTTNA AAC TGTGCAATGT ATTAATAACG TTTTTTTATA TCTAAATGGT 300  
ATTCTGCACG AGANGNTACA CTGGGTCCCA AAGGTGTAAA AGCTTTTTAA GAGTCATTGT 360  
ATTATAAAN TNNNTTAAT CTNTGGTTG AAATCTTNA GTGNANAGT ATTN 415

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SEQ ID NO:4299  
SEQUENCE LENGTH:156

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05113

SEQUENCE DESCRIPTION:

GATCTAATCT NAGATGTAAA CATTCAAATT NACCCTGTAG ACTNGGGTGA CAAGTTTCGN 60  
TTGGTCATAG CTAGTACCTT GTATGANGAT GGTACCCTGG ATGATGGTGA ATACAACCCC 120  
ACTNATGATA GGCCTTCCAG GGCTGACCAG TTTNAN 156

SEQ ID NO:4300

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05114

SEQUENCE DESCRIPTION:

GATCTTACTT TCATCCAGTC TAATAGGTTT GGAGATTAAA CCTTNTCTCA ACTTGTGCTG 60  
TTTATATAGC CAAGCTTCCG TCAATAAGGC TTCATTGTGA CTTTAACAAA CATNATCTTC 120  
CCACATACCA GGAACATATTG GACATTTATT TTACATGGGA AAAATTATTT GGAATAATAA 180  
AGCAGGNACT TTNCCTGANG TTGCAATTA TACTGTATGG CTNCTNNTTC ATGTTTCATC 240  
TAGGTTTTAN GAAGTGAAGT ATANGTAAAT NTNGGTTTCGT TAAATNGTGA TGGCGCTGGN 300  
NATTACATGN 310

SEQ ID NO:4301

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05115

SEQUENCE DESCRIPTION:

GATCACTCAA GCACAGGATT TTAAGACCAG CCTGGGCAAC ACAGTGAGTG AGACCCTGTC 60  
TCTACAAAAA AATTAAAAAT TAGCTGGATA CTGTGGTGTG TGCCTGTAGT CCCAGGTACT 120  
TGGGGCATTG AGGCAAGAGG TTACTTTNAG CTCGGGTGTT TGAGGCTATG ATGAACTATG 180  
ATTGTAGTGC TGTACTCCAG CCTGTGCAAA ANAGTAAAAC CTTGTCTCAA A 231

SEQ ID NO:4302

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05116

SEQUENCE DESCRIPTION:

GATCGGGCCA CTGCACTCCA GCATGGGTGA AAAAGTGAGA CCCTACCTCA AA 52

SEQ ID NO:4303

SEQUENCE LENGTH:419

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05117

## SEQUENCE DESCRIPTION:

5 GATCACCAAC AGCCGTCCTC CCTGCGTCAT CCTGTGACTG CACAGGACTC TGGGTTCTCTG 60  
 CTCTGTTCTG GGGTCCAAAC CTTGGTCTCC CTTTGGTCCT GCTGGGAGNT CCCCTGCCT 120  
 CTTTCCCCTA CTTAGCTCCT TAGCAAAGAG ACCCTGGCCT CCACTTTGCC CTTTGGGTAC 180  
 AAAGAAGGAA TAGAAGATTC CGTGGCCTTG GGGGCAGGAG AGAGACACTC TCCATGAACA 240  
 CTTCTCCAGC CACCTCATA CCCCCTCCCA AGGGTAAGTG CCCACGAAAG CCCAGGTCCA 300  
 CTCTTNGNCT CGGGTAATAC CTGTCTNGNT GCCCACAAGA TTTTATTNA TTCTCCCCTT 360  
 10 AACCCNAGGG CAATGTCANN NTATTGGCA GTAAAAGTGG GGGTTACAAA ANCACTAAA 419

SEQ ID NO:4304

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05118

SEQUENCE DESCRIPTION:

20 GATCTCCCTA GGGCCCCACC TGGACCATT TCCCTCCGTT TTATTTTGTT AATTAAATTC 60  
 TTTCCAAATT GAAA 75

SEQ ID NO:4305

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05119

SEQUENCE DESCRIPTION:

30 GATCTCAGTT CACTGCAACC TCCGCCTCCN AGGTTTCAGGT GATTCCNTTG TCCCAGCTAC 60  
 TTGGGAGGCT GAGGCAGGAG AATCACATGA GCCTGGGAGA TGGAGGTTGC AGTGAGCCGA 120  
 GATTGCACCA CTGCACTCCA GCCTGGGCAA CGAGCAAACC TGCNNCTCAA A 171

SEQ ID NO:4306

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05120

SEQUENCE DESCRIPTION:

40 GATCCCTGGT GTGTTGTGTG GGCCTCTTTA ACGTTTGCCA CTGAGCCTTA ACCTCACTGT 60  
 ACTTCACTGT ACTTCACACG CATTGGTGTT AACATTTTAA TCTTAGAAGA CCCTGACCCA 120  
 CTGAGGGTTT GTTGTGAGAA TTGCTGAAGC CACGTAGAAG CACCTTGAAA TCTGTAAAAC 180  
 CACAAGAAAG TACTTTATAA AAGGTATCCT TATTTGAAGT GGATAAATCT TGTAACCTCGA 240  
 45 AAAGTTGTGA TTTAGAAGAC AGGATTGTTT TTGAACATTA GGAATTAAAG GCTATATCTG 300  
 GTCCTTAAA 309

SEQ ID NO:4307

SEQUENCE LENGTH:587

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05121

SEQUENCE DESCRIPTION:

5 GATCTAAAAA CTCATCTTTG GGGTAAAGAG TTAAGTGTCC AAAGGTTGTC ACAGTTCATG 60  
 AGGTCAGAGG GAGCTAGCCT GGCACCTGGA CTCTGCCCAT CCACAGCTGA CAGATTCCAA 120  
 CAGAAGTGTA TTAAATTCT CCAGTAGACA ATGCTGGGTA AGGGAGGGGN TAGNNCTGGG 180  
 TTATTAAGAT ACAGGCTGCT GTATTTTACA TTGGTTGTGG GGAAGGGGA GCCTGGAGAA 240  
 AACAAAGTCA CTATTCCCTT TTTTGAAACA GGAAAAAAA TTATTTTTTG TTCAGTAAAA 300  
 10 ATGGGTAGGN GAATTCCAAT GTCCCTAGCC ACAAGGNCC AGTTTCCACT GAGGAAGTGA 360  
 ACCAGTGGGG AACTCAAAAT TTCCAGGNAA CATTGGGGGG GAGGGGGAAA ANTTGGGCTT 420  
 TTCNCTTAAA TTTGGCAGNT NTTNCCAGT TGGGGNCNGG GNGGGGGGCT CCTGTTTTTT 480  
 TTTTTTGGGG NTTGTGNTTA NTGNTNNTAT NGTACCGNT TATTTTGGC CCCGGGGTTT 540  
 15 TTCTTGGGNT TTNTNAAGGG TTNCCCCAAA NTTGGGTNA AACNTN 587

SEQ ID NO:4308

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05122

SEQUENCE DESCRIPTION:

20 GATCCCCCA TCTCTNCAGC ACTCTCTTGC TCCTCTCCCT TTTCATTTCC TTACTTTGTA 60  
 25 TCTTNTCAGA TTAGAACATA TTTNNTTGT CATGACAAAG GACTCTCCAA A 111

SEQ ID NO:4309

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05123

SEQUENCE DESCRIPTION:

30 GATCTNAACT CCTTGCTTC TTTACTTAGT TCAAGCCCCA GCCTAGGAAA GCCAGTTACA 60  
 35 TAAAAGTTGG CTCAGGAGTC TTAGAGCTTT ACCTAAATAT GAGCCCAGAA AACGGAGGAT 120  
 GGGGGTGGGG CGCCTTCCTG GAGGTGACAC TTGATGGGGG TGTGTTCTGG TTACTGTTCT 180  
 AAGGCTGTGC CATCAGCTCC TTCCTCCCT GTTCATTCTG CATTCTCTAG TCAGTTGGCT 240  
 AAGAAGTGAC TCTTGCAACT AAAAAATTA AGAAATTCAC TTCCCTCTA GGAGGTGATG 300  
 40 ATAGGGTTTT N 311

SEQ ID NO:4310

SEQUENCE LENGTH:366

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05124

SEQUENCE DESCRIPTION:

45 GATCAGAGTT TCTGTGAAT TCTGTTTGT AAATCAAATT AGCTGGTCTC TGAATTAAGG 60  
 GGGAGACGAC CTTCTCTAAG ANGAACAGGG TTCGCCCCAG TCCTCTGCC TGGAGACAGT 120  
 50 TGATGTGTCA TGCAGAGCTC TTACTTCTCC AGCAACACTC TTCAGTNCAT AATAAGCTTA 180  
 ACTGATAAAC AGAATATNNA GAAAGGTGAG ACTTGGGCTT ACCATTGGGT TTAAATCATA 240

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GGGACCTAGG GCGAGGGTTC AGGGCTTCTN TGGAGCAGAT ATTGTCAAGT TCATGGCCTT 300  
AGGTAGCATG TATCTGGTCT TAACTCTGAT TGTAGCAAAA GTTCTGAGAG NAGCTGAGCC 360  
CTGTTN 366

SEQ ID NO:4311  
SEQUENCE LENGTH:240  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05127

SEQUENCE DESCRIPTION:  
GATCACGCTG ACCTGGCAGC GGGATGGGGA GGAACAGACC CNGGACACAG AGCTTGTGGA 60  
GACCAGGCCT GCAGGGGATG GAACCTTCCA GAAGTGGGCC GCTGTGGTGG TGCCTTCTGG 120  
AGAGGAACAG AGATACACAT GCCATGGTGC AGCACGAGGG GCTNCCCCAG CCCNTNATCC 180  
TGAGATGGGA GCAGTCTCCC CAGCCCACCA TCCCCATCGT GGGCATCGTT GCTGGCCTTN 240

SEQ ID NO:4312  
SEQUENCE LENGTH:96  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05128

SEQUENCE DESCRIPTION:  
GATCTTTTCT CCATCATGTA CTTAGTATTT CCCATTAACC TACACACTGA TTTTNTGCT 60  
ACTCCTTGTA GAAACAAAAT TNTGGNTGGA CTCAGN 96

SEQ ID NO:4313  
SEQUENCE LENGTH:354  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05129

SEQUENCE DESCRIPTION:  
GATCTGCTGG TCCTTGCAGG CAAAGCTACA GCCAGANTGT CCGTTTGANA CTCCTAGCTC 60  
ATCTGTCACC GAGCTTNATC CGAATGTGCC ACGGAGCTTN CTCTCCACTT CCTCCGTGCA 120  
GCGGCCCTGC CACAGCCCTC CCTCGGCACA CTTTGACCCT TTGTAGGGTT GGNATTAGCA 180  
GGACTCGGCT ATTTAAAGCA CCAGTCTGGG GTCGCCTGGG CCCCTGCTGA CCCNTTCCTN 240  
CAGAGCAGCC AGCCAGCCC GGAACAAGA CGGACTTNCT ATNCCTTCGG ACTCACAGCC 300  
TTTGAAGAGT CAAGCTNCAC TTNAAGCTCA CTCAGTAATA TCCTTTCAAT GNGN 354

SEQ ID NO:4314  
SEQUENCE LENGTH:161  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05130

SEQUENCE DESCRIPTION:  
GATCCGCCAC TTTCGGCCGG AGCTCGAGGA GCGGATGCAG CGGTTTGCCC AGCAGCATCA 60  
GGCCCGGCAG GCTGCCTCTT AGCCCACCAC CCTGGCCTGC TGTCTGCGT CTATCCATGT 120

GGAATGCTGG ACAATAAAGC GAGTGCTGCC CACCCTCCAA A

161

SEQ ID NO:4315

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05132

SEQUENCE DESCRIPTION:

GATCCTGGCT TTCCAGGGTG GGCAAGGGCA AGGAGCAGGC TTGGAGCCAG GGACCAGTGG 60  
 GGGCTGTAGG GTAAGCCCCT GAGCCTGGGA CCTACATGTG GTTTGCGTAA TAAAACATTT 120  
 GTATTTAAA 129

SEQ ID NO:4316

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05133

SEQUENCE DESCRIPTION:

GATCTTTGAG GTGAACAACT TGCCTGTGGA ATCGTGGCAG TAACTGTTTC CACTCACAGC 60  
 CTGAAATTCT CCTNTGTCCC AAACCCAGG GGGCCCCAGC AGCTTCGAAC CTACACCTGA 120  
 GGGCTACCAG CAGGTGGCGC TNTGGCTTTG CACTGCAAAA ACTGGGGACC AGCCCNCTTC 180  
 TNCCACAAAT AAAGCCCAAT AAAGCCTGAG AAGTGAGGAA AGCCAAA 227

SEQ ID NO:4317

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05134

SEQUENCE DESCRIPTION:

GATCTCCGTG GATGAACTGC GTCTGGACTC TTAGATTCAT AAAATATTCG AGGGTTTGGG 60  
 AGTNACAGAC CCTCCCCTCT CCTCAGTGCA CTTTGGCATT TNCACGGTGT CTTCCCCGGA 120  
 CAGCACAGCA ATAAATNGNG TGATTGCGTG GAAA 154

SEQ ID NO:4318

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05135

SEQUENCE DESCRIPTION:

GATCAGGTTT GGNCTTCTCC CACTGAGCAT GACAAGCACT CGAAAGGCTA AATCAACCAG 60  
 AAACATCGAA AAAAAAGCTC AGTACGATGC CAACTNTTAA GCCTGCAGGA NTCCTCCTGG 120  
 GTTGTCCCC CGGCACGNTC CACAGCTGGT NGACCCGGCA GTTCCTGGNT CCTTGTTTCAG 180  
 N 181

SEQ ID NO:4319



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SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05136

SEQUENCE DESCRIPTION:

GATCTGCCCT TGNTNGCCTC ATACCTCTGT GCTCCACACT GCGGCCAGGC CAGCTGAGTC 60  
CCTCCATCCG TGGATGCTTT CCTGCAGCTA TGTGGTATGG GGGTCATTCC TGCCTCTTGG 120  
CACCAGGTTG GGGGGCATGT GCTTGTGGG CACCAAAGTG ATGGAACCCT CAGGTGCTCT 180  
CCGGGAGCCT GAACCTCCTG ACTGAGGAAC ATGGGCAGAA CATGTTTATT GCACAGAGTG 240  
GGCGCTGCGC ACAGGCGTGG CTGTACACGT GCTCTCAGCT CATCATCCTT TCCAGTAACT 300  
TTAAAAAAC ATCCN 315

SEQ ID NO:4320

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05137

SEQUENCE DESCRIPTION:

GATCGNGNNA CTTGGGGNGN GGCCCTAGGC ACTACCAGCA GCGCACGCTC ACCTTCGCCC 60  
TCAGGGCTGA CGACCCCTG CTCAAGCTCT TGCAGGAGGC TCAGCAAAGC TGAATTAACT 120  
CAGGCAGAAG AGCACAGATG TGTGGGATTG GGGGAGGAGT GGGGACAAGA TTTTNNATCT 180  
CTAAGTGAAT TTTCTAAAAA TGTATTTTAT ACCGGCTTAT TCCTAGTATT GNATAAACTA 240  
GCGGGNTCAN TCAAA 255

SEQ ID NO:4321

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05138

SEQUENCE DESCRIPTION:

GATCAACAT GCATGGNTGG GTCCTCACGC AGACACACCC ACAGAAGGAC ACTAGCCTGT 60  
GCACGCGCGC GTCNATCTAC ACACACACAC AAGAGTTCAT AATGTGGTGA TGGCCCTAAG 120  
TTAAGCAAAA TGCTTCTGCA CACAAAACCTC TCTGGTTTAC TTCAAATTAA CTCTATTTAA 180  
ATAAAGTCTC TCTGACTTTT TGTGTCTTCA AA 212

SEQ ID NO:4322

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05139

SEQUENCE DESCRIPTION:

GATCGAGTTA TTATGATAAC TGTGGTAATT TGTTGTTATA AATAGCAGTA ACATAGGAAG 60  
GTTTTGTGTA CTNCTGACAA GAAATTTNAT GTAGAGAGTT AATTCGAGC ACATTAAAAAT 120  
GACTGTCCCA CTCAAA 136

SEQ ID NO:4323

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05140

SEQUENCE DESCRIPTION:

GATCTGCATT ATTCTNGGAN AGTATTCAAG TGGTATCTTG ACTATTAAAC TACGTATAGT 60  
 GTTNNTGNAA TAGAAAGAAA ACAGCATTGG AATTGGATTG ATGTATCGTG GGATACAGGT 120  
 GTTATTTTCAG GTGATGTACT TGCATTATTT TCTTTAGCCA TAGTAACTTT TTGTCACAAT 180  
 AACTAAGTAT TCAATTATAT ATAANGAGTG AAACATTAAA ATGGNAAA 228

SEQ ID NO:4324

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05141

SEQUENCE DESCRIPTION:

GATCCTGCCA CTGCACTCCA GGCTGGGCAA CAGAGTGAGA CCATGTCTCA AAAAATAAAA 60  
 ATAAAATAAA ATAATATCAG GNTGCATACA TCAGAGGCTG TTCCTAGTGT AAAGGCACTT 120  
 TGGAGGGAGA AGACTTTCAG AGTTAGGCAG ACCAACTAAG AGGTCAGCTG ANGCACCTAA 180  
 CCAGTTGTAA GGAGGTGAAA GACAGCACCC CAAGANGAGA TGTGCAGGAN GGAGGAAAGA 240  
 GGCTTGGTCA TAAAGGNTGG AGGAATTCCA AAGTGACACT GANACAGGCT GCGTTTN 297

SEQ ID NO:4325

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05142

SEQUENCE DESCRIPTION:

GATCGTTCTG CTGAGTATGT TAAGCTCTTT ATGACTGTTT TTGTAGTGGT ATAGAGTACT 60  
 GCAGAATACA GTAAGCTGCT CTATTGTAAA 90

SEQ ID NO:4326

SEQUENCE LENGTH:411

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05143

SEQUENCE DESCRIPTION:

GATCTGCTGC TGCCATTTTA ATCTTGCTCA TTAACCTTAC TCCTTTGAGA ATTCTTTAAC 60  
 AATATTTAAA ATTGGTAACA AAAATAGTTT AGCCATAATT GTTTAGCCAT GTGAGTTTCA 120  
 GGTGCTGACA CGTTCAGACA GAACTGCTGT ATCACATTCC AATTTTGAAT AGCCAGTGAG 180  
 CAATCAAGTG TAGAGAAATG ATAAATGGCC TAAGAAGGCA TACAGTGGCA TAAACGATGC 240  
 TCTTCCTAGT AGCTTAATAG GCCACAAGCT AGTTTCTGTT GCACTCTGAA ATAAATATG 300  
 CTTTAAAAAT GTAGGGANCA GTGCTTAGAA AAGCAAAANC TAGGTGTGTC ATTGANATAA 360  
 TAGGCATAAN ACTTAAATGT TCCATAGGCC ACTATTGGA AGGGGGCCTT N 411

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SEQ ID NO:4327

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS05144

SEQUENCE DESCRIPTION:

10 GATCTACACA TTTTATAGT CATTTAAAT TGTATGACTC TGTCAAATNA TTAAAGTAAT 60  
TTTGGTGGAT TTTTAAAAAT AAAAAAATAA AAATAGAAA 99

SEQ ID NO:4328

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS05145

SEQUENCE DESCRIPTION:

20 GATCAGTTTT TATAGCATCT ATGGACATAG AAAATCAGTC ACTGAAAAAA ATAAACACAG 60  
CTTTCAATGT CTCACTCAA 80

SEQ ID NO:4329

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS05147

SEQUENCE DESCRIPTION:

30 GATCCAGAAT CACCAAGACC TCCAGCCCTG GATGATGCCT TTTCCATCCT GGACTTATTC 60  
CTGGGACGTT GGTTCGGTC CCGGTAGCCT TGTTAACCT CAGAGGCCTT CAAGTCCTTT 120  
CCACCTNTCA CCCATTGCCC ACCATTAANA AGCTTAGCTG NNTCTTGCCA CCTCAGGGGC 180  
TTGGATATGT GGAATAGTGA ACTGGGNCCA TGTCAGTTTG TCACTNACCC AAAGTGACCA 240  
ATAAACCTN NATTTATGNT AAA 263

35 SEQ ID NO:4330

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS05148

SEQUENCE DESCRIPTION:

GATCCTAANN CTGACAAGAT TCAAAGNACT AAATTTAATT CAGTCATNAA CACTACCAAT 60  
TACCGTTTAT NGGTAGACAT CTTTGAAAT TTCCACAAGA GCAAGCTAGG N 111

45 SEQ ID NO:4331

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

CLONE:HUMGS05149

## SEQUENCE DESCRIPTION:

GATCTGACCT GTTTATTGTT GCGCTTGT GAAAACGAGC TTTCTTTCCC ATGATAGTGC 60  
TTCGTTTTTG AAGTGTGAA GCTGTGCTCC CCTNAAATCG TGGCAGGAGA GATTAAGGTA 120  
ATTACAACAC TCAGTTCTAT GTCTTACAAG CACTTTGTCT TGTCTCTGCA AGAAAATTCG 180  
ATNCCNGTCA TNTCCATAA AATACAGNCA TTTTACCANC ATANTATGCT TTGATTGANG 240  
CAGCANTATG CTTTTGGGCA GTAN 264

SEQ ID NO:4332

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05150

## SEQUENCE DESCRIPTION:

GATCCTCCCG CCTCAGCCTC CCAAGTAGCT GGNATTATAG GTGTGTGCCA CTGTGCCAAG 60  
CTAATTTTTT AATTTTTNGT AGAGATGNGA TTNACCATG TNACTCAGGC TGGTCTCAAA 120  
CTCCCAGCCT CAAGCNATGC TCCCACCTCC ACCTCCCAA GTGCTGGGAT TACAGGCGTG 180  
AGCACCATAC CTGGCGCATG CATATTTTNN AAGAGTACCC ACTGGNGTCT AATATATAGC 240  
CTGGGNTACC TGGGATGAN 259

SEQ ID NO:4333

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05151

## SEQUENCE DESCRIPTION:

GATCTAACCA ATTTGAATAT GACTTCCTAC TCCAACGTAT CACCAAAACA CTGAAAAGCA 60  
ATAGCTGGTT TGGTTGTTAG AAATGGTGTA ATTAATGGTT TTNGTTAGTT CACTTCAGCT 120  
TAATAAGTAT TTATNGCATA TTTGCTATGT CCTCAGTGTA CCACTACTTA GAGATATGTA 180  
TCATAAAAT AAAATCTGTA AACCATAGGT AATGATTATA TAAAATACAT AATATTTTTC 240  
AATTTTGAAA 250

SEQ ID NO:4334

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05152

## SEQUENCE DESCRIPTION:

GATCGCATTT ATATAACATT CTTGAGGTGA CAAAATTATT GAAATGAAGA ACAGATTAAT 60  
GGTTGCCAGG GATAGGGACT GGAGGGGGTG TGGGGTATGT ATGACTATAA AGGGATGACG 120  
CAAGGAGTTC CTTTGTGCTG ATGGAACAGT TCTATATGAT TATGATGATT ACGATGTTGA 180  
TTATAACATT TGATTATGAG GTTAAGCACA TGAGTCTTTA CCTGTNCTGA AGTTGTATGG 240  
ACCTACATAC ACACAAATGN 260

SEQ ID NO:4335

SEQUENCE LENGTH:261

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05153

5 SEQUENCE DESCRIPTION:  
 GATCAAGACG AGCCTGCACC GCCTGAAGCC CGACACGGTG CCAGCGCCCT GCTGCGTGCC 60  
 CGCCAGCTAC AATCCCATGG TGCTCATTCA AAAGACCGAC ACCGGGGTGT CGCTCCAGAC 120  
 CTATGATGAC TTGTTAGCCA AAGACTGCCA CTGCATATGA GCAGTCCTGG TCCTTCCACT 180  
 10 GTGCACCTGC GCGGGGGAGG CGACCTCAGT TGTCCTGCCC TGTGGAATGG GCTCAAGGTT 240  
 CCTGAGACAC CCGATTNCTG N 261

SEQ ID NO:4336

SEQUENCE LENGTH:145

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05155

SEQUENCE DESCRIPTION:

20 GATCCTCAGT AAACCTCTGAG AAATAATGAA TGTGTTGTGT TTTAAATGG TAAATNTTGA 60  
 GGTATTATGT TATGTGGCAA TAGATAGCTA ATATATAACT NATTTGANTC AAACAATATG 120  
 TTAANTTAAA GCNCAGAAGA NTAAA 145

SEQ ID NO:4337

25 SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05157

30 SEQUENCE DESCRIPTION:  
 GATCTAAGGA AAGAAATGGA GCAACTAGTG CTTGACAAAA AGCAAGAGGA GACAGCCGTA 60  
 CTGGAAGAGG ATTCTGCAGA TTGGGAAAAA GAACTGCAGC AGGAACTTCA AGAATATGAA 120  
 GTGGTGACAG AATCTGAAAA ACGAGATGNN AACTGGGATA AGGAAATAGA GAAAATGCTT 180  
 CAAGAGGAAA ATTAGCTGTT CCTGAAATAG AAGAATAATC CTTAACAGTC TGCAAATGTA 240  
 35 CATTAAATTC TAGATGTTGA CAAA 264

SEQ ID NO:4338

SEQUENCE LENGTH:109

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05158

SEQUENCE DESCRIPTION:

45 GATCGGGGCG GGGAAACAGC NGGAAGANGG NCGCACCCGG TCTGACTACA ACANCCAGAA 60  
 AGAGTCCACT CGGCACGTGG TCCNGCGCGT GAGGGGGGGT GTCTAAGTN 109

SEQ ID NO:4339

SEQUENCE LENGTH:195

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS05159

SEQUENCE DESCRIPTION:

GATCAGTATA CAGTGTACGT AACTACACC ATCCTCAAAC CCCGGAAAAGC AAAGCAAATC 60  
 AGGAAGAAAA GTGGAGGTTA GCAACACACC TNTGGCCCCA AAGNACAACC ATCTTGTTAA 120  
 CTATTGATTG CAGTGACCTG ACTCCCTGCA AGTCATCGNC TGTAACATTT GTAATAAAGG 180  
 TCTTCTGNCA TGAAA 195

SEQ ID NO:4340

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05160

SEQUENCE DESCRIPTION:

GATCTAATAT TCAGGAATTT TTCTCCTAAA GACACCCAGT AAAAATATCA CAAA 54

SEQ ID NO:4341

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05161

SEQUENCE DESCRIPTION:

GATCACTGTG TAAAACTAAG TNTCTCTAAA TGTAATGCAT CGATTTAGTG TCTGGAACAT 60  
 AATAAATATT TGCTCTCATG ATTGCTAAA 89

SEQ ID NO:4342

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05162

SEQUENCE DESCRIPTION:

GATCTACATC CCCATCCACC TATACGGACA TCTTTTCCGT TGTGGTTTGA GAATGTTCTT 60  
 ATAATAAACC CCTCTGCTTT GTTCTTAAA 89

SEQ ID NO:4343

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05163

SEQUENCE DESCRIPTION:

GATCGTCTTG TATGGTGAAT TTTCTAGGAG CGATGATGTA CTGTAATTTT ATTTTAATGT 60  
 ATTNNGATTT ATGATTATNT ATTAGTTGNN TTAAATGCT TN 102

SEQ ID NO:4344

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05164

SEQUENCE DESCRIPTION:

5 GATCAATTNT GCANCANACA NCAATCTTAA CCATTTCCAG AACTACTAG TTATATTAGG 60  
CACGTTTTAA AACTTAAAC AAAATAAAGG CCATCCCAA CCCTGGGCTG TTGTCGGGTT 120  
ATTTTGCAGC AGGGTTGTGT TCAAAANCTT CCTTTGACTC CCTGAGACTT TATCTNCTNC 180  
TTGCAGAGTA AGATGGAAAG CCANTCAGTG TTTGCGTAA TGTAATACAG NGTAGTGCCA 240  
10 TTCNGGNN 248

SEQ ID NO:4345

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS05165

SEQUENCE DESCRIPTION:

20 GATCCAAACT TCTACAGCAA AACTTACTT CTTTtagGAA AGACATACTT GAAACTACAC 60  
AACAAAAAGC TTGCTGCTTT CTGGCTAATG AAAGCCAAGG ACTATCCAGC ACACACAGAG 120  
GAGGATAAAC AGATACAGAC AGAAGCTGCT CAGTTGCTTA CAAGTTTCAG TGAGAAGANT 180  
TGAGAACTTT TCAGAGAAGA TTTATGAAAT AGCTAATAAA CATTGCCTTT TCTTTTAA 239

SEQ ID NO:4346

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SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05166

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SEQUENCE DESCRIPTION:

GATCAAAAAA TGTCTCCGCT CAGGGATTTA TGGTGGATTA TTGCAGACAN TGCTAAAAAT 60  
ATAGAGCACA AGACAAGTTT ACTAAATTAA AATTTTATTT TTTGAGAAAC TGTTATTTGT 120  
ATAAATTATC AAGATTTGTA GGCTTTTCCTT TNGTAGAAAT AATTGTTTTA TGTGCCAGAG 180  
35 AATTTCAATT TNGTTTTCAA CAATAAAGCA TTGATAAGAG AAA 223

SEQ ID NO:4347

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS05168

SEQUENCE DESCRIPTION:

45 GATCATTGT TTATTAAT GTGTCCTATT ACACAGTGAG TTAACCTCA AA 52

SEQ ID NO:4348

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS05169

SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

GATCCGAGCG ACCATGGTGG CCCGGGTGTG GTCGCTGATG AGGTTCTCTCA TNAAGGGAAG 60  
 TGTGGCTGGG GGCGCCGTCT ACCTGGTGTG CGACCAGGAG CTGCTGGGGC CCAGCGACAA 120  
 GAGCCAGGCA GCCCTACAGA AGGCTGGGGA GGTGGTCCCC CCNGCCATGT ACCAGTTCAG 180  
 CCAGTACGTG TGTCAGCAGA CAGGCCTGCA GATACCCCAG CTCCCAGCCC CTNCAAAGAT 240  
 TTTACTTTCC NATCCGTGAC TCCTGGAATG CAGGNATCAT GGACGGTTGA TGTCAGNTCT 300  
 NNTNGGTGGC CCCTTTCAAA GGGNCNGGTG AGTN 334

SEQ ID NO:4349

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05170

SEQUENCE DESCRIPTION:

GATCCATCAA ATTGAACAAT CTGTTGTAAT TAAAAATTTT GGCCACTTTT TTCAGATTTT 60  
 ACATCATTCT TGCTGAACTT CAACTTGAAA TTGTTTTTTT TTNCTTTTGT GATGTGAAGG 120  
 TGANCATTCC TGATNNNGGC CTCNNN 146

SEQ ID NO:4350

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05172

SEQUENCE DESCRIPTION:

GATCTCAAGC CTCTTCTGAA CCCCAGGCTT TCTTGAGTCT CCATATGAGC ATTTGCCTCT 60  
 GTGGGCACAA CTTCAAGTGT CCTTTGTGAG GAAATGTGCA TCTCTGGNTG GTGAACTTCC 120  
 ATCCCTCAGA GAGAAATAGA AGCACAAATT TGAAACAAGC TGTCTGTCTG NGNNNNNNCT 180  
 TTATGTCTTG GAAACTTTAT TTATCCATCC AAGCTTTNTT TTTTTTTTAG CCTTTNNGGG 240  
 CAGGNAACCA TCCAGGN 257

SEQ ID NO:4351

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05173

SEQUENCE DESCRIPTION:

GATCTGTCTA CTGAGAAGAC CCAAATCTTG GTTCTAAAT GCCATTCTTC AATAAAAGGA 60  
 ATTGGGTTTC AAA 73

SEQ ID NO:4352

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05174

SEQUENCE DESCRIPTION:

GATCTCCTTC TCCNTCCTGT CCTGTCCTTG CCCCTCAGGA CTGCTGGAAA ATAAATCCTT 60



TAAAATAGTG AAA

73

SEQ ID NO:4353

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05176

SEQUENCE DESCRIPTION:

GATCCAAGCA GGGGGATGAA AAACCTCAGCA GAGAAATTCG AGACCATTTT CCAAGACTNT 60  
 CCCCTTCTCC TCAGGACCCC CTGGCTCAGT NCTTGAAAAA CGGTGTCATA TTTAGTCAGA 120  
 GGCCCCACCC CCAGGAAGCA TGGATGGGGA TGAAGGCACA GGCGTCTCCA ACCTCAGAGG 180  
 CCCTTTGTGG GGTGAGGACA CAGAGTGGGN AGANGAGACT GATGCAGGCC TACCAGTNCC 240  
 TGGCTTTTGT TCTGGGGCTG GAATAAAGAG GTGNCTTCAG CTGTTTGGNN CGAGAGGCAG 300  
 GGTAAG 306

SEQ ID NO:4354

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05177

SEQUENCE DESCRIPTION:

GATCAACTGG AACCTCTGTA TCATGCGGCT GAATTCCTTT TTTCTTTTAC TCAATAAAAG 60  
 CTACATCAGA CTGAAA 76

SEQ ID NO:4355

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05178

SEQUENCE DESCRIPTION:

GATCAGGCTT TTAGGACCTA GGAAACAAAT AAAGAGGAAT TTGTTGCTGA AA 52

SEQ ID NO:4356

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05180

SEQUENCE DESCRIPTION:

GATCCTTATT CTAGCTACAA GTCAAAGATA ACTCCTGGTC CAGACAAAAC ACCTGGCCTA 60  
 TCACAAGCTG ACTAAAAATC TGCACCTTGG GCCAGCGCAG GCAACAGTAA CTNTGACAGG 120  
 TTCAAATTAG ACCTCACACT TTCTACTCAT ATTCTAGTCA CTGGACCCAT CTGANTCAGT 180  
 AATCCCTNCT GCCCGGTCCT GGAGTAACTT CTTAGAGATA TTATAGCAAG TGGCAAAANT 240  
 AAAAGAGGGA TTTGCTANGA NTATCAAA 268

SEQ ID NO:4357

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05181

SEQUENCE DESCRIPTION:

GATCTCAAAT ATAAATTTGA GATTATACAT GTAGTTATGT ATAGNGNCAT GTAGTTACAC 60  
ATAGTTTGT ATTTNCCTGT TTTTCTCA TATGAGCATT TNCTTATTAA NGTN 114

SEQ ID NO:4358

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05182

SEQUENCE DESCRIPTION:

GATCTACACG TGTTGTTTTG TTTTNCCTTT ATTGATGCAC GNATGCTTTT GAACAGTAGA 60  
GNGAAATGCT AGACATGGAG AATCTGCTCT GTTGTCTCTN TATACATTTC TGTAGTTAAC 120  
AGAACTGT AATGTGCCTT GGAGCTTAGT AACTNGTAAT AAATTCAATN GATATTAAA 179

SEQ ID NO:4359

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05183

SEQUENCE DESCRIPTION:

GATCCTAAAT CCTATGTAGG CTNNGGTTAT TAGTGTATAT TTGTGTCTTA AAACAATTTT 60  
GAAAGTNAAA AAAATATTTT TTAAA 85

SEQ ID NO:4360

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05184

SEQUENCE DESCRIPTION:

GATCTNATTT TGAGATTAAA AAAAATACTT CTAGCTTTAG CCAGGTGTGC ATGTNGCTGC 60  
CATTTTGCAT TTTTGAATCA TCTTGTGTAA TTGTCACCAT GAAAGTGTTA CTCAGAATNG 120  
TCATAGATTT NNTNTTCTTT GTGCAAAAAC ATGGAAAATT GTCAGTACT TTGTTTGTAG 180  
GTTTCCCCGG NNNN 194

SEQ ID NO:4361

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05185

SEQUENCE DESCRIPTION:

GATCTGCTGT ATGTTACAGT TATGTAATTT GACTTGTTC AAAATTATTA AAGTTTAAAG 60

TGTATGCATT CTACTGGTCA ATAAGTAAAT ATATTCAGGC TCTGAATGTA GACAGATAAA 120  
TATATAAATA TAGAAAGTAC ATTTGTTAGA ATACAAACAA GAATAAAAAT TGAGTACAGA 180  
NTGAAAACCT TATTAAATTT TATCACTCCA TATAAA 216

SEQ ID NO:4362  
SEQUENCE LENGTH:333  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05186

SEQUENCE DESCRIPTION:  
GATCAAACTC AAGCTCACAC CTGTACCTGA TGGGAATGAA CATAATGTGA AGAAACTTAT 60  
TTCCCAGTGT AAACGCAGTT GTACAGAAAA AAAATGTTTT GGGTATAAAT CTGGGTTTTTC 120  
AAAACCAGCT TTNTTCTATA TATAAATNAT GCTGCTATTA CAGATTTAAC ATTNCTGTT 180  
AAAGGAAAGT CTACATTTTC TGCCTGTNCA GAACTGTTTA ATAGCAGTNN CTCTTGAGTG 240  
TATTTNCCTT GGTATGTTTT TNAACCTATT TTCCTTNAAG CCGAAATAT TGCCAATTGG 300  
ATANGGTTAG CCTTANNAAG TNNAATAAAN NAN 333

SEQ ID NO:4363  
SEQUENCE LENGTH:185  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05187

SEQUENCE DESCRIPTION:  
GATCAGCCAG TCTCTTTCAT CATCAAGCAG ACATACTCAA GGTACCAACA CAGCAAAGGC 60  
ACAAAATGTC TCTATATCAG TATTTTTCAT GGTATATGTG AGACCCATTA GTGAGGCATG 120  
AAATCAATTC TGTGAGTCAC AATGAACATT TGTCTAAAAA ACATAATAAA NTGTAAAATA 180  
CCAAA 185

SEQ ID NO:4364  
SEQUENCE LENGTH:108  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05188

SEQUENCE DESCRIPTION:  
GATCCTTTCC CATTTATTCT GGGAAGATGT TTTTCAAAC CAGAGACAAG GACTTTGGTT 60  
TTTNTAAGAC AAACGATGAT ATGAAGGCCT TTTGTAAGAA AAAATAAA 108

SEQ ID NO:4365  
SEQUENCE LENGTH:201  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05190

SEQUENCE DESCRIPTION:  
GATCATTTGG CTCTTTTTTT CCTTCCAGAA GAGTNGCATC AACAAAGTTA ATTGTATTTA 60  
TGTATGTAAG TAGATTTNAA NCTTCATTAT AAAATATTGT GAATGCCTAT AACTTGTTN 120

NCAATGTGNT TGTGTGTGTT TCTAAGGACT TTTTCTTNGG NTTGCTAAAT ACTGTAGGGT 180  
TGAAAATGCT TCTTTCTACT N 201

5 SEQ ID NO:4366  
SEQUENCE LENGTH:118  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS05191

SEQUENCE DESCRIPTION:  
GATCCTTCAT GGACANTATT CTAAGTATA CGTAGACACT TACTTGAAA TTTTGGACA 60  
TTATATTAAA TGAGTGCTAT CTGTGAAATT GGTTATATTA GGTGGCTNNN NCTAATGN 118

15 SEQ ID NO:4367  
SEQUENCE LENGTH:277  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS05192

SEQUENCE DESCRIPTION:  
GATCTGAGGT CTCAAGCTAG GAGAGACTGA GAATTTTAAT CAGTTTGGGC ATATAGTTTG 60  
GACTGAATCA CATCTGTAGT ACTTAGCCAA AGACAATTG GAGGAGAATA TCAGCCTTCT 120  
25 GGAAGTAGCT ACTTCCTGNT CAATGTAAAG TGTCGCAGAT ATTCAATAAA ATGGCAACCT 180  
GTTATAATTT TTTTGAATAT CAGCCTTCTG GNAGTAGCNA CTTCTGTAN CAAANGTAAA 240  
GNGTCGCAGN TATTCAATAA AATGGCAACC TGTTTTN 277

30 SEQ ID NO:4368  
SEQUENCE LENGTH:209  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05194

35 SEQUENCE DESCRIPTION:  
GATCTCTTGA CAANTGTGTA TGTTAACTTT TTAGCACATG TTTTGTACTT AGTACACGAG 60  
AAAACCCAGC TTTCACTTT TGTCTGTATG AGGTCAATAT TGATGTCACCT GAATTAATTA 120  
CAGTGTCTTA TAGAAAATGC CATTAAATAA TTATATGAAC TACTATACAT TATGTATATT 180  
40 AATTAAAACA TCTTAATCCA GAAATCAAA 209

SEQ ID NO:4369  
SEQUENCE LENGTH:58  
SEQUENCE TYPE:nucleic acid  
45 TOPOLOGY:linear  
CLONE:HUMGS05195

SEQUENCE DESCRIPTION:  
GATCGTGTGCG GAGACTNTNA CACAGTTTAA ACACATCAAT AAATACTTTA ACTTCAAA 58

50 SEQ ID NO:4370  
SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05196

5 SEQUENCE DESCRIPTION:

GATCGAGGTA GTAAAGGCCA TCCACATTTT AAAGGGTTAT TTGTCTNTNN TATAATNCGT 60  
TTGCTTTCAG AAAATGTTTT AGGGTAAATN CATAAGACTA TGCAATAN 108

10 SEQ ID NO:4371

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05197

15 SEQUENCE DESCRIPTION:

GATCAAACAG GGACACAAAA GCAAGTATCA TGGGAGGAAC TTGAAATCTC TGNGGACAGC 60  
AGAAGCTGAC TTCAACTCTN ATAATTGTGG CATCCATAAA TTGCAAATAT AGCCCTGAAT 120  
AGATACACAC AAATGTCTAT AATGAAGGCC CAGCAGAATG GAATGTGTGA CCATCTTCAG 180  
20 GAAGAAAAATN 190

SEQ ID NO:4372

SEQUENCE LENGTH:241

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05198

SEQUENCE DESCRIPTION:

GATCAATCCC TAGTAAAAGC CCTGGACACC TAGGCATGGG TGAGCTACTN TGGTTGGTAA 60  
30 TACTCTGTGC ACACATCATT GTAGCCACAC ATCATTGCTG GGAGAATTAA GCATTATCCT 120  
GAAGACTCTG CCAGGAGAGG ATAATTGGAA GTTCTCTTGG ACCTTACCTT ATGTGCCTTT 180  
NTTCATTGCT GATTTTAATC TGTATCCTTT CACTGTAATA AACTGTAAT ATGNGTGCAA 240  
A 241

35 SEQ ID NO:4373

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS05199

SEQUENCE DESCRIPTION:

GATCGTTCAT TGCCTTTCCA GGGTTATTTA GTAAAGTTTG TTGAAAACAA A 51

45 SEQ ID NO:4374

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05200

50 SEQUENCE DESCRIPTION:

GATCTCAGGT GATTCACCCG CTTCTGCCTC CCAAAGTGCT AGGATTACAG ACATGAGCCA 60

55

EP 0 679 716 A1

CCGCACCTGG CCATACAATT GCCTTCTATA TGTTTTTNAT TTAATATGAC ATTTGTATTT 120  
CCCCATGTTA TTAATAAATT CTNTATAAGC AAA 153

5 SEQ ID NO:4375  
SEQUENCE LENGTH:103  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05201

10 SEQUENCE DESCRIPTION:  
GATCACCCCA CCCTGTGAAG AGGCAGTTGG TGCTGGCAGT AAGCTGGTTT CCTCCTCTCC 60  
AGGGTTTTCC TAGTAATAAA GGTGTTNCTG TTGANGCCGT AAA 103

15 SEQ ID NO:4376  
SEQUENCE LENGTH:390  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05203

20 SEQUENCE DESCRIPTION:  
GATCACATTC ATTCCATAGG TAGCTTTACG TGTGGCTACA ACAAATTTTA CTAGCTTTTT 60  
CATTGTCITT CCATGAAACG ANNTGANGAA AATGATTTTC CCTTTGCAGG TTGCACACAG 120  
TTTTGTTTAT GCATTTCCCT AAANTTAATT GTAGTCTCNA GGATACAAAC CATAGTAGGC 180  
25 AATACAATTT TAGAATGTAA TATATAGAGG TATATTTAGC CTCTTTTAGA AGTCAGTGGA 240  
TTGAATGTCT TTTTATTTTA NNTTTTACAT TCATTAAGGT GCCTCGTTTT TGACTTTGTC 300  
CATTACATT TATCCATATG CCTTTGCAAT ANCTAGNTTG GTGNAAAGCT AACCAAGTGT 360  
TGTAACCANT AATCCNTTGT TTNGNGGTGN 390

30 SEQ ID NO:4377  
SEQUENCE LENGTH:144  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05204

35 SEQUENCE DESCRIPTION:  
GATCATATGC AGGACTCTTT CTTAATGCAG CCTGAGACAA ATCTTGCAAT ATGAAGAGAT 60  
GATTTCCAGG TTTTATTGAA TAAATGAATT GTAATTTTTC CTTGAAATTA TCTTATTTAG 120  
40 TATAATAAAT ATTACAATAT TAAA 144

45 SEQ ID NO:4378  
SEQUENCE LENGTH:386  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05205

50 SEQUENCE DESCRIPTION:  
GATCCACAG CGAAACACTG GCCACTGGCT ACCAGTATTN CTTCCAGAG CTAGGGGCTG 60  
CCTTAAAGGA AATTGTAGCC TAAGTAGGTC GTGGCAAGGG CCTGAGGCCT GTTCCTCACA 120  
GGCTTCCAGG TTAGGCACTG TGAATAGGCT CAGCTCCTCT AGAGAGCTGA AGCCATCTGG 180

55

EP 0 679 716 A1

5 TTCTTAGATT CCTCTCCCAG TCCTCTTTCC CATTGTTCTG TTGCTCCACC TTATTGTCTC 240  
AAGGCCGTAA TCTCATCAGG TTGGGACATT AATCTTTTCA ACTCCTTTGT AAAGATTTCC 300  
CAGTTTGGTT TCTCTACATG TNCTGCAGCT GGCCNCAATT CTCCTTTNAC GTTGTGTAGA 360  
GAATGNTCTG CAGTTTTAGG GCAAGN 386

10 SEQ ID NO:4379  
SEQUENCE LENGTH:174  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05206  
SEQUENCE DESCRIPTION:  
15 GATCTAAACG AAAAATAGTT TCTTGTTTAA ATTACATAA GGCAATNAGA TATGGAAAGA 60  
TGACAAGATA CGTATAACA TTGGTTTGCA TTTTATTAAT TNATTCTAAT GCAAATCTTG 120  
TATAAAGAAC CCATGATGTT TTGTAACCTT CTAATTAAAA TGTCAAAAT GAAA 174

20 SEQ ID NO:4380  
SEQUENCE LENGTH:207  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05207  
SEQUENCE DESCRIPTION:  
25 GATCTTGGTC AATAACTGGG AGATGGACAA ACTAGAGATG GAAGATGCAG TCACATTTTT 60  
GAAGACTAAA ATCTATTGAG TAGAAGCTCT TCCTGTTGCT GCTGTAAATG TGCAAAGCAC 120  
ACAATAAAGT GAAAATCAAC CTTTTCATAT TAGGAGACAT GCATTTGTAA AAATTAATAA 180  
AGATGACAAG TCAGTTGTCA ATGGAAG 207

30 SEQ ID NO:4381  
SEQUENCE LENGTH:189  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS05208  
SEQUENCE DESCRIPTION:  
GATCAGCACC TTGGCCGTGA TTCCCAAGGT CCCAGCCAAA GCAAAGGGCC AGTTGTTTCA 60  
GTTTAAACAG ACATGTCTTT AGTCTAATAA AATTAGTTAA CTGCCAGTAA AGTTATTTGT 120  
40 TAGCTTTGNT GAAAGCTATG NNGGTATCTT TCCCTAATCA TCAAAGTAAA TAAAAANTCA 180  
TTTCTNAAA 189

45 SEQ ID NO:4382  
SEQUENCE LENGTH:502  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05209  
SEQUENCE DESCRIPTION:  
50 GATCTGTTCT TTTTAAGTTG ATTCGGGAGT GGCATTCTTT TATACCCAAA GACTGTAGTG 60  
CATCTTGAAG AGCTCAAAGC ACATGACCGC ACAAATGCTT ACAGGGTTTC CTCCCGAGTA 120

55

EP 0 679 716 A1

ATCCAATCTC ACTCCCCTTG TAAGGGAATT CTGGGGCAGC TATGGTTTGA GTATGCAGTT 180  
TGCATCGTGT TTCTACCTTT AGTACCTTGC CACTCTTTTA AAACGCTGCT GTCATTTCCC 240  
ATTTCTTAGT ACTAATGATT CTTTGATTCT CCCTCTATTA TGTCTTAATT CACTTTCCTT 300  
NCCTAAATTT GGTGATTGG CATATCAAAT TCTGGTAAAA TNGTTTNGG TAAANCATAT 360  
TTACCCNCAC TTGGGGTAAA TCCCAATTCC TGGNTAGGGN CTTTTAAAAA NGGGTTTTTN 420  
NTAATNNGG NNAATCCAAT TATTAATAAN GGGGGNCCN TTTTTNAAG GGNGGAANAA 480  
ANGGNGAGGG GGNAGNTNGN GN 502

SEQ ID NO:4383  
SEQUENCE LENGTH:383  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05210

SEQUENCE DESCRIPTION:

GATCTCTGGT CAGAGTGAAC TCTTGCTTCC TGTATTCAGG CAGCTCANAG CAGAAAGTAA 60  
GGGGCAGAGT CATACGTGTG GCCAGGAAGT AGCCAGGGTG AAGAGAGACT CGGTGCGGGC 120  
AGGGAGAATG CCTGGGGGTC CCTCACCTGG CTAGGGAGAT ACCGAAGCCT ACTGTGGTAC 180  
TNAAGACTTC TGGGTCTTN CCTTCTGCTA ACCCAGGGAG GGTCTTAAGA GGAAGGTGAC 240  
TTCTCTCTGT TTGTCTTAAG TTGCACTGGG GGATTTCTGA CTTGAGGCC ATCTNTCCAG 300  
CCAGCCACTG CCTTCTTTGT AATATTAAGT GCCTTGAGCT GGAATGGGGA AGGGGGNCAA 360  
GGGTCAGTCT NTCGGGGTNG GNN 383

SEQ ID NO:4384  
SEQUENCE LENGTH:258  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05211

SEQUENCE DESCRIPTION:

GATCAAACTG TTGGAGGAGA AGCTGAAGGA GGCTGAGACC CGAGCAGAGT TTGCCGAGAG 60  
GTCTGTGGCA AAGTTGGAGA AANCCATCGA TGACCTAGAA GAGACCTTGG CCAGTGCCAA 120  
GGAGGAGAAC GTCGAGATTC ACCAGACCTT GGACCAGACC CTGCTGGAAC TCAACAACCT 180  
GTGAGGGCCA GCCCCACCCC CAGCCAGGCT ATGGTTGCCA CCCCAACCCA ATAAAACTGN 240  
TGTTACTAGN CTNTNAAA 258

SEQ ID NO:4385  
SEQUENCE LENGTH:174  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05212

SEQUENCE DESCRIPTION:

GATCAATGAA AGGAGACATC TGGAGTGTGC GTGCTTCTTC AGAGGGACGG GTGATGGGCA 60  
GATTGGAAAA AGCACCAGCAG ATGGGAACCT TAATCTTCT TTTCTAAAAT TGATGCTATG 120  
AAAATTTGCG TTTCTGTAA CTTGTAAAAA CTAAAGTTG CTTGTCTACT GAAA 174

SEQ ID NO:4386



SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05213

SEQUENCE DESCRIPTION:

GATCAGGCAA AAATAGTTT CCAAAGTTAT TTTAATAAA GTATATACAA AATTCTTATA 60  
AA 62

SEQ ID NO:4387

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05214

SEQUENCE DESCRIPTION:

GATCTAACGC CACACCTCCG TGAAAACACA ANTCNCACAG CAGGAACCAC NTGAACCTGG 60  
ACATCAGCAG TTTATTGAGC AGATGCTTCA GGCTCTTCTT GGAGTAAATC CTCAGCTACA 120  
GANTCCAGAN GTCAGATTTC AGCAACAACCT GGAACAACCTC AGTGCAATGG GATTTTNGAN 180  
CCGNGAAGCA AACTTGCAAG CTCTAATAGC ANCAGGN 217

SEQ ID NO:4388

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05215

SEQUENCE DESCRIPTION:

GATCTATGCA GACAACTGTG TATTCTGTTT TATAACAGTT TGTTTGAATT TACTTACAGT 60  
TAAAAAATTT AAATATATTT ATGTTTGTAC GGAAA 95

SEQ ID NO:4389

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05216

SEQUENCE DESCRIPTION:

GATCTGGGTG AAGGGGAGAA CCTGCCATCT TATCCCTACC CCCCCGGGGC CCTCAAGCTT 60  
ATTTTCTTGT TGAAGAAACA CAAAACCTC GAGATTCATG TACTGTATGT TGGAGAAAAA 120  
AAATTACCTA ACTGTTCCCC CAAAAAAGTC AGTATNTTTT GTACTTTGTA AAAGTGTTGG 180  
TTAAAAATGA AA 192

SEQ ID NO:4390

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05217

SEQUENCE DESCRIPTION:

GATCTGCAGC CTTTTGGGTA TCAAATGGGT CAAAACCATG GGACCTGCCA CCTCCCATCA 60  
GCAATTCTGG AAATGCACTA TTTCTACTGG TGNTCTTGCT TTTTTTTTTT TTNNATTTTC 120  
TNGNTGAANT GCCAN 135

SEQ ID NO:4391  
SEQUENCE LENGTH:270  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05218

SEQUENCE DESCRIPTION:  
GATCGTANTT AGTCCTTTTC ATCTCAGCTG CTCCTTAAAT CAGTGCAACC CCTCCAAATT 60  
AATGTGAATT GAAACTTGCA TTGCTTTTCA ACTTAATTGA ATACTTACTA TATGTGAACC 120  
ACTGCACAAA ATAGGGGAAG AAGATGTGGG AGACAAAGAT GTGGAGCCTG TCTTCAATAA 180  
ATTTACAGTT AGTTTCAGGG TACATTGTTT TNCTNCTGCT GTTAATTAGG TGTATCCCCA 240  
AGACAATAAA TACATGGNTG GGAAAGTAAA 270

SEQ ID NO:4392  
SEQUENCE LENGTH:123  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05219

SEQUENCE DESCRIPTION:  
GATCAAAAATT GGNTAAATTC TATTGTAACA ATTTGTTGG TCATTTTGGG CCATAAAATT 60  
TTTTTGTAAT AGGAATTGT ATAAAGCATT ACTCTTTTTC AATAAATTGT TTTTAATTT 120  
AAA 123

SEQ ID NO:4393  
SEQUENCE LENGTH:288  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05220

SEQUENCE DESCRIPTION:  
GATCNCACCA GTNTNCTNCA NCCTGGGCCA CAGAGCAAGA CCTTGACTCA AAAACAACAA 60  
CAACAACAAC AAAAATTCTT GAAGATTTTG CATTCTGTCC CACTATCCAT TGGTTTTTCAT 120  
GTCAAGATAA TGTGAGAAAT TCTTTACAAT TGCTTCCAGA AGGANTAGCC TTTTGATTTA 180  
GTGCACAGGT GTCCAGTCTT TTGGCTTCTC AGGCCACAT TGGAAGAAGA ATGCTCCTGA 240  
GCCACACATA AAATACACTA NTGNTAACAA CAGCTGATGG AGCTTAAA 288

SEQ ID NO:4394  
SEQUENCE LENGTH:156  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05221

SEQUENCE DESCRIPTION:  
GATCCTNCGT TCTNTTGTTA TAGATTAGTT TGC GTTTTCCT ACAATTTTAT ACACATGGAA 60

TAATACTATA GGTACTCTTG TTTGGCTCCT NCCATCCAGC ATAATAAGTT TGAGATTCAT 120  
 NCATGTTGTT ATATGCGTCT ATGTTTCATTC CTNNNN 156

5 SEQ ID NO:4395  
 SEQUENCE LENGTH:149  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 10 CLONE:HUMGS05223  
 SEQUENCE DESCRIPTION:  
 GATCCTNCTT TTCCTTCATG NCAGCACAAG TGCTCACC GGCCAGAGCC AGGGCATGGA 60  
 TATGACAAGC AGGGCAGCCT GGACACTGCC CTCACAGGAC AGCGCCAATA ACAATACAGT 120  
 15 GTCTGAGTAT CTCCAGGGGA AAAAATAAA 149

SEQ ID NO:4396  
 SEQUENCE LENGTH:204  
 SEQUENCE TYPE:nucleic acid  
 20 TOPOLOGY:linear  
 CLONE:HUMGS05224  
 SEQUENCE DESCRIPTION:  
 GATCCTGCTT GGNCTATCAC AGAGCATTGA CCATTGGCTT CCCTCATCTG AGNCGTGGGA 60  
 25 GAGCANACTG GATAGATGAG AATTGTTTTA AAACAATTGT GAACAGAAAC TGNAGATGGT 120  
 ACAGTNCTAC ATCTGCACCT GCCCTTTTTT CATACCACAA AAGTATTTTT NNAGTACTGT 180  
 ACTGGACTTT TTGCNAGTNN CTAN 204

SEQ ID NO:4397  
 30 SEQUENCE LENGTH:213  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05227  
 35 SEQUENCE DESCRIPTION:  
 GATCCTGATG TATGAGGAAA AAGCGAGAGA AAAGGAAANG CCAACAGGCC CCCAGCCAA 60  
 GAAAGCTATC TNTGAGTTGC CCTGATTGGA AGGGAAAAGG GATGATGGGA TTGAAGGGGC 120  
 TTCTAATGNC CCAGATATGG AAACAGAAGA CAAANTTNTA AGCCAGAGTC AACAAATTAA 180  
 40 NTAAATTACC CCCTCCTCCA ANAANTANTT TNN 213

SEQ ID NO:4398  
 SEQUENCE LENGTH:67  
 SEQUENCE TYPE:nucleic acid  
 45 TOPOLOGY:linear  
 CLONE:HUMGS05228  
 SEQUENCE DESCRIPTION:  
 GATCCATCTG AGGAATCACT CTGTGTTGCA CTTATGCCCT CATAAAANAT ATTTATTGAA 60  
 50 GAATAAA 67

55 SEQ ID NO:4399

EP 0 679 716 A1

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05229

SEQUENCE DESCRIPTION:

GATCAATGCA TTTNATACGG ATATAGACCT AGGGCTCTGG AGGGTGGGN ATTGTTAAAA 60  
CACATGCAAA 70

SEQ ID NO:4400

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05230

SEQUENCE DESCRIPTION:

GATCTCTATA GAGGCTGGAA TGGCCACAGA GAATCTAAAT NTGAAAACAA ACATGTCCTG 60  
AGGGTGTGCT CCAATACCAC CCNNTAATAC TCTCCTGAGA TGTGAAGGCT NGAAATGAGA 120  
ATGCCATNTT ATTGTNACTT NCAAAACGN 148

SEQ ID NO:4401

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05231

SEQUENCE DESCRIPTION:

GATCCTTGTT TTGAGCTCTC AGAATCACTC AGACAACATT TTGTAAGTGC TGCTGTTGCT 60  
TTCTACATAC ACCTTATAAA GTGACATTTT AAAAGAAAATA AGGTGCCACA GTTTTAAACC 120  
AGAAGGTGGC ACTCTGTGGC TCCNTGTAGT ATTATAGCTA TACTGGGAAA GCATAGATAC 180  
AGCAATAAAG TACAGTAATT TTACTTTAAA 210

SEQ ID NO:4402

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05232

SEQUENCE DESCRIPTION:

GATCCTGTTG CAAACTGTGA ATATTCTGAT GATGCCAGTA CAGTTTGATT TATTAAATGT 60  
GGGTCCTCAA A 71

SEQ ID NO:4403

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05233

SEQUENCE DESCRIPTION:

GATCTGAACC CGTCTCCCGG GTGCTGTAAA TAGTCTGATA AACGTTTACA CAGTCTAAAA 60

EP 0 679 716 A1

TTACCCTTTA TATTTGCTGA ATACAACTCA TCTTTTGTAG TTTAAAATTT CTATTGTTTT 120  
GGAGCTAGCT GTGAGTTTCT AGAAGTGTAC AGAGTTGCTC CNGTGTCCC GGGTCANGTT 180  
GAGTAGGGAA TAAATAAATC TGATGCNGCC TCCTGAGGCT GCCGGGGGGT TTCTGCTAAA 240

SEQ ID NO:4404

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05234

SEQUENCE DESCRIPTION:

GATCAAGNAT ATTTTTTATT TTTAAGAAAG CATAACCAGC AATAAAAATA CTATTTTTGA 60  
GTCTAAA 67

SEQ ID NO:4405

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05235

SEQUENCE DESCRIPTION:

GATCTAATTC CAAGGACTTC TCCACAGCTA AGTNAGATGC CTCANACCAT TAGGTGATGC 60  
TTTGGACAGA ACAGAGTATT TNAATCTTGT GTTTAAAGCA ATTCCTTGGC TTCGGCTCCT 120  
CACCACCTTC TATGCCAGTN TCCCATTAT GTCCCTAGTA ATGCCTATGC AAA 173

SEQ ID NO:4406

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05236

SEQUENCE DESCRIPTION:

GATCCCAGCA GTGATGTTGG TTGAGGCAGC AAACAGATGG CAGGATGGGC ACTGCCGAGA 60  
ACAGCATTGG TCCCAGAGCC CTGGGCATCA GACCTTAACC ACCAGGCCCA CAGCCCAGCG 120  
AGGGAGAGGT CGTGAGGCCA GCTCCCGGGG CCCCTGTAAC CCTACTNTCC TCTNTCCCTG 180  
GACCTCAGAG GTGACACCCA TTGGGCCCTT CCGGCATGCC CCCAGTTACT GTAAATNTGG 240  
CCCCCAGTGG GCATGGAGCC AAA 263

SEQ ID NO:4407

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05237

SEQUENCE DESCRIPTION:

GATCAGAATG TTCTAAATNT TGACTIONTAT CTTTTTATTA TGAGTTAATA TAGTTTAGCA 60  
GTAAA 65

SEQ ID NO:4408

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05238

SEQUENCE DESCRIPTION:

GATCTCTATA TTAAATNCTA AAATGGGATT AAAAGAAGAG TTGGAGAATT CACACTTATT 60  
GAGTAACTGA TGTCATACAA CCTGGAATTT CTGAATTCCA AATAAATAAA TTCACTCTT 120  
TAAA 124

SEQ ID NO:4409

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05239

SEQUENCE DESCRIPTION:

GATCTATGCA GTATACATTT TNCAGGCTGA AATCAAGGG GAATCATTCT GATTATNCTT 60  
ACTACAAATG GAGATGGCTA TTATGAAACA GCATGAGCAT GAGCCTTTNA TCTNTNATAC 120  
TTAGTGATAT ACTTTGCTTG AAAATCACTC AGCAAAGTAG TTCACATGAT GTGTTATCAT 180  
ATTTGANGTG TGGNTTNTCT CAAAATCATT GNCTTTAAGG NGCTCATTNC TGAN 234

SEQ ID NO:4410

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05240

SEQUENCE DESCRIPTION:

GATCTNTTTG TATGTNACGT GTTAAGGGCT TGTTTGGTAT CCCACTGAAA TGTTCTGTGT 60  
TGCAGACCAG AGTCTGTTTA TGTCAGGGGG ATGGGGCCAT TGCATCCTTA GCCATTGTCA 120  
CAAAAATATGT GGAGTAGTAA CTNAATATGT AAAGTNGTAA CATACATACA NTTAAATGG 180  
ANATGCAGAA A 191

SEQ ID NO:4411

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05241

SEQUENCE DESCRIPTION:

GATCACCTGA GCTGCCTCAG ATTCCATTTG GTCCTCTCCT TCCTGGAAGG CTTCTTTTAA 60  
TGTTTTGTTT TAATCCCAAA TGTCTGAATG TTTTGCAGTG TGAGGGGTT TGAGCCCTT 120  
GTTCAATTCTC CTTCTTTTTT CCTCCCGCTT CCCTCTCCAT GAAGTGATTC TGTTGACAA 180  
AATGTATACT GCGCGTNCTC TTCCTGTTT TATCTGCAGA AATNNCTCTG GGCTTTTNTC 240  
GGTGTAGAT TCAACACTGC GCTAAAGCGG GGATGTTCCA TTGAATAAAA GAGCAGTGTG 300  
GTTTTAAA 308

SEQ ID NO:4412

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05242

SEQUENCE DESCRIPTION:

GATCCACCCA CCTTGGCCTC CCAAAGTGCT GGGATTACAG GCGTGACACN CAAACCCAGC 60  
CACCAATTTT ACTTTAGGTA AACTTTTATT TTCAAGCTTT TGTGGTGTT GCAAGTGTA 120  
ATCTGTTTAA TAAATGTTT TATAAATATA ACCACTATTC CTTGTAAGCT ATTTAAATA 180  
AATTTTAAAG TCTTTCAAGT AAACACCAAA 210

SEQ ID NO:4413

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05243

SEQUENCE DESCRIPTION:

GATCTGAATT TAGGNACATT TCCTTTTTCT GTGGGAATCA CAAGAGTTTA TCCACTAAAA 60  
AAAGATATGT AAAAAAGATA CTTTCCAGCA CATAAATAAA GGCTGGAATT TTACAACCTG 120  
ATGTATATAT TAGACAGTTC TAGGATGTGA GTTCCCTNCA TNCCAGAGCT ATGCTTGTGA 180  
TACAGCCCCT TTTCTTATAA AGTCAGTTAG ANGGACTTCC TTAACAATGA CTATTATAAT 240  
GNCTTNCTTA AAATACAGTT TTGTATTCTG TCAATGCAAA TATAAGACAG GTTGTGCCNT 300  
AATCATGTAN CANGNNTATT TTGNAGNTT ACATATN 337

SEQ ID NO:4414

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05244

SEQUENCE DESCRIPTION:

GATCAGCTAG CTACCTTCTA CTTTCCATTT TTCAAGTGGA TTGTTCTCTT AATTGTGATA 60  
TAACCTGTTG TCTAAATTTT ATGTACAGTC TTTTATAATA AACCATTCTC CTATATGAAA 120

SEQ ID NO:4415

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05245

SEQUENCE DESCRIPTION:

GATCTGGCTC ATCCATCTGC AACTGACCA CGCTAAGAGC TGTCTGCAGT GATGGAAACC 60  
TTCTCTAGCT GTGCTGTCCT CTATAGTGGC ACCAGCTGCC TGTGGCTACT GAGCACTTCA 120  
ACTGTGGCTG CAGAGACTAT GTTAAATTGT ATTTAATCAT AATTAATTTA ATTGTAAACA 180  
ACAAA 185

SEQ ID NO:4416

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05246

SEQUENCE DESCRIPTION:

GATCTTAAAA TTCGTTTGCC TTTTAAAGC TATATTAATA ANGTATTGTT GAATCAAA 58

SEQ ID NO:4417

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05247

SEQUENCE DESCRIPTION:

GATCCACAAG ATTNAGAAAA TATTATATAG TTAGATAATA ACATTCTTGT CTAATGATAT 60  
CCNANCTNGT TACAAAATTN TTTAAACTT AAATAAAAC ATGCATCTN 109

SEQ ID NO:4418

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05248

SEQUENCE DESCRIPTION:

GATCCCTCTA CAGAGCTTCC CTGACTCATT CTGAAGGAGC CCCATTCTTG GGAAATATTC 60  
CCTAGAAACT TCCAAATCCC CTAAGCAGAC CACTGATAAA ACCATGTAGA AAATTTGTNA 120  
TTTTGCAACC TCGCTGGACT CTCAGTCTCT GAGCAGTGAA TGATTCAGTG TTAAATGTGA 180  
TGAATACTGT ATTTNGTATT GTTCAATTG CATCTCCCAG ATAATGTGAA AATGGTCCAG 240  
GAGAAGGCCA ATTCCTATAC GCAGCGTGCT TTAAAAATA AATAAGANAC AACTCTTTGA 300  
GAAACANCA TTTCTACTTT GAAGTCATAC CAATGAAAA ATGTATATGC ACTTATAATT 360  
TTN 363

SEQ ID NO:4419

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05249

SEQUENCE DESCRIPTION:

GATCACATTC AGGATAAGTG TACAGAAGAA AATACGGGTG TTTACTCTTT AGGGAAGTGG 60  
AAACACTCCC TGCATTGATG TACATTTTAA GAATGGCACT TTTGATACAT GTTATCATAA 120  
AGGTGCTTAA TAGAGCTGAA TTAAAGTTTT TCAAATCTGT AAACANNGCA AAAANGTAAA 180  
TTGTAGTCAT TTGATTATTT TTAAATNGG NGCTTTATAT TTNGTNTCA CTCAGAGTAA 240  
AAGCTGCAAT TTATTGTNCA CCCAAA 266

SEQ ID NO:4420

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



# EP 0 679 716 A1

CLONE:HUMGS05251

SEQUENCE DESCRIPTION:

GATCAAAGCA ATTTACAGAT TCAATGCTAT TCCTGTCAAA CCACCTATGA CATTCTTCAC 60  
AGAACTAGAA GAATAAACTA TTAAGGTTT GTATAAAGTT TAAA 104

SEQ ID NO:4421

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05252

SEQUENCE DESCRIPTION:

GATCTCAACA GTGTGGGGTG AACAGAAGA CTGTATCTTC AGCCTTTTTC CTATAATCAT 60  
GGATGATTG GTCTTATTCA AAAGGACCGC ACATATTAGT ACTCTTAAGA GCATCTTCCA 120  
AGACTCCAGC AGNGAGCATT TAGAGAGTGT GTTGTCTTCC AGAGTCATGA ATGATTTTGT 180  
TTAGCTATCA GGTCTACTAC CTCTAAGGAC ATTTTCATAGC AGCATCTCTT GAGTTGCCTG 240  
CATCAGTGTG GTGGTN 256

SEQ ID NO:4422

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05253

SEQUENCE DESCRIPTION:

GATCTGAATA TAATTCTGGT AACAGCTGT CTTTATTTT NTCCTCTAAA GAACTTAATT 60  
CATTTGTAC ATAAAATATA AGGAAATCTT TGTACTATTT TACAGTAACC ACAATCTAAA 120  
TATTTACATA TACCAAAAAT TANTTATGC TCATATATTA GGATGTGAGA NTATCATCTG 180  
TTTATGGACA CATGAAACCT CCTAATGACC TGAATTTGT AGANTATNTG ACTTTTATA 240  
TGCAAAGTTT TTCGN 255

SEQ ID NO:4423

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05254

SEQUENCE DESCRIPTION:

GATCCCGGT GGTTTGTGC TCAAAATAAA AACTGATTAA ACCTTTGTGG CTGTGAAA 58

SEQ ID NO:4424

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05255

SEQUENCE DESCRIPTION:

GATCCTTTTC TTCTCTTATA AATCATCCTC TTAATGAAAA TTAGCCTAAC AAAAGTTTGG 60  
AGACTGGAAT CCTACTTTGA GCCACTGACT TGAAATAACT CTTTGGCAA GTTGCTGAC 120

ATCCTGTCTT ACCAAGGTGG CAGGTTTGCA TTTTACTGC TAAAAACATT TTTNTTTTTT 180  
TAACCATCTT NANCCAAATT NATCATATNN GNGGTNGGCC TANCAGGNTT TTNN 234

5 SEQ ID NO:4425  
SEQUENCE LENGTH:200  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS05259

## SEQUENCE DESCRIPTION:

GATCCACCTG CCTCAGCCTC CCAAANTGCA NGGTATTACA GNCANGAGNT TCTGCGTCTG 60  
GCAATAATGT AACTTTGAAG CTAAAAAATT AATCCCAGTT TGTAAGCAATA ACAGAAGACT 120  
15 ATCTACAACG GAAGAAAGAA GCAACTGCCT TACAGTTCTG TAAAGANTTG GCAAGAAAAAT 180  
AAAGCCTATA GTTGCCGAAA 200

SEQ ID NO:4426  
SEQUENCE LENGTH:84  
20 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05260

## SEQUENCE DESCRIPTION:

25 GATCTAGTCA TCTTCTGTAG CTACATAGTA CTCCTAATGT TAAGATTACC AAATTCAGCA 60  
ATAAAGCCAA AATCAAAACT GAAA 84

SEQ ID NO:4427  
SEQUENCE LENGTH:75  
30 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05262

## SEQUENCE DESCRIPTION:

35 GATCATAAAC CAGTGNNATC AGACCTATGT GTAATAAGAC TCCTGTTAAT AAAAAAATAA 60  
AAAGCTAAAA GCAAA 75

SEQ ID NO:4428  
SEQUENCE LENGTH:424  
40 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05263

## SEQUENCE DESCRIPTION:

45 GATCTCAAAAC TTGTCTTAAA TCAACAACCT TCTACTCATG TTAATGTCTT GATTAAATAT 60  
CACAATGCAA AATACACATT AAGTAAAAGA ATTCCAGCTG GTAAACATGA CCTGGACATT 120  
TGTAAGAATA TATTTAATAT ATGTNCACCC ATTATGTTTT TAGGTAACAG GNGGNNAAAT 180  
GCANCNAAT TTTTTTCTC TTGAAAGGCA CTGTCATTTA ANCATAAACC TGGAGTACTC 240  
GAAATAGAAT TCAGGTTTAC ANGATGAAAG CGTGTGGAGA AGTGTGAGAT GGCAGTGGNA 300  
50 GCATGTGTGT TTCTAAAANG TAAAAANTCTC AAGGAAACCA NGANATGGCA TGCTTTTACC 360  
CATCTTNCCT TAGTGAAAAG NGTGCTTCAG GTTTGANATT GTTTTAAGAA AGNTAGCCGG 420

GNTN

424

SEQ ID NO:4429

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05264

SEQUENCE DESCRIPTION:

GATCTGCTCC CTCTCGCTCT CTCCTCCAC TACTTTTGG AACAAAGTGA TGGCAGAATG 60  
 CGGTGGTGGT GGGGGTCTTT TGTACTGTTG GATTAATAAA ATGATTNAA ATTNCNNNTA 120  
 AA 122

SEQ ID NO:4430

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05266

SEQUENCE DESCRIPTION:

GATCAGTATA ATTTTNNAAA GTTACTTTGT NAGAGGCACA AAAGGGTTTA AACTGNTTCA 60  
 TAATAAATAT CTGTACTTCT TCAAA 85

SEQ ID NO:4431

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05267

SEQUENCE DESCRIPTION:

GATCACGTAG ACATGTAACC CAGCAGCAGT TTGCTTCTGT TGTCCACTGA TTAATCAGCC 60  
 TATGTGCCTG ACACTGGTCT TGCAGTACAA CTGNAAGCCA AAACAAGGTG GAAGATGTCC 120  
 TGAATTAAGA TGTTTTACC ACATTGTATT ACAGAGACAG CCAATAAATC TACTATTTGA 180  
 TTTCAAA 187

SEQ ID NO:4432

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05269

SEQUENCE DESCRIPTION:

GATCTTTTAT TTNTGAAACA CTCAAACACC TTACAAAGTG CTGAGTAGGT AATAGTGACC 60  
 CAACTTGTGT GCTAAATGAT TATTTGTTTA AATCTGTACA GTTTTAAGTG TTCATTATA 120  
 CAAAGAGTGT ATATACTTTC AAATAATTNA AAATGCTTTA NATTATNNGG CTAGAAATTG 180  
 CNGTTTTNAA TAAATGTGAA TNTNTAAAA N 211

SEQ ID NO:4433

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05270

SEQUENCE DESCRIPTION:

GATCTGTTGT TAGGATTCTA GTTAACACTT TTNTTTTAA AACTAAGGA CAAATGAACA 60  
AA 62

SEQ ID NO:4434

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05271

SEQUENCE DESCRIPTION:

GATCCAGGG GAGGGGTCTC TCTCCCATC CCAAGTCATC CAGCCCTTCT CCCTGCACTC 60  
ATGAAACCCC AATAAATATC CTCATTGACA ACCAGAAA 98

SEQ ID NO:4435

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05272

SEQUENCE DESCRIPTION:

GATCGTATCC CGCTGACACA GAAGGNTGCC GGGTGGGGGG AGGGCACCCA TGAAATTCAA 60  
AGAAAACCTT AAGTGTGGAT GTTCAGAATT TTGGAAAAAT GTCCTGAAG TGATTGAAAG 120  
AGTGCTTGGC ATGCAAGGNT AAGAGGTTCT TTACATAACA TTTCTTAAAT GCTTAATAAA 180  
CGTTTGTTC ACTTGGTTTT GACATTGCCA ATGGGGTTTG AACCAGTGCT CTCTCTAAA 239

SEQ ID NO:4436

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05273

SEQUENCE DESCRIPTION:

GATCTGCAAT GACTGGAAGT TGCCGGTGCC TGGGGTGCCT TTCCCCCAGC CAGGGTCCAA 60  
AGAAGCTTGG CTGGGGCAGA AATAAACCAT ATTGGTCGGA AA 102

SEQ ID NO:4437

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05274

SEQUENCE DESCRIPTION:

GATCTTCTTT TGGGAGGATT TGATGTAAGT NACTGACAAG CCTCAGCAAA CCCAAAGATG 60  
TTAACAGTAT TTAAAGAAGT TGCTGCAGAT TCCTTTGGCC ACTGTATTG TTAATTNCTT 120  
GCAATTTGAA GGTACGAGTA GAGGTTTAAA GAAAANTCAG TTTTGTNCT TAAAANTGCA 180

TTTAAGTTGT AAACGTCTTT TTAAGCCTTT GANGTGCCTC TGATTCTATG TAACTNGTTG 240  
CAGACTGGTG TTAATGAGTA TATGTNACAG TTTAAAAAAG AAGTTGGTAT TTTATANGCA 300  
CAGTCAATNC TNATGGTAAC TTTTGGTNGT CTN 333

SEQ ID NO:4438

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05275

SEQUENCE DESCRIPTION:

GATCAATGTT TCAGCCCTAG ACTGCCCAAG GAGTATTATT AATTATTAAT AAATGAATTC 60  
TGTGCTTTTA AA 72

SEQ ID NO:4439

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05276

SEQUENCE DESCRIPTION:

GATCAGATTA TTTTACTACC AACAGTTATA GTTTGAAAGT CCAACTGTAT TAATTGACTG 60  
ATAATATGAT AATATAGAGA TTAAATTGTT TGTNTTCAAA 100

SEQ ID NO:4440

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05278

SEQUENCE DESCRIPTION:

GATCACAAAG AGCAAACAAA TGTCAATATC TCTTATGAAT GGTGAAAAAA AGGAATTAAT 60  
CGATGCAAAT AAACCTTTCA CAGTATTACT TTAAAA 96

SEQ ID NO:4441

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05279

SEQUENCE DESCRIPTION:

GATCTAGCAA GCCATGGCGA CAGGTAGCAT TTNTAAGATG NTGNACAGGA GCAGNATTAT 60  
CCCCAAAGAT ATTACAGGGT AGACACGTTT TAACTAAAAT CAATCAAGNT AACTTN 116

SEQ ID NO:4442

SEQUENCE LENGTH:411

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05280

## SEQUENCE DESCRIPTION:

GATCTGACAT ATATCACCTT CTGGGNTATT TACTCATTGT GCCAGGACCT GGCATTTTCA 60  
 TGTGCCTTTG ACCAAGTGTT CAGAATTTGC TTGNCTCTAA CCTGGAGAGC TTCTTAAGTG 120  
 ATGCCCTTTC ATGGAGCTTC TATGACAGTG AATAAACTAT TAATTGAAGG AAAATGTTAT 180  
 AATTAANGTA TCTATTTGCT GCATTGTATA TGGATTAANT GNTAAAAAAC AAGTAATCTA 240  
 CCCTCAGAGC CATGTATTTG AGAATGCTTT CAATCATATT TNCCTATGNA CTTTTTTTTT 300  
 ATAACTTAG TTTTANGCCT ATGTTGTAAA ANTGGGAAGG TTNGTAAACN TATGTTTGGN 360  
 AAAANTAGGG GAAATGTNGG CTTAAANTTN TTTTNCANTT ATNTTNGTTT N 411

SEQ ID NO:4443

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05281

## SEQUENCE DESCRIPTION:

GATCTATCTG GGGGTCTTAG TGTACCACAA GCTGAACCTG AAGATTTGGA AAAATGTTTC 60  
 TAATTAAATA AAACAGAGCA AAAAGACAAA 90

SEQ ID NO:4444

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05282

## SEQUENCE DESCRIPTION:

GATCTACATT TAAGTGGAAA AATTAGCAGT ATTTGAAAGC TCAGTTTNAA TCATTGTCTT 60  
 AACTTCAGAT ACAAATAACT GAACAGAAAAG TTTTAACCTT TAATATCTCA TGTNCTGTTT 120  
 NTTATTAGT ATTTTCTNT ATGTTAATTC AATTATATAC TTCTGAATGG CACCTTACTT 180  
 TTTGGAAACA AATCTTCTGT TATTTACAAA ATAATAATTT TTANAAAACA TTTAAAAAAA 240  
 ATCCAAAGCT GCTCTCGATA ATAGTCAACA TTTGCATATA TATGGAATTT CTTACTTTNT 300  
 TTCTCCCAAA CTCTATTTAA TAAACTNATT TTAATGGTTA AA 342

SEQ ID NO:4445

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05283

## SEQUENCE DESCRIPTION:

GATCACAAAA ATGTATTTTA TAAAATGTTT TGTACAATAA AGTTACACCT CAAAGTGTA 60  
 A 61

SEQ ID NO:4446

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05284

## SEQUENCE DESCRIPTION:

GATCATTATC AGTAATTTCA TAGCAACTGT TCTAGNGTTT TGNGTTTTTA AAACAGAATT 60  
AGGAATTTGA GATATCTGAT TATATTTTTC ATATGAATCA CAGCTGTTGA CAATGTCCCA 120  
TATATTTAAG AAATTATATC ATACTGATAC TATTTGTAAC ATTTTGATTG GATTTAATCT 180  
CCAGGGACAG AAATAATTCA TTGGTAAAGN GTAATAATGC GTTTTTTAAA AATGCTTTGA 240  
GAGGTAATTA CTTGCATATG AGAGAAATAA AACATTTGGC ACATTGTTTA CAGGTGTGAA 300  
A 301

SEQ ID NO:4447

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05285

## SEQUENCE DESCRIPTION:

GATCAGACCG AGAAGCAGGG TGAGAGATTC TAACGACTGG ATGCTGCTAG TAACACATTG 60  
TTTGTATTGC TTTACCATTT TTAAGTGTGA GATTTGAGAT GAACATACAT TTTGCTTTT 120  
TAATAAATGT TTAAGAAG TCCACATAAG AAA 153

SEQ ID NO:4448

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05286

## SEQUENCE DESCRIPTION:

GATCACTACA GTGAAGTATT ACAGTTGTAC AGTTCCAGT CTGGCCTTGG CTTGCTCGGA 60  
TAAAACTTTG TATGTATTTT GTATGGCATA GATTCTATAT TGTAATGATG TCCTATGCAA 120  
AAAGAAAAAT TAACGAAATT GTAAATTTTA TTGTTTAAAC GTGTATGCAT GTTTAGTGAC 180  
GTTTACATTT TGAAATAAAA TTTATGATTC ATTAATA 216

SEQ ID NO:4449

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05287

## SEQUENCE DESCRIPTION:

GATCTGGAAG CGTTTTGTAC CGATTATCCA CAGCAAAACA AAAATAAGCT TTTATTTTAT 60  
TAATAATTTT GTTCCTCTTG TGCCCAATCA AATCTTTTAG GAACAACTG CAAGAAAAGC 120  
TAAGAATGTT TTAGAGTGAA CTAAATACAG ACATTGCTTA CTTGTTTGA AA 172

SEQ ID NO:4450

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05288

## SEQUENCE DESCRIPTION:

GATCTCCCTG TGGCAGCAGG CATGGAGAGT CAGGGCTGCC TTCATGGCAG TAGGCTCTAA 60  
GTGGGTGACT GGCCACAGGC CGAGAAAAGG GTACAGCCTC TAGGTGGGGT TCCCAAAGAC 120  
GCCTTCAGGC TGGACTGAGC TGCTCTCCCA CAGGGTTTCT GTGCAGCTGG ATTTTCTCTG 180  
TTGCATACAT GCCTGGCATC TGTCTCCCCT TGTTCCCTGAG TGGCCCCACA TGGGGCTCTG 240  
AGCAGGCTGT ATCTGGATTC TGGCAATAAA AGTACTCTGG ATGCTGAAA 289

SEQ ID NO:4451

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05289

SEQUENCE DESCRIPTION:

GATCTCTTAA AAATACCACA GTTTGTATTT TTCCTTTAAG GAGTAAAGAT TTGCCTTTAA 60  
ATAACTTGGT ATTTTCCTGG CTTTCGTTTA ATACAATAGA AAATAAAGTA TTACACCGAA 120  
A 121

SEQ ID NO:4452

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05290

SEQUENCE DESCRIPTION:

GATCAATGTG ACGGCAGGGA AATGTATGTG TGTCTATTTT GTAAGTGTAA AGATGAATGT 60  
CAGTTGTTAT TTATTGAAAT GATTTCACAG TGTGTGGTCA ACATTCTCTCA TGTGAAGCT 120  
TTAAGAACTA AAATGTTCTA AATATCCCTT GGACATTTTA TGTCTTTCTT GTAAGGCATA 180  
CTGCCTTGTT TAATGTTAAT TATGCAGTGT TTCCCTCTGT GTTAGAGCAG AGAGGTTTCG 240  
ATATTTATTG ATGTTTTTCAC AAAGAACAGG AAAATAAAAT ATTTAAAAAT AAA 293

SEQ ID NO:4453

SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05291

SEQUENCE DESCRIPTION:

GATCTAGGTC CTTCTATCTC GTCCCTCTAC AGATGTATTT TCCACTTGCA TAATTCATGC 60  
CAACACTGGT TTTCTTAGGT TTCTCCATTT TCACCTCTAG TGATGGCCCT ACTCATATCT 120  
TCTCTAATTT GGTCTGATA CTTGTTTCTT TTCACGTTTT CCCATTTCCC TGTGGCTCAC 180  
TGTCTTACAA TCACTGCTGT GGAATCATGA TACCACTTTT AGCTCTTTGC ATCTTCCTTC 240  
AGTGTATTTT TGTTTTTCAA GAGGAAGTAG ATTTTAACTG GACAACTTTG AGTACTGACA 300  
TCATTGATAA ATAAACTGGC TTGTGGTTTC AATAAA 336

SEQ ID NO:4454

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



CLONE:HUMGS05292

SEQUENCE DESCRIPTION:

GATCTGCTGC AACCATATC TTNGTTCTTG AGTTCATCAT GCATTAAAA TGAGATGCAA 60  
 GAGCATTTAG CATACCATGT AAATATGGAC CTTTAAAAAT TAAATACTA TTGGAAGTGC 120  
 TTTCAACTCA GCCACATCTT AGCTATTAGT TCTTTGTGTT GTCTTATCAA AGTTTAATGG 180  
 ATACAGTTCC ACAGTTGTTG ATGTGTTTGT GTGTATATTC GATTNNNNNA AAGATGGTAG 240  
 TAAGTCAATA AA 252

SEQ ID NO:4455

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05293

SEQUENCE DESCRIPTION:

GATCATACCA CTCCACTCCA GCCTGGGCAA CACAGCGAGA CTCCATGCTC CCCCCAA 57

SEQ ID NO:4456

SEQUENCE LENGTH:564

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05294

SEQUENCE DESCRIPTION:

GATCAGGCTC TCCTCATGCT GTTTAGTGAT GGCACGTGCC AGGTGAACTN CTACGGGGAC 60  
 CACACCAAGC TGATTCTCAG TGGCTGGGAG CCCCTCCTTG TGACTTTTGT GGCCCGAAAT 120  
 CGTAGTGCTT GTACTTACCT CGCTTCCCAC CTTCCGGCAGC TGGGCTGCTC TCCAGACCTG 180  
 CGGCAGCGAC TCCGCTATGC TCTGCGCCTG CTCGGGGACC GCAGCCCAGC CTAGGACCCA 240  
 AGCCCTGAGG CCTGAGGCCT GTGCCTGTNA GGCTCTGGCC CTTGCCTTTG TGGCCTTCCC 300  
 CNTTCCTTTG GTGCCTNACT GGGGGCTTTG GGCCGAATCC CCCAGGGAAT CAAGGGACCA 360  
 GCTTTACTNG AGTTTGGGNN CGGGNTTGTT TTCGNTGGNT TCCTACCCCA TNTCCAAGAT 420  
 AAGCCTTNAG CNTTAANTCC CANGNTAGGG GGCCTTATTT NATGGACCAA TTTTAAATTT 480  
 ATTNTAAGAA ANTTTNTTTA NTTGGGGATT TTAAGCCCAA AGGGGGGCCC TCNTCCTNAG 540  
 GTNANAAAAAN AATTTTTTAA GAAA 564

SEQ ID NO:4457

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05295

SEQUENCE DESCRIPTION:

GATCTTTATT TTGATTAAT TTGTTCTGAT TTTTGGTTT GTTTTTTAAG GAACTGTAAT 60  
 GAACAAATGT CAGGATATCC AATGCCAAAT AAAGATGTTG TATTTATTTA AA 112

SEQ ID NO:4458

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05296

SEQUENCE DESCRIPTION:

5 GATCACACCC NGGTGAACCC ANGGTGCTAA GANTGAAAAT AACCTTGGTG AAATGTACAA 60  
NTTAAAGACA AAGAACTACA TGTGAAGATA GACTTGCTTT CTATTTTNAATCAGTAGTA 120  
GTACTGTTGC TGAATAATAC TAGGTTTTNN CN 152

10 SEQ ID NO:4459

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05297

15 SEQUENCE DESCRIPTION:

20 GATCTGGTGC TGCTTTCAGA TGTTTATCTT TTATTTTTTT CCCTTAAGCT TTAATCTTCG 60  
TCATTGTCTT AAAGTCAACT GGTGTTTCTT GTTCATTGAC TTTGGTACGA TGGTGCTTTG 120  
CAAGGATGTA TTTATGTTAT AATGGCCAAC ATTTGGTCAG CCCTTGTCCTTATTCACT 180  
TCCCTCCNTT TGTAATAATA GTGCTTTAAT TATAAACTGT ATAAAAATAC CTTGTATAAA 240  
CCCCTTTTTT GATTATTACA ATAAATAAGC TGAATTGTAA CAAATGAAAT TTGATTTTGT 300  
TAATAAAACA GTGGAAAAGT AAA 323

25 SEQ ID NO:4460

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05298

30 SEQUENCE DESCRIPTION:

35 GATCCTTTTT AGTTAATACT ATGACAGTAC TAAAAATATA TGAATAACAT TTCAGATACC 60  
ATTATATTAA AATATTTGTG TATGTGTACA AAAGCGTTGA TAAATACTAA TCTTTAAAGT 120  
TTGTGGAGTT CCTTTATTG TAATATATGT GCTCTTAAAA GCAATGGGAT GTGAAATTAT 180  
GAAAGTATTT TATTGTTTCAT AGAAATAAAA AACACAGTTA CTTTGCAA 229

SEQ ID NO:4461

SEQUENCE LENGTH:135

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05300

SEQUENCE DESCRIPTION:

45 GATCTGGACC TAATGAATTC CTCAGAAAAT TCCCATGAGT CAGCTGATTT CAGTGCTGCT 60  
GAACTAATTN CTGTGTCTAA ATTTCTTCCT ATTTCTGGAA TGGAAAAGGA GGNCATTCTG 120  
AGCCACACTG NNNNN 135

50 SEQ ID NO:4462

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS05301

SEQUENCE DESCRIPTION:

GATCTGGGTA AAGGACCATC TGGGGATTCT TTGTACTATT TTTCTTTCCG CAACTTTTCA 60  
AGTTTCAAAC TATTTGCAAA TAAAGAGTTT TTGTTTGTTA AA 102

SEQ ID NO:4463

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05302

SEQUENCE DESCRIPTION:

GATCACATGG CTAAGGTGGT GTGTGCCAGG TTTCTCCACT GTAAAATTAG GAATTTTCCC 60  
TTTGAAATTA ACAAGAATCT TCCACTTTGA AGCTGTGTGA ATGTCTTATT CTAAAAATTT 120  
TGCCTACTGA TTTNANNNN CATCATCAAT GATTCTTGCT TATAACAGGT ATTAATGTTA 180  
TGCTTGAAA 189

SEQ ID NO:4464

SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05303

SEQUENCE DESCRIPTION:

GATCATGTGA ATTTAAAGCT TTATACACAT TGTTGTTTTT GCTGGTCTCA TCTTTGGTAA 60  
TATGCTATAC CCCACTGCTG CCCGACACTG CCCTNTAGCT GCAGAGCTGG ATTAGCTGTT 120  
GACCATTGTA TGCTGTTGTC TGTCTGGCAG GGAAGTGAATG ACCTGATGTC AGATTTAGAT 180  
TCTTCCTGGG GATTACACAG CTATGAATGT ATTTGCTTCT AAAACCTCCC AAAGTGAATC 240  
TAATCTTAAA ACTACAAGTT GTAAGTATTC TGAAATTGGG AAACATTTAT NTNAAATGCA 300  
ATCAGGNNAG TGTTGCTTTT TACAGCATAA TNAATATANG TNTCAANNAN NGTGGANGGT 360  
NGTN 364

SEQ ID NO:4465

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05304

SEQUENCE DESCRIPTION:

GATCACTTGA TGTCAGGGAG TTTGAGACCA GCCTGGCCAA CATGGTGAAC CCCATCTCTA 60  
CTAAAAATAC GAAAATTAGC TGGGTGTTGT GGTAGGCACC TGTAATCTCA GTTACCTAGG 120  
AAACTGAGGC AGGAGAATCA CTTGAACCTG GGAGTTGGAG GTTGCAGTGA GCCAAGATTG 180  
TGCCACTGCA GTCCAGCCTG GGTGATGAAA CAAGACTCTT TGTCTCAA 229

SEQ ID NO:4466

SEQUENCE LENGTH:496

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05305

## SEQUENCE DESCRIPTION:

5 GATCTCTAAG GAACTCCTGT TGCTAAATAT GAAGAGTATG GAACATTCAT ATAGTCTCTG 60  
 TGAAGCATGG GGGGAGGGAA GACATTTCTN TTNCTTATAG GCTTTATGCT CAAATGTCAT 120  
 AGTCTCCTTT CAAAGAATTG TGTTCGATTT TAAATGCACC CAGCTTAAGT AGAAGACATT 180  
 GAAGGATGCA TTAATTTTCA GGAACATTTT TGGATTATGA AAAGATTCCC AATTGAAAAA 240  
 ATTATTCAAC AAGTAAAAGC TAAGAAATTN CATTGAAATC ATAATGGCAG TTAAAGCATA 300  
 10 AATTTGATAA ANAATAGCTG TGTACTACTA AATTAATTAG GAAAATTGNA TTCCAANCCC 360  
 AAGNNGAAGG AGTCCANGGT GGAAATATCC GGTTTGTTTT TATTTTGNNC TTAGGNTGAN 420  
 GTTTTCCTTT GGTNAACCGN TTGNNTTTTT TATTTAANAT NGNTTAATTA TTTTNGGTT 480  
 AANGNTATGC CCCNTN 496

SEQ ID NO:4467

SEQUENCE LENGTH:415

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05306

## SEQUENCE DESCRIPTION:

20 GATCTTGGA GATATTAATA TCTGCTGGCC AGACCTAAAA AAAACTGAAG GCCCAAGGAA 60  
 AGTGACTGGA CTCACTGGAA AGTNTCTAAC AAATACTTTG GATTCCAAAG TATTTCCAAT 120  
 25 ACCTTGAAGA TTCCTTTGAA AACATCAAAG CACAACTCA AATCTGCACA AGATTACAAA 180  
 AGCACAATTT TGGTGTATT TTTAGANTNC AATACACAAA GCTATTGTTC ATTTCTNTCA 240  
 GCAAGCATT TCCTGGGTAG TAGTAATAGC TTAGGAATCA AATGCCACTT TTNTTTTCC 300  
 TTTTTCAC TAGTTGAAA TACCACAANT NACAGGTNAG TCAGTCTCC CAGAGGNNA 360  
 NGGNCAGTCC TAGGGNGGNA TCAACAGGNC TNGCAAGNCA AGNCCCACAA NTTNN 415

SEQ ID NO:4468

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05307

## SEQUENCE DESCRIPTION:

35 GATCGCAAAT TGAAATATGG ATATTTGTAC CAGGCTGCGT GTTTTTCATT TTAACACAC 60  
 AAGATTTAAT TGAAAGGACA TCAATAATCA TAATTGTGTA TTAAACAGGT GGTTTNTAT 120  
 40 TAGTTTTCTN GTGTTTCAGA CTTTATGCAG CCATATAAAC TGTTCTCTAG GCATGCTGTG 180  
 ACATTTTAAT AAAAAGCAAA AGGAGCAAA 209

SEQ ID NO:4469

SEQUENCE LENGTH:353

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05308

## SEQUENCE DESCRIPTION:

50 GATCGCACCT TTTATACCAG AGACCTGAGG CAGATGAAAT TNATTTCCAT CTAGGACTAG 60  
 AAAAAGTGG GTCTCTTACC GCGAGACTGA GAGGCAGAAG TCAGCCCGAA TGCCTGTNAG 120

TTTCATGGAG GGGAAACGCA AAACCTGCAG TTCCTGAGTA CTTTCTACAG GCCCGGCCCA 180  
GCCTAGGCCC GGGGTGGCCA CACCACAGCA AGCCGGCCCC CNCTCTTTTG GCCTTGTGGA 240  
TAAGGGAGAG TTGACCGTTT TCATCCTGGC CTCCTTTTGC TGTITGGATG TTTCCACGGG 300  
TCTNACTTAT ACCAAAGGGA AACTCTTCA TTAAAGNCCG TATTTCTTCT AAA 353

SEQ ID NO:4470

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05309

SEQUENCE DESCRIPTION:

GATCCTCTAA CACTGTACTA AAACATTTCA ATAAAATCAT TCTGACTGCG TTCATAAAAA 60  
CAAA 64

SEQ ID NO:4471

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05310

SEQUENCE DESCRIPTION:

GATCTATTAC TGACCGTATG ATGAGGCCAA CTTTTTNNCC TTGTGGTTAG CAAGACTGCA 60  
AGAGATGGAA AAAAAGTAGT TTGAATGTTT TGTGTGTAAG GAGTATACCA TGAGATGAGA 120  
TGACCACCAA TCATTCCTT GGGGGGAGGG GGTGTCTGCA CCNTAGAAA 169

SEQ ID NO:4472

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05311

SEQUENCE DESCRIPTION:

GATCACTTGA ACCCAGGAGT TTAAGTCCAG TCTGAGCAAG GCAGTGAGAC CCTGTCTCTA 60  
AACAATAAAA ATTAAATATA GTATTATCGA GAGTTCCTGG AGGGGTGAAA TTAAAGACTT 120  
TCAAACTTA AA 132

SEQ ID NO:4473

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05312

SEQUENCE DESCRIPTION:

GATCACCAGG CTGCCAAGG GTGCTGTGCT CTACAAGACT TTTGTCCACG NGGNTCCTGC 60  
CAAGCCTGAG GGCACCCGTC AACTGGTAG CTATGCTTNG ATGCCTGTT GAGGCCATCG 120  
GACAGAGACT GGAGCCCANG TGACAGGAGA TGGTGATACC AGAAGTCAAG GGTGGGGTG 180  
GCGACACGGC CTCCCAGGA AGAGGTCTGC TTGATGGTGA CTCTGCAGGA GACTCTGAAG 240  
TGACTGCTGG GAAACCCTTT GGGAGACCTN ACCTGNGGCC AAAANTAAAG TNNGCCAGCN 300

TCATGAACCG CATNCTATTT AAGGGAAA

328

SEQ ID NO:4474

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05313

SEQUENCE DESCRIPTION:

GATCTGGACA TGCTGTNACA AGAAATAGTG ACCTTGGGGA ATATGTACAG AAAAGACCTT 60  
 TTTCTAAGAG TTGGGAGGGG GTGGGGGACT GTATAATGAA AAGAATTAGC TTACAAAAAA 120  
 GAAATTGATA TTCAAAGTAT TTTAGGCAAA GCCAGTCAAA ATGCTTTCAT GATATTTTGA 180  
 GATGTAAATT TTGTCTGATT TGTATTGTNC TTTTCATTG CCTTCTTAAC TTTATATGTG 240  
 ACCTGAATTT TCCATAACTT GATGACTATA GATTGCACCT AGGCATTCCA ATAAAAGCCA 300  
 ACCCAAA 307

SEQ ID NO:4475

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05314

SEQUENCE DESCRIPTION:

GATCGTAAAA ACATGTCTTA TGCGGAACTT TCATGTCAGA TGCCTGGAGT GTGAAGTGTT 60  
 CATTGGACAT TCCATTTTAC TGTTCGAAGT ATGGACTTAC ATATCAAATT AAAAGGCTCT 120  
 TTTGTTCTGC AAA 133

SEQ ID NO:4476

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05315

SEQUENCE DESCRIPTION:

GATCAACTGT CCTTAACCAC AGCAGCATGA TACGCTGGNT TACCCAATCG CTTGTAAGGN 60  
 AAGNCAGAGA TGACGTTATC CTGACTGCTG AGATGAGCAG TTTACCCTAG GAGGNCCNAT 120  
 TNGGACTATN 130

SEQ ID NO:4477

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05316

SEQUENCE DESCRIPTION:

GATCAGCCAC ACAACTGTTT TGTACATACT TATTTTCTCA TGCACCTTTC TGTATGCAAA 60  
 TAAAGCTATA AATTTACTCA TTTCAATAAA CTGGAGTGGC AGAAA 105

SEQ ID NO:4478

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05318

SEQUENCE DESCRIPTION:

GATCTGGGAC AGANTTCACT CTCACCATCA GCAGTCTGCA ACCTGAAGAN TTNCAACTN 60

ANTACTGTCA ACAGAGTTAC AGTGCCCCGT GGACGCTCGG CCCAGGGACG AAGGTTGGAC 120

GTCAAACGAA CTGTGGCTGC ACCNTCTNTT TTCATCTTN 159

SEQ ID NO:4479

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05319

SEQUENCE DESCRIPTION:

GATCTGAAAA GAAGGTGAAT ATTTTGCCT TTTGATACTC TTAGGAACAA ATAACCTATT 60

TGGCAAATTG TTTNTTTTTT ATGTTTTGGG TGTGTGTTTT GTTTTTTGAC TTTTTTTGTA 120

TTGTGAACAG GCACTGAAGC TGATGTTATT TTAAGATTAC AGAATGGAAA 170

SEQ ID NO:4480

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05320

SEQUENCE DESCRIPTION:

GATCATGTAA AATTACAGTA CTCAACCCTT CTAGCAAAGT ATTTGGNTGA AAAATAAACT 60

AAATGCCTTT AAA 73

SEQ ID NO:4481

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05321

SEQUENCE DESCRIPTION:

GATCCGCAGA GGGTGGTTGG GATACACCGG ATACCTCTGC TCTCATTGCT TGTTTCCAAA 60

TGCTCTATGG ACATTTGTGT GCTAAATCCT ATTAAATAAA AAAGACGGGT TAAACCCAG 120

ATGCTGTAAA 130

SEQ ID NO:4482

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05322

SEQUENCE DESCRIPTION:

GATCAAATTG AGAGACAATA AGTGTACATT GTTGAATAAA AAATTTTAAA GTTAAA 56

EP 0 679 716 A1

SEQ ID NO:4483

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS05323

SEQUENCE DESCRIPTION:

10 GATCTTGAGA GTATGTTCTT ACTCATTTCT GTAATTGCAG TAGTGTAGTC ATCTGCATAT 60  
AGTTTAAATA AATGCATGTT AAAATTTAAA 90

SEQ ID NO:4484

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS05325

SEQUENCE DESCRIPTION:

20 GATCACGCCA TTGCACTCCA GCCTGGGGGA CAAGAGTGAA TCTGTGTCTC ACCAGAAA 58

SEQ ID NO:4485

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS05326

SEQUENCE DESCRIPTION:

30 GATCTGGTGA CTGTNCTCTC CCTGTTTTC TTTCTTTTGG GGTGTTTGAG GAGCANNNGCT 60  
TAGCTTGAGA CACACACAGA CACTGTGTAC TTCAGTNAAG GGCTTAATAN ACAGN 115

SEQ ID NO:4486

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS05327

SEQUENCE DESCRIPTION:

40 GATCATTTCT ATGTGTGTGG GTAATCTGGT CAGTAAGATT GAGACTTAGT TAAGATTCCC 60  
CTTGGAATTT CCTTAATGTT TATTAGCTTC TAACTAGTGT TGTAAGTCCG ATGCCAGAAT 120  
TTGGAGATTT GAGTTCTTCT TTTTCATGGCT TTTATTCAC GTGACTAATA AGCTTCCTAA 180  
TAAATCCTTG CCAGACTTAA A 201

SEQ ID NO:4487

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS05328

SEQUENCE DESCRIPTION:

50 GATCTAGTTC GTGTATAACT GTTAACTCAT TTTACATTTT TTNCTTCGTT GAATGTTTAT 60

55



EP 0 679 716 A1

CAGATTATAA ATATAGAGGC ATTTCTNCAT CCTGTTTAAT GTTTATTTTG TAATCATTGG 120  
 AGTATGTGAA AAATTTTNGT TTGTTTTGCT TTGGTCTCTA AGTAAACATG TTCAGCAAAG 180  
 TATTTNTNTT TTNAAGAAAT AAATNGNGNT TTGTATGTCC TNCCTTTTAG GTTTGAGGCA 240  
 AAGAGGAGAT GGGAANCCAA AGGCAACANG GGNN 274

SEQ ID NO:4488

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05329

SEQUENCE DESCRIPTION:

GATCTNTGCC ATGCAGAGCA TCTTCCAGAA GACCAGGACT CTGGGAGGCG AGGAGAGCTG 60  
 AGCTGGGCCA CCTGGTCTCA GCCACCTGTT CTTGGCTCCC CAACAGACTC TGCACTGCAC 120  
 CATGGGAGGC TCCTGGGATG TTTGGAAGAA GAAACGGGCT TCTCCTTGAG GGGGTAGTGG 180  
 AGGGATTTTT TCCCCAGCAG TGGCCTCTGA GAGTNNNTCA GTGCCTGGTG GGGCAGGGCA 240  
 GGCCTCTTGG AGCACCTCCT CCCTGGNTCA GGGCCTGGAT GCAGGTGCCA AGCTCTCCAT 300  
 GTGGTGCATG TTNGACCCAG CCACGTGGTG AN 332

SEQ ID NO:4489

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05331

SEQUENCE DESCRIPTION:

GATCTTAACT ATGAGTAATT CACTATCAAG AGCTAATTAT TTGAAAAAAT ATAAGATGTT 60  
 ATGGAGCAGA TAGCTCAAGC AGTAAAAAGA AATTNTGCAA CTNTAATTCT NTTCTTATT 120  
 TTAATACTAC TACTTAATAA ATAGTATTTG CTAAG 155

SEQ ID NO:4490

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05332

SEQUENCE DESCRIPTION:

GATCAAATCA GAGATTGACA GCCTGTGGAG GGTGCTGAAC TATACAGAAT TAGACACAAC 60  
 TATGTCATTA TTTTGTGTAC CTACTGNTCA GAATAAAAAA ACTTGAAATA TGAAG 115

SEQ ID NO:4491

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05333

SEQUENCE DESCRIPTION:

GATCCCTTCT GTTGGTGTCA TGTTGTAAAC ATTTCTTTCA ATAACTAAA GAAAAATTAT 60  
 TAAAGGAACA CATACTTTG GTTAAATAGT CTAGACTAAA AGATTGAGAA GTTACTTTCC 120

ATTGCTATCT ATTGATAATT TAGACATTGA GTTCAAATTG CCTTCATTTT ATGATAAATA 180  
 ATGATTTAAC TGACAAA 197

5 SEQ ID NO:4492  
 SEQUENCE LENGTH:79  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

10 CLONE:HUMGS05334  
 SEQUENCE DESCRIPTION:  
 GATCATTTTT ATTTTGTAAG TATTACCTAA CTTTACATAA ACTATATCAT AATAAACTAT 60  
 TTTTGCATCA CCCTTTAAA 79

15 SEQ ID NO:4493  
 SEQUENCE LENGTH:377  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

20 CLONE:HUMGS05335  
 SEQUENCE DESCRIPTION:  
 GATCTCCAAG CTGAAACTTA CACGTAAAA CTTTGCCTG TAAGAATTG CACATGAATG 60  
 TTAATGGAAA ACACAAAACCT TAAGATGGCC CAAACNAAA GCCACAAACA GTTCATCATT 120  
 25 TGGTGCTTAG TCTTTGTAAG GGCTCTCTGT GGTTTGACTT ACTCCAGCTA CCGTTAGATG 180  
 AGGGCAAATC ACCTTAGAAC ATGTTTCAATTT GATTCATAAC ANGGAAAATT GGGTCTATGA 240  
 TTTTNGCCA ATCTTAGCCT AAAAGAAATT GCTTTAGCTT CTGGTCAGCA CTGATTAAAA 300  
 TGTGAATAGT GAAGTGGCTA TCCTAAACTG GTTTATCTCC ACCCACACTA TCATAGANTT 360  
 CTTAGGTAAT ACAATTN 377

30 SEQ ID NO:4494  
 SEQUENCE LENGTH:170  
 SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear  
 CLONE:HUMGS05336  
 SEQUENCE DESCRIPTION:  
 GATCAAACAC ACACACCTAT ACACATACAT ATTAANATGC AGAGGATTTT AAATAATTGC 60  
 AAATGTCTTG TGGCTGTTTT ATTTCTACAA AATTCTGTAA GATGTATACC AGAAAAACATA 120  
 40 ATAAAGATAA GCTCAGTTCT TCATTGGGNA AAANTATTTT TAAGNNNNNN 170

45 SEQ ID NO:4495  
 SEQUENCE LENGTH:57  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS05337  
 SEQUENCE DESCRIPTION:  
 50 GATCTGTAAT GTGTCAAAGC ATTTTTCCTT TTTCAAATAA AGATACCTAT AATGAAA ... 57

SEQ ID NO:4496

55

SEQUENCE LENGTH:373

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05339

SEQUENCE DESCRIPTION:

GATCAGAATC TNCCAACTTT AGAGGTGCAA TGGAAGACAC TACGCTACTT GGTGAGCCT 60  
 GGTGAAGAAT GTATTAATGA GACTNCTTTG CATAAACTG GGAAGAAAGA GAAGACAGTT 120  
 GGAGATGGAA GATGGTTTTN TATATATNTN GGAACCTTAG TTCCTCTGTA AGACGAAAGA 180  
 GGAGAGCTAT GTTTNNNTNC ACATTGTCTG ATATATATNG TGTACCTGTC AGGTGAGTTG 240  
 ATTTAGACAN CATAGCTGAC CTTTATGAC ANGGCAGTTT GANTAGGGNC TATTGTAATA 300  
 CCCTCACACA TTATAGGGGC ATCAGAGNAT GGCCATGGNA GGGACAGTCT TACAGGGGGC 360  
 TTTANGGNGN CCN 373

SEQ ID NO:4497

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05340

SEQUENCE DESCRIPTION:

GATCTGAAGA AGTTGCTGTT CTGAAACAGA AGTTGGAGCG ATGTCATTCT GCTGAGCTTG 60  
 CACTTAACGT AATCACGAAG TAGAGGAAAG GCTATGNAGT TGATGATTAC GTCTCAAAGA 120  
 AATCCAAACA TGAGGAGGAA GAATGGACTG ATGACGACCT GGTAAGATCT CTCTAACCAT 180  
 TTGAAGTTGA TTTCTCAATG CTAACATAATC AAGAGAAGTA GGAAGCATAT CAAACGTTTA 240  
 ACTTTATTTA ANANGTATAA TGTGAAAACA TAAAATATAT TANNCTTTN CTATTGTTTT 300  
 CTTTCCCTTT CACAGTAACT TTATGTNAAA TAACCATCTT TCAAAAGGGC TANAANNAN 360  
 ANANNTNN 368

SEQ ID NO:4498

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05341

SEQUENCE DESCRIPTION:

GATCACATCA CCTCTCTGCC TCAGTTTCCC CATCTGTAAA ATGGGAGAAT AATACTTGCC 60  
 TACCTACCTC ACAGGGGTGT TGTGAGGATT CATTTGTAAT TTTTTTTTTT TTTTAAANA 120  
 GNGTTTAAAN GNNTAAAAAN CAGTNAATN 150

SEQ ID NO:4499

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05342

SEQUENCE DESCRIPTION:

GATCTCCATC ATTTCTTACA GGTTTCTCCTC CCTCAAGCAA TTCGACATCT CAAGTGAAGA 60  
 CATGGCCCCCT GAAGGGCAAT AAAGCTGCTA GTTTATTAAT ACAGTCAAA 109

SEQ ID NO:4500

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05343

SEQUENCE DESCRIPTION:

GATCTACAGG NCAAGGGAG GGAGCAAGCC CTA CTCTGGAT GGGGCACGGA CTGTCCACCT 60  
 TTNCTAATGT GTGTTGTCAG CCTGTGCTGT GGCATAGACA TGGATGNGNG GACCACTTTG 120  
 GAGACTGGGG TGGCCTCAAG AGCACACAGA GAAGGGAAGA TGGGGCCATC ACAGGATGCC 180  
 AGCCCCTGCC TGGNTTGGGG GCACTCAGCC ACGACCAGCC CCTTCCTGGG TATTTATTCT 240  
 CTATTTATTG GGNNNGNTG AAGAGGCATC CTGCCTGGNT GGGNCAGCCC CTTCAGCCCC 300  
 TTNTNCCCTN CCCGN 315

SEQ ID NO:4501

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05344

SEQUENCE DESCRIPTION:

GATCAGACTG TTGCTTTCGC ATGNTGTATG TAGTGTCTCA TGNCTGGAGT TTGCTTTGTT 60  
 TTATAGTATC TGTACTCCTT GTATTTTCA AGAGCTATTT TGTAACAGA TGATGTATTT 120  
 CTCCATTGAA AACACAATAA AAAAAANCA GCACAAA 157

SEQ ID NO:4502

SEQUENCE LENGTH:397

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05345

SEQUENCE DESCRIPTION:

GATCTAGTCT TTACTTTCAG TTGTNTGTTA GGTCCATTCT GTTACTAGA CGGATGTTAA 60  
 TAAAACTAT GCGAGCCTGA NTGANTTCTC AGCCAAATTT AGTCTTGNT CTCATCTGA 120  
 TTGGNTAAT TCCAAATTCT AAAATGATTC ANTNCACAAT AGCTCTAGGG GATGANGAAT 180  
 TTGCCTTACT TTGCCAGTT CCTAAGACTG TGAGTTGTCA AATCCCTAGA CTGTAAGCNC 240  
 TTCAAGGAGC AAGAGGCGCA TTTNCTCCGT GTCATGTAAT TNNNCTAAGG TGCTTGGCAG 300  
 CACTCTGTAC CCTGTGGAGT ACTCAGTACC TNTGGTTTGA NGTTGCTGAC AAGACCTGAA 360  
 AAAATCCCT TAAAAANNA ACCCTTTAAG GTGTGGN 397

SEQ ID NO:4503

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05346

SEQUENCE DESCRIPTION:

GATCAGACTT GTTAAGTATG CCGCAAGTAA GAGCTAATTC ATTCATTCCA TGTNTGCCAC 60

TAAATAAAGA GATTGAGCAA GAAA

84

SEQ ID NO:4504

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05347

SEQUENCE DESCRIPTION:

GATCTNAACC CCAGACATCA AGGATAACAT CGTTGCTCAG CTGAAGCAGC TGTACCGCAT 60  
 CCTTNAACC CAGGAGAGCT GGCAGCCCAT GCAGCCCACC CCCAGCATGC AACTGCCCCC 120  
 TGCCCTGCCT CCCAGTAAT TGTNAATGCN ATCTTCTTCC TTCTNTTTT TATAATATTG 180  
 TACATATGGA TTTTNNAGN GNTTAGATTT AACCAGCTTT TAAATCTCTC TTNNTCTAA 240  
 CAGTGTTAGA AGTTTGTNAT TCTNCAAATA TGCCTAGATT TAAAGCTGNT TTGAATTTAT 300  
 GGNAAAAAAA AANAAN 316

SEQ ID NO:4505

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05349

SEQUENCE DESCRIPTION:

GATCAAAGTG TTAGGGGAAA AAAATTCCAA AAGTAGTTAC AAGCTATATC AATGTCAAAG 60  
 TAAATNCACT TCATCAAAGC TAAGAAGTCA CAGGAATTGT NCTCAGGTTT TAAAAAAAT 120  
 TTTNCCTGAA TTCAGGAAGT GTCTTCTGAA TAGCAGCTAG CCANNTAAAG CGGTGTGTGT 180  
 GTACTGCAGC TGTAGGTGAA CTTAAAAATA ATAATAAA 218

SEQ ID NO:4506

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05350

SEQUENCE DESCRIPTION:

GATCAGCCAG TTACCTTCTC CATTGTNTTA GTTCTGTCAC CCATTTCGTC AAGTGACCTC 60  
 TCATCTTCTA TAACTAATA CAGGAATTCT TTCCAAAGCA ATGTCTAAAA ACTCTTTTTT 120  
 TTAAAGTAAC AGTTTGGTAT GTTTATTGTA GATAAATNAT TTTNAGGCC TTCATTTTAG 180  
 CTAAGTTTAG AATTNATATT AGGCANCTAT GATTGAGTG GTTATNCATT GAGTAANTTT 240  
 CCACTATAAA GAATTTNATT GANCANTTGT TAAAGNATNN TGGTAATGCA TGGNCAN 297

SEQ ID NO:4507

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05351

SEQUENCE DESCRIPTION:

GATCAGAGCA CTGAGAACT CCAGAGGCTT CTGGTTCACC GCCCTGATTC CACAGATGTG 60

# EP 0 679 716 A1

GGTCAGAGGC AGAGATGGAA GTTGAATGG ACAAGCCTGC CCTCTCCTCA GCTCTCCATG 120  
GCTCTGTGCT CAGGCTGTTT CTGCAATTG ACATGAGGCC TGGCCCCAGG GAAACCAGTG 180  
GGGCCTCATC TCCTCCCTGT GCTGCTCTGA GGTGGAGCCT TCTNAGGGTC AGTCCAGCTC 240  
TGGAGNCCCT CTCCAGCTCG GTCACCAAAG CTGTCTGGTC CCAGGGCGGT GTGGAGTGAC 300  
AGGCACGGCA GCCCAATNCN GN 322

SEQ ID NO:4508

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05352

SEQUENCE DESCRIPTION:

GATCGCGCCA TTGCACTCCA NCTTGGGTGA CAGAGTGAGN CTCTGTCTCA AAAAATAATA 60  
ATAATNAATT AATTAATTAA TAAAAAATA AACAGTGGGT TAGTTATCTC AAAAGTGGGC 120  
TTGTTATAAA ANCNNGN 137

SEQ ID NO:4509

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05353

SEQUENCE DESCRIPTION:

GATCATAAGA CTGTCATGTA AGAGGTGCTC TCCTGGCACC CAGAGAAAAG GAGCATCCTT 60  
ACCTCCAAAA GCACAGGGAC ACAAAGAGGA ATCTAAACAA ACAGGCCTCT NAGTTTCCCC 120  
CAGTTTATTA CATTTAGCTT GTTCACACTT TGCCCTATGA CATTNCTACA TCACTGGNTG 180  
CTCTTCATCA AACCTACTAT AANNNNCATT CAAGTTCAAC TGTTTCTTTG GGCCTTNNTT 240  
NNCTTATGGA GGCCCTCGTG TCGTGTA AAA CTTNTATTNG GTNAN 285

SEQ ID NO:4510

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05354

SEQUENCE DESCRIPTION:

GATCAGCAGA GTGGAGGCTG AGGATGTTGG GATTTATTAC TGCATGCAAG CTCTACAAGT 60  
CCCGGTCACC TTCGGCCAAG GGACACGACT GGAGATTA AAA CGAACTGTGG CTGCACCATC 120  
TGTNTTCATC TTGCCGCCAT CTGATGAGCA GTTGAAATCT GGAAGTGCCT CTNTTGTGTG 180  
CCTGCTGAAT AACTTCTATC CCAGNGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT 240  
CCAATCGGGT AACTCCCAGG AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG 300  
CCTCAGCAGC ACCCTGACGC TGAGCNN 327

SEQ ID NO:4511

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS05355

SEQUENCE DESCRIPTION:

GATCCTCCAC TCCAGAGCAC CTGAGAAGGC CGGGACCAGA GGCCCTGTGT GATGTGTACT 60  
 CCGCAGCTGT TTGGGGTGGG ACATTTCTGT ACTTCTCGAT TTGCTTATGG CTCAGCCATT 120  
 ACCTGTGTCA GTCCATGATT CTGTTGTAAC AGTTTAAAGA GTAAATAAAT AAAGCTGCCT 180  
 GATGTCCCAT CAAA 194

SEQ ID NO:4512

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05356

SEQUENCE DESCRIPTION:

GATCACTTTT CCCTGTCTAA ACTCCAGGNT ACAGTATCCA ATANATCCAA ACAGAACTCT 60  
 GGTGTCAAAG TGTAANTAAT NGTGTAATAAT AGCCTTCCCA AGNTTN 106

SEQ ID NO:4513

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05357

SEQUENCE DESCRIPTION:

GATCTCACCA CTGTACTCCA GCCTGGNTGA CAGAGCGAGA CCCAGACTCA AAAAATAAAA 60  
 ATAAAAACCC TGAATATCTT CCTTCTAAA 89

SEQ ID NO:4514

SEQUENCE LENGTH:366

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05359

SEQUENCE DESCRIPTION:

GATCTCTATA CCTCAGCTTC TTCATCTGCA AAGTGAGATA ATTGTACTAT TCTACTTTCC 60  
 TCATAGTGCN NTTATAACAG ATTATGATAA TATTACAAAG TACTTAATAC TTGGCATATA 120  
 GTATATATAT NANTATTAG TATTTTGCAA TTTGGGGATA TTGAAAATTA GAAATTGCNT 180  
 GTTAGTTCAT GCTGCACTAC CATATTGTCC TTTGGGGCT CTTCAATGGG TGAAATTCCA 240  
 TTTNACAGTT TATCATGTGC ATCTGTATCA CAGGNGTATT TTGGCAAAAT GATTCTGTNC 300  
 CAAAAAGGAG TACTATANN NGNGGGTGCC AAATATATTG AGTCTNTTAT GGGGAAAANA 360  
 AATTTN 366

SEQ ID NO:4515

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05360

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCTCTGGT AAAAAGCAAC ATCTGAGAAA ATTNCTTGTT TTTAGGAACC TGTGTACATT 60  
 CATACTTAAT TCTNCCAATN ATGCTTTTCA GTTTTTTGGA TTAACACTCA AAAGTAACAA 120  
 GTCCTCAAAA TTAGGTTTGT CCTGTTGTTT TAAGTGGACC TTTGGCAAGA GATTTCTAGT 180  
 GAAGCTTGAT TCTNAGTACT TTCCTCATGT ATTA AAAAAGA GGCTGGAGGA GGGAACTGG 240  
 GACGTGGAGA GTGAGGAGTG ATAGCCTGAG GTTCTTGTT TGCCAACCTG GGGAAACCT 300  
 GTCTCTACTT AAA 313

10 SEQ ID NO:4516  
 SEQUENCE LENGTH:73  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05361

15 SEQUENCE DESCRIPTION:  
 GATCACTAAA CTATCTCCCC TCTTGCTGAA GTTCTTTGTA GTAATAGCTC ATAAAAATTT 60  
 GTTTATTAAT AAA 73

20 SEQ ID NO:4517  
 SEQUENCE LENGTH:247  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05362

25 SEQUENCE DESCRIPTION:  
 GATCTTTTAA AAAGAGATTA AACCGAAGTG ANTAAAAAGA CCTTGAAATC CATGACGCAG 60  
 GGAGAATTGC GTCATTTAAA GCCTAGTTAA CGCATTNCT AAACGCAGAC GAAAATGGAA 120  
 AGATTAATNN GGAGTGGTAG GNTGAAACAN TTTGGAGAAG NTAGAAGTTT GANGTGGAAA 180  
 30 ACTGGANGAC AGAAGTACGG GAAGGCGAAG AAAAGANTAG AGAAGATAGG GAAATTNGAA 240  
 GNTAAAN 247

35 SEQ ID NO:4518  
 SEQUENCE LENGTH:95  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05363

40 SEQUENCE DESCRIPTION:  
 GATCGCAGAA CATACTGTAT TTTNACTATA TCTTTTTTTT TAAATCTGAC AAACTTTTTT 60  
 NCTTTNATTT NAATTGACAT AATTGTACAT ATAAA 95

45 SEQ ID NO:4519  
 SEQUENCE LENGTH:134  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05364

50 SEQUENCE DESCRIPTION:  
 GATCTGCTTT GGAAATTAAT TGCCTCTAAT ACATACCTAA GTAAACATAA CATTAAATACC 60  
 TAAGTAAACA TAACATTACT TGGAGGGTTG CANTNTCTAA GTGAACTGT ATTTGANACT 120

55



NTTNAGTNTA CTTN

134

SEQ ID NO:4520

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05365

SEQUENCE DESCRIPTION:

GATCTGGCAC TGAGCTTTTT GTCAGTGAAC CTTCCCGATG CCAGCTGGGC TCTTGGACTC 60  
 CCCTCTTCCT CAAGGGTAGA TGAGAGGAAC GATNNNTAGA GGTTGGCTGT GGGTCCTGGG 120  
 TACCACCTTC TGAGCCTCAG TTCCTCATC TGTAAGTGG GGAGAAAAGT CTGTTTGCCT 180  
 CAGGAGTGTG AGGACTACAC TAGTGAAAGC NCCTGGCGGG CAGCCGGCGA TGCCCAATAA 240  
 ATGTGTGNTT TGCTGTTTGT TAAGTGAAA 269

SEQ ID NO:4521

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05366

SEQUENCE DESCRIPTION:

GATCAGTTTG TAATTTTTTT NCTCCTTGAA GGCACAAAAT AATTGGTTTN AGGTATGTAA 60  
 AACACTAGAG GTCAACCTTA CATAGTATAT AGAACTNATG GGTTTACCCA GCTACCCAGT 120  
 AGCATAACTT TNCACAGCTC GGGGATGAAT TAACATGGCT GAAATAAAAC TAAAAGTATG 180  
 GTTTTNAAA 189

SEQ ID NO:4522

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05367

SEQUENCE DESCRIPTION:

GATCACAGTA CACCATATGC ACTCTGGTAC CTTAATTTTT TTTTATAAAT AATAAAAGTG 60  
 AATATTGAAG CTTCTTAAA 79

SEQ ID NO:4523

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05368

SEQUENCE DESCRIPTION:

GATCTGTTGA ATTTGGGAAG CCTCCAGTTT TAATAAAATT TTTTATTAT GGTGGAAACN 60  
 TGTCTGTAAA NCTTAGGACT ATAGAAATGC AAAGAATAAA GANCTGAGGG AGTTACACAC 120  
 ATTTGTAGTC AGAAATTAAG TTCAAAANAT AATTTAGGTC ATTTGCATTT TTTAGTATGC 180  
 AAAATAAATG GAAAANTTAA NGTGCAATAN ANNTATAATT NGGGAAATGA ATGCAGTAAA 240  
 NTTGANAACA TTGAN 255

SEQ ID NO:4524

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05370

SEQUENCE DESCRIPTION:

GATCTGTCAG GGCCACTTAG TGATAATAAA TTCTTCCCAA CTGCAGACAA A 51

SEQ ID NO:4525

SEQUENCE LENGTH:353

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05371

SEQUENCE DESCRIPTION:

GATCCGCATC GACTTGGCCG TGGGCGACGT GGTCAAGACC TGGCGTTTCA GCAACATGCG 60  
CCAGTGGAAT GTCAACTGGG ACATCCGGCA GGTGGCCATC GAGTTTGATG AACACATCAA 120  
TGTGGCCTTC AGTGCGTGT NTGCCAGCTG CCGAATTGTA CACGAGTATA TCGGGGGCTA 180  
CATTTTCCTG TCGACGCGGG AGNGGTCCCG TGGGGAGGAG CTGGATGAAG ACCTCTTCN 240  
GCAGCTCACC GGGGGNCATG AGGNCCTCTG AGGGCTGTTT GATTGCCCTT GCCNTGCTNA 300  
ACAACCTGTN ACAGGCACCT CCAAGGCCAG AACCACAGGG GCTNACTNTC GAN 353

SEQ ID NO:4526

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05372

SEQUENCE DESCRIPTION:

GATCTGGAAT AATTATGGTA AAATAATAGT ATTTGCTAAG ACTAGATGAT TGGTGTACTG 60  
GATTCATCC GCTATTTTCT AAGTTTGTTA TGAACGCTTA AAATATATAT GTATGTAGTA 120  
AAATTAATGT AAATTTGTAC AAATAAAAAT AAATGGCATG TGATATATGG CAAA 174

SEQ ID NO:4527

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05373

SEQUENCE DESCRIPTION:

GATCATGTGT TTGGGGGCTT TTAGGGGACC CAGCTGCACT GGGGCACTGC CCGTGGCCTG 60  
GGTAGGACAT TTCCCAGCAA GGGCTGGAGG AGTTGCCGTG CCTTCAGCCT GAATCGAATG 120  
TCAGAACCAG CCAGCGGTGC TTCACCCTCT TGGGGATAAC TTGCTTAGTT TTTAATAAA 180  
TGTTCTTGGT TGGTTTTCAA A 201

SEQ ID NO:4528

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05374

SEQUENCE DESCRIPTION:

GATCTATGAA GCCACCAAC AAGGCCGAGG GGCTCTGGAG GCATTGCTAT GTGGGGGACC 60  
 CCAGGGGGCC TGCTCAGAGA AGGTGTCAGC CACAAGAGAA GAGCTCTAGT CCTGGACTCT 120  
 ACCCTCCTCT GAAAGAAGCT GGGGCTTGCT CTGACGGTCT CCACTCCCGT CTGCAGGCAG 180  
 CCAGGAGGGC AGGAAGCCCT TGCTCTGTGC TGCCATCCNG NNNGGNTCCT CCAGCCTCAG 240  
 GGCACCTCGG CCTGGGTGGG AGTCAACGNC TTCCCTCTG GACTCAAATA AAACCCAGTG 300  
 ACCTCAA 308

SEQ ID NO:4529

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05375

SEQUENCE DESCRIPTION:

GATCTTCTGA GCTTGTTCCT CTGCTGGGTG GGACAGAGGN CAAAGGAGAA GGGAGGGTCT 60  
 AGAAGAGGCA GCCCTNCNTT GTCCTCTGGG GTAAATNAGC TTGACCTAGA GTAAATGGAG 120  
 AGACCAAAAG CCTCTNATTN TNAATTTCCA TAAATGTGA GAAGTATATA TATACATATA 180  
 TATATNCCTN TAAN 194

SEQ ID NO:4530

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05376

SEQUENCE DESCRIPTION:

GATCTTGATT GATAACTGCC ATGATATTTT GCTTTGATGT GTTTCTACAT GTGGTTGCAC 60  
 ACGGTTTCAGT AAAAATAATG CTGCTATCGA GTATGCAAAT ATTGAAGTAT GATGGTTTGA 120  
 CTGTATGGNA GTGTTGTAGC AGCCTCTTGT TTTTTTCCCC ATTGCCTCTT TTTTAAAAA 180  
 ACTTATAAAG TCACTNTTNA TTTTNCCTCA GTCTTCAATG ACGAGAGCAA TATTAAGANG 240  
 ACATTGCTAT CTAATNNTNA ATCTTNTTAA ATGAAAAATT CCTATGTTCA GTAGCGTGGT 300  
 TGATGCTATT GTGN 314

SEQ ID NO:4531

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05377

SEQUENCE DESCRIPTION:

GATCGAGTCA GCATAAATTT CTAAGTCAGC CTCTAGTCGT GGTTTCATCTC TTTCACCTGC 60  
 ATTTTATTTG GTGTTTGTNT GAAGAAAGGA AAGAGGAAAG CAAATACGAA TTGTACTATT 120  
 TGTACCAAAT CTTTGGGATT CATTGGCAAA TAATTTTCAGT GTGGTGTATT ATTAAATAGA 180  
 AA 182

EP 0 679 716 A1

SEQ ID NO:4532  
SEQUENCE LENGTH:314  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05378

SEQUENCE DESCRIPTION:

GATCATGAAA CTGGTTTCTG TTTTATGCAG TTGTCATTG TAAAGNCTAA TAAAATATNC 60  
TCTATAATTN CTTCTAGATT ACAAAAATAT GACAATCTG TAAGTAGCAG ACTATGGAGA 120  
AAAATGAGTT ACCTGGNGGG TCAGGTAAC TGCCTAACTN AAANGTNTGT TAGTTGAGGC 180  
AAAGTCCTAA GCAAGGTTGT GCTATCANGG CTCAGCATAC CTTCTGTTGGC CTTTGANTTA 240  
CCANCACTGG AANTGCCTGC CANCTAATCT GGGGTAGATT CTTTAAGGCA TTCCACTTAG 300  
CTTGCCAGTT GNGN 314

SEQ ID NO:4533  
SEQUENCE LENGTH:311  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05379

SEQUENCE DESCRIPTION:

GATCAACTAA TAGCTCTGCT AGTAATTGAT TTATTTTNC TCAATAAAGT TGCATAAACC 60  
AATGACTTAG CTGCCTGGAT TAATCAGTAT GGGAAACAAT CTTTGTAAA TGCAAAGCTG 120  
TTTTTNGTAT ATACTGTTGG GATTTGCTTC ATTGTTTGAC ATCAAATGAT GATGTAAAGT 180  
TCGAAAGAGT GAATATTTTG CCATGTTTCCG TTAAAGTGCA CAGTCTGTGA CAGGTTGACA 240  
CATTGCTTGN CCTGATTAT GCAGAATTAA TANGCTATTT GGATAGTGTA GCTTTAATGT 300  
GCTGCACATG N 311

SEQ ID NO:4534  
SEQUENCE LENGTH:330  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05381

SEQUENCE DESCRIPTION:

GATCGGAGGA CGACCCGAGT CCCAAGAGTG GGGTTTTGCT TTTTAAAAGG AGAGAGGAGG 60  
GGTGATGGCA GGGGAGTGGA GGGTGGCCGG GCAGGTCTCT CCGGCGCAGG GAGCCCTCTG 120  
CCCTTCACAC TCTCTCCAA AAGAGCCTCC ATCTGTAAGG AAGCAGGTCT CCGCGAGGGG 180  
TTTCTTTCCA TGTNTTTTCC TCCTGTNGTT TTAGAACTTT TTNGAAAAAA ACNGNCCTCG 240  
TTTTAGATTT ATAGCATTGA CTTTACACA CATTACACA AGANAAAAAT CCTTNCAAAA 300  
TTCTTAAANT NNNCTGGTNC CNNCTTTNNN 330

SEQ ID NO:4535  
SEQUENCE LENGTH:204  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05382

## SEQUENCE DESCRIPTION:

GATCTCAGCT CCCGTTCCCC AAGCACACTC CTAGCTGCTC CAGTCTCAGC CTGGGCAGCT 60  
 TCCCCCTGCC TTTTGCACGT TTGCATCCCC AGCATTTCCT GAGTTATAAG GCCACAGGAG 120  
 TGGATAGCTG TTTTCACCTA AAGGAAAAGC CCACCCGAAT CTTGTAGAAA TATTCAAACT 180  
 ANTAAATCA TGAATATTTT TAAA 204

SEQ ID NO:4536

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05383

## SEQUENCE DESCRIPTION:

GATCACTTGG AGACTCTTTT TTTGCTGGTT TCTAGATAAC TCAGGTAAAT CAGACCTTTA 60  
 CAGAGTACAG GGCTAGGTGA NAGANTTACT GANAAATCAC CTTGAAAATC CGANGGGCTG 120  
 ATATACCCCTT NNTGTN 136

SEQ ID NO:4537

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05384

## SEQUENCE DESCRIPTION:

GATCTATGCT GTGTTTGCTT ATTCTTTAGT TGAACACACT ATGAAGAATT CCAGGTGTAC 60  
 TAGTGAATGT AATTTATAGT TGCCAAA 87

SEQ ID NO:4538

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05387

## SEQUENCE DESCRIPTION:

GATCGACAAC GAGGCCCTCT TCAGCTGCGA GGTCAAGCAC CCAGCTCTGT CGATGCCCAT 60  
 GCAGGCAGAG GTCACGNTGG TTGCCCCAA AGGACCCAAA ATTGTNATGA CGNCCAGCAG 120  
 AGCCCGGGTA GGGGACACAG TGAGGATTCT GGTCCATGGG TTTCAGAACG AAGTCTTCCC 180  
 GGAGCCCATG TTCACGTGGA CGCGNGTTNT GAGCCCGGNN NNGGACGNN AGCGCTGAGT 240  
 TCGACGGGAA GGANCTTGGT GCTGGAGCGG TTTCCGNCG AGNTCAATTG GCTCCATGTA 300  
 TTNGN 305

SEQ ID NO:4539

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05388

## SEQUENCE DESCRIPTION:

GATCATAAAA TGAATTCTTT ATTGTATCTA CACACTCCAC ATTCTTTACT GTGTCCTACT 60

ACTGTATCTT GGCTCCANTG CTGTATTAAA CACCATCTTA AGCAAA

106

SEQ ID NO:4540

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05389

SEQUENCE DESCRIPTION:

GATCCTCCTT TGCATGCAAC TGTAGCTGCA TTTAATGAAT AGTTTGAACC CTTGTNAATN 60

CATTTTTTNA AAAAGAAAGA AAAAAAAAAAC TTCGTGTATG NAACTCAAAG CATGNAACCT 120

TAAGATGTTG CATTCTAAAC TNACANTAAA GACCTTTCCC AANTAAA 167

SEQ ID NO:4541

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05390

SEQUENCE DESCRIPTION:

GATCCATACG TGGCCGCACC CACACAGCAC GTGCTGTGAC NGATGGCTGA ACGGAAAGTN 60

TACACTGTTC CTGAATATTG AAATAAAACA ATAACTTTT AATGGTANAA A 111

SEQ ID NO:4542

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05391

SEQUENCE DESCRIPTION:

GATCAGTTCT GCAAGATGCC CATCAACAAC AAGATGGCCC AGTGGGGCAA CAAGCCTATA 60

TGCTGAGCAG GAGGCAGACT TGCAGAGCTT GTTTTGTTC ATCCTGTCCG TAAGGGGTCA 120

GCGCTCTTGC TTTGCTCTTT TCAATGAATA GCACTTATGT TACTGGTGTC CAGCTGAGTT 180

TCTCTTGGGT ATAAAGGCTA AAAGGGAAAA AGGAAA 216

SEQ ID NO:4543

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05392

SEQUENCE DESCRIPTION:

GATCGAAAAT AGTTGGAAAA AAGAAGAAGA GTTGCATCTC TACTGAACAT GTACAGACTT 60

TCTTCTTCTT ATTATTCCTT AAACAATACA GTGTAAACT AAA 103

SEQ ID NO:4544

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS05393

SEQUENCE DESCRIPTION:

GATCAGAACA NTNCAAAAAA TTCACACCCC CAAAAAAGNC AAGCTATTAT ATGGCAATTT 60  
CGTGATAAAA TATTCATCCT ATTTGTCCTG CATTTCTAAT TTTCCCGTAA CTAGACACAT 120  
CAGTTTATA ATTAGGGNAA AAATACCTTN TAAAAGTAAA GCGAGCANAG GTTTCNNTTG 180  
CANTGTTCAT TCCN 194

SEQ ID NO:4545

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05394

SEQUENCE DESCRIPTION:

GATCTGGTAG GTTGCAGCAG AGAAAAATAA TGTGACTTGN GAGNCCACTC AGAGAGGGTC 60  
CAAGGGTGAT GGAGAAGGAA GCATGGCCTG GNAGCTTGGA AGGNANGN 108

SEQ ID NO:4546

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05395

SEQUENCE DESCRIPTION:

GATCTGCTCT TGCAATGGCC TCACCATCTG GNAGGAGCGA GGCCGGCCCA TCGTTGGCAA 60  
GGGCCGAAAG GAGTCAGCGC ANCCCCTGCC CACCTTTNAG CAGGACCTCA CCTTGGCTCT 120  
GTTGCTGTCC TCCAGGGCGA GCACTTTCCA CTTCCAGAGG GGGCCAGAGG GACTTTGCCT 180  
GCCCAGTCTT TGGAGAGCTC AGTACAGGGC AGGAGCTGCT GTGGTGTTCC CTTGGCAAAT 240  
NAAAGTTTAA TTTTCGTTTG GGNAAA 266

SEQ ID NO:4547

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05396

SEQUENCE DESCRIPTION:

GATCTCCGTG TGTGCATGTN ACTGTGCTGG GTTGGAATGT GAACAATAAA GAGGAATGTC 60  
CAAGTGTTCA AA 72

SEQ ID NO:4548

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05398

SEQUENCE DESCRIPTION:

GATCATGGGG GTGGATTCT TATGAATGGT TTAGTACCAT CCACTTTGTA TTGTCCCCGT 60  
GGTAATGAGT GAGTTCTTAA GAAATCTGGT CATTGAAAAA TAAA 104

SEQ ID NO:4549

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05399

SEQUENCE DESCRIPTION:

GATCTTCACA TCTTGGACCT TNGTCAGTTT TGCTATTCAT TATTAAACAC TAAAACTTTG 60  
GCGGTTNTTG CAAA 74

SEQ ID NO:4550

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05400

SEQUENCE DESCRIPTION:

GATCTGAAAT CACATCCAGC TCCTGATGTT TTCTTCTCCC TCTGACTGCA GAGGAAGTGT 60  
TCCTACCTGC AGGAAGGCAC CTGTCACACA GGGCGTTCAC TCAGACCATC TGTGCTCTGC 120  
CCTGAGTTCA GTTGAGAAAA TCCTATTATC AAATTTGGNT TTCCTGGCCC CAGAACTTCC 180  
CAAAGACCTG TAAAATGGAG GGATTTACCA CCTCACATAT GTCCAGTTAA ACAGTTTGTG 240  
GACTTGTAAC CGTCGCAGCC CANTGGTACA ACAGTAGTTT AATCACGGGA AA 292

SEQ ID NO:4551

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05401

SEQUENCE DESCRIPTION:

GATCGGATGG GCAAGTCCCT GCCAGGGTCT CCAGATGGCA ATGGAAGCTC CTCCTTGCCC 60  
CACTGGGAGT AGCGGCTAAA GCTGGGGGAT AGAGGGGCTG CAGGGCCACT GGAAGGAACA 120  
TGGAGCTGTC ATCACTCAAC AAAAAACCGA GGCCCTCAAT CCACCTTCAG GGCCCGGCCC 180  
ATGGGCCCCCT CACCGCTGGT TGGAAAGAGT GTTGGGTNGT TGGCTGGGGG TGTCATAAAA 240  
GCTGTGCTTG GGGGTCGCTN GGAAA 265

SEQ ID NO:4552

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05402

SEQUENCE DESCRIPTION:

GATCTATGCT CTTTCAAATG GAGACTGGGA TATTGTTGTT TTAAGACCAC TGTTTTCTG 60  
TTTCTCCCA AATNTTAGTC ACATATATNA TTACCCTTAA GTTGGTCACT ATCTATCTAT 120  
CTGTCAATAA TTCAGGATTA AAGTTTGAAG TGTAATTACA TTTGANTTTT AAA 173

SEQ ID NO:4553



SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05404

SEQUENCE DESCRIPTION:

GATCGACCAG CAGGTGGTCT ATATCCATCC TTCCAGTGCC CTCTTCAACA GACAGCCAGA 60  
 ATGGGTNGTG TACCATGAGC TNGTGCTCAC CACCAAGGAA TACATGCGTG AAGTTACCAC 120  
 CATCGACCCT CGGTGGCTTG TGGAGTTTGC CCCAGCCTTN TTNAAGGTCT CAGACCCANC 180  
 TAAGCTAAGN AANCAGAAGA AGCANCAGCG TCTTGGNACC GTTGTACAAC CGNTATGAGG 240  
 ANCCCAATGN CTGGGAGAAT ATCTCGGNGN 270

SEQ ID NO:4554

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05406

SEQUENCE DESCRIPTION:

GATCGGGTTG AGCCCAGGAG GTTGTGGCTG CAGTNAGCTG TGATGTGCCC TTATGCTATA 60  
 GCCTGGGCAA GAGCGTGAGA CCCTGTCTCA AAGAAGAAAA AAAGAGAAAA ATAACTCTTT 120  
 TGAACAAACA GNCAAATTAG CTAGTAGTAT GGAGATGTAT ACCCTCTATT ACACACATAA 180  
 AACCGTAACA AAATTCATTG NGGTGTATTA TAGTTAGTTT TGTGAATAGA GAAATAAAGC 240  
 ACTGATGNTT AANNTTGGTT ACAGTGAATT TTAGAAGGNN TTNNTTGNTG GTTCACATTN 300  
 GTCAGAANTT TTTTCCNNC NNGGCTGGTT CAN 333

SEQ ID NO:4555

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05407

SEQUENCE DESCRIPTION:

GATCTCCCC TTCCCTTGNG GGGCACAGCT GGCCTGGGCC TCCAATCCTG CGGANTTTCC 60  
 TGGGTGTGGC TTTGACCTCA GAAGTGGCTC TGGTTTGGCC TCAGGAGTGT GGCCTGGCCC 120  
 AGCCTGCTGC AGCCTCCTGT GGNNGGCCCT TNATGCCACT AATCCCCNGA CCCCCGGAT 180  
 NTTNCAAAC GNACAGACAC ACGNATTGTT AAGGCCGCTT ANGGCCTCCA GCGTGCACTC 240  
 TTNTTTANGN 250

SEQ ID NO:4556

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05408

SEQUENCE DESCRIPTION:

GATCAATGCA NCGACGNGG GCTCATGGCC TACCTCGGCA CCATCACCAA AACGNCAAC 60  
 ACCATGAACC ATTTTGTGAA CAANTTCAAT GTCCTCTACG ACCGACAAGG CATCGGCAGG 120  
 AGAATGCGCG NGCTCTNTTT CTGATGAGGG TACTTGAAGN GGCTGATGGA CAGGGGTCAN 180

NGCAACTATC CCAAAGTGGA GNGCACTACA N

211

SEQ ID NO:4557

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05409

SEQUENCE DESCRIPTION:

GATCTTTTTT CCATTGGTTA AACATTTAAC TCCATGNCAG ACCTTGTTTT AACCCCTCTC 60  
 ACATCATGTT CTTTCCTTTT TTGCGAGTTA TTTTGCATTA ACCAACTTTG TCAGTGACAG 120  
 ATCGGTATCT GAGGGTGTCA CACACGACCN TCAGCAGGGA AGACTTCTGG GCCATGGAGG 180  
 GCCGTCTAAT ACATGGACTT ATAAACTGAC TGCNTGGGCA ATGAAAAGGC CAAATTATTTC 240  
 TGAATTTTTT TNGAATCACT GTAAAAAAC TGATTNTTN NTGTATAGAG ANCACTTAAA 300  
 CGGTGGAN 308

SEQ ID NO:4558

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05410

SEQUENCE DESCRIPTION:

GATCCAGCTG GTCATCCCA GCCCAGGTGG GCCAATTATT CAATTTTNAA GAATTTTGTT 60  
 GCAAGCCAGT TGTCAAACAC AGCCATTATA ATTATGTAA TTTGCAANTT ATGTTAAAAA 120  
 CAAGGACAAT AAATATTCAA AATGCATCCC TAATTACTAC ATTTGACCAC GNAAA 175

SEQ ID NO:4559

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05411

SEQUENCE DESCRIPTION:

GATCTTNACA ACTGTTTAAT CAGTTTTATT TTTGTACAGT ATTAGTGACC TAAGTNATTT 60  
 TGCTGTCCCG TTTTGTAAA TCAANTGAAA NTATAAAGA GGCTTGTGAC AGTAGGTATT 120  
 TTGTACATAT GTATATATGT TGTCCAAATA AAATTAATAA ANTGGTNAAA GGCTGAAA 178

SEQ ID NO:4560

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05412

SEQUENCE DESCRIPTION:

GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA GGNAGGCAAA 60  
 ATGCCGCAAA AAAGAAA 77

SEQ ID NO:4561

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SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05413

SEQUENCE DESCRIPTION:

GATCCCAGGA ATATTGTAAA TTTTCTAACT TTACTCTGCA TTTTGTATAT CTGGCCTCTA 60  
 TTGCCCTTGA AGGTGAAGAT GAAACTGTCT TTAGAAGATA TCTCTTTGAT TCTGTGATAG 120  
 AAGTCCCTCA CATCTTGTAT TAATTTTATG TATATATCAA CGGTGGTTGG TCTTTAAAAA 180  
 AATAAATCAA AAGAATANGT AAA 203

SEQ ID NO:4562

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05414

SEQUENCE DESCRIPTION:

GATCAACCCA CATTAGAGTG TCTAAGGACT CCTGAGAATT CCTGTTACAG TAAACAAAAC 60  
 TAACGTAATC TACCATTTC TACACTATTG GAGCATGGAA ATCATAGTCC CCACTCTGTG 120  
 AAAACTTAAC GCTTTTGGGA AGACATTCT GTAGCATGTC AGTTTGGAGA AATGATGAGC 180  
 TACGCCCTGA TGAAAGAACC GTGTTGGTGC TGCTAAGTTT AGCCATTATG GTTTGNGCCN 240  
 TTNTCTNTCT TAAGGCCTTA TTCTTTCAAC TAAAAAGNTG GGGGATTNAG GNGCCAAGGN 300  
 AGNTTGGGGG GGGGNTNNTG NAAATTAANT TTTNTTGAGG GGTNGGCNTA GN 352

SEQ ID NO:4563

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05415

SEQUENCE DESCRIPTION:

GATCCGCAAC CTGGACCCCA GTGAGAGGCG GTGGGCTGAC TGGGAAGNAG AGGCCCCCAA 60  
 CCTACTCAGG ATTTNCACGT GTGAACTAGG CTGCCTGTGG GGTGCCCCCTT AGGCTTGGAG 120  
 AGCCCCAGAT TGGAGGCAGA CAGACTGCAC CACCCCTTCC CCCCCTGCAT CTCAAGAATA 180  
 AAGCAAGCTG CCTTTGTACT TGGTTGNAAG 210

SEQ ID NO:4564

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05416

SEQUENCE DESCRIPTION:

GATCANATAG TTGCTGTTTT GTAAAATGTA ATGTATATNT GGTTTTAAGT AAAATAGGGC 60  
 ACCTGTTTCA CAAA 74

SEQ ID NO:4565

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05417

SEQUENCE DESCRIPTION:

GATCCAGAAA CTGAGAAGCT TATCCGAGAG AAAGATGAGG AGCTGCGGCG GATGCAGGAG 60  
ATGCTACACA AAATACAAAA ACAGATGAAG GAGAACTATT AACTGGCTTT CAGCCCTGGA 120  
TATTTAAATC TCCTCCTCTT CTCCTGTCC ATGCCGGCCC CTNCCAGCAC CAGCTCTGCT 180  
CAGGCCCTT NAGCTACTNC CACTTCGCCT TACATCCATG CTGACTGNCN AGAGACTNAN 240  
GNGGCANTAA AGTTTAATAA ATCTGTAGGT GGCNNANAGA AAAAGAAAAN AACAAAANAA 300  
AAA 303

SEQ ID NO:4566

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05418

SEQUENCE DESCRIPTION:

GATCGTGT TTAACTTTTCT TTTTCCTGTT TTTATTTTGG TATTAAGTCG TTGCCTTTAT 60  
TTGTAAAGCT GTTATAAATA TATATTATAT AAATATATNA AAAAGGAAA 109

SEQ ID NO:4567

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05419

SEQUENCE DESCRIPTION:

GATCTGGAGG CAGCAGTGCT GGATGGAATT GTCTAGGCTG TGGCATGTTG GTTTTGTCTT 60  
TCTTTTCTCC TTTGATTATG TAAGAGCTAT TTCATTATAA CTTATTATGG TGATTATACA 120  
GGCAAGAAGA CAAAAAGGAG AGAAAAATGTA CCTCTTCTAC TGGAATAATG TTTATGATTA 180  
CAAGTGAGAT AAGGTATTTT NATCAATATG AAGGCAACCT TGGCTGATAA AACCTCTATA 240  
GTGAATACTC ACATCTTTNA CTTCACTCAC TATCAATAAT AAATATATTT NCTGACAANG 300  
AAA 303

SEQ ID NO:4568

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05420

SEQUENCE DESCRIPTION:

GATCTCTTTT GTAGAGGATT TCAATGTATT TCTTTATCAT TTGAGTGTGT GTGTGATGGA 60  
CGAATATGTG TGTGAGTTTG AGAAGCATAT CGTTCGTGTC CAGTTACTTT GCAAATTTGT 120  
GGACATTTGT GATTGGACAG AGGGGTTTGT GCTGTGGCCT AACACTTGCC AAGTGAGGTG 180  
TAGGTTATGC CTATATGCAA ATTAAACTTC ACCTTTCTTG AATATTCAAA 230

SEQ ID NO:4569

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05421

SEQUENCE DESCRIPTION:

GATCCCAAT TGA CTCAGAG TTGAGGAGT TAGTATCACA GAATTAGATT TTTTAAAGC 60  
ATTTGTACGT TTCCATTCCC AAATATGTAG CTGTGTTTCT TGAAAACACA TCCTACATTG 120  
CATATGGGCA TAGCAGTTTT TGACCCAGGC AGAATAAGTT AATATTTAAT TAAATATTGC 180  
TTTGAAGATG GCGCTCTGGG CATGAGCATG GGGCTCCATG ACTTCCCTTC TATCCCATG 240  
AGCCCTCCT NCATCCAGCG ACAAGCCATG GGCATGCATA CAATGCAGCA AGACCAACAC 300  
ANGNGCAATA TTGAATTGGN TCATTCTATC TAAAAATTAC ATGGGGNGGG ANGTN 355

SEQ ID NO:4570

SEQUENCE LENGTH:353

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05422

SEQUENCE DESCRIPTION:

GATCAGAAAT AAACGACAAA TAGTGTGAGA TGTGTTGTGA ACAGGCATGG TGACCGTGGT 60  
CAGCGCCACT CTTGTTTCCT GAAATGTGCT TCTAAGACAG AAAATGTATT TNCTCATCAA 120  
GGGTGTCTGG AGACACAGAC CGTGACCTTG GCGCANGGTG TGCATCAGAG GCGTGTGCTG 180  
AGAAGGGTGG TGTTAAGCTG TGGAAAATGA CTCAAGAGCA ATAAATCAGT GCCAAAGCTT 240  
CCCTGCGCAT CTGAATAGNC ACAAGTGAAG CCCGTGTGCG CACAGTGCAG AGGCCNAGNC 300  
TGTATTTCCA GGTAGNGTGG CTTTATTTGA CTGTGAATCC ATTTACCTGT TAN 353

SEQ ID NO:4571

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05423

SEQUENCE DESCRIPTION:

GATCGGGTCT ATTTACCCA ATAGTCACTT GTGTGTCCCC CGAAATTGGG ATGGGTGAGC 60  
ACCTTGCTG TGGTGTAAC TTCCTGTTAT TTAATCTCCC CCACGGTTTC ATTTTNTNT 120  
TCTGTTAATA CTTAGAACTT TCTAAGAAAC TCCATGAAAT GAGGAAATAC TGTTTCTAAT 180  
AATATGAGGA AAGANGTAAA ANTGTTTATT CCANGTGGCA AGTCTTATTG GACACATTTT 240  
ANATAAGNTC ATGCATACCT GATAAA 266

SEQ ID NO:4572

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05424

SEQUENCE DESCRIPTION:

GATCGCCCGC ATGAGGTGCT GCTGTGCTCG GACCTGGTCA AGGCATACCA GCGCTGCGTG 60  
AGCGCCGCCC ACAAGGGNTG AGGAGCAGAC ATCATTCCCT GCCCTGGCAG TGACTTGGAG 120

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CCCTGAAGAA GGGCCAATCA TGGGACCACA GCCACTGTGC CCTGCCGTTT CCTGCTGGGC 180  
CCCTGCATAT GCCCCTGAGC CTGGGGCTGC CACGTGTTTA GGAAACAAAG TATGCGCTAC 240  
TGTCTGAAAA CAAATAAAGC AGATGCCTTT GTTTTCAAA 279

SEQ ID NO:4573

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05425

SEQUENCE DESCRIPTION:

GATCTAGGCC AGTGGCTGCT TGTCCTTG TG GAGCTGTGTG TNTNCTNCTN TAAGCAGCTC 60  
CTCCCCGGAG TCCCCAGCA CAGTCCCAGG AGATGACAGG AAGGAAGCAC CAGGGCAAGN 120  
CGGACGNTCA N 131

SEQ ID NO:4574

SEQUENCE LENGTH:413

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05427

SEQUENCE DESCRIPTION:

GATCTCACCT TCCACCTCCT CCGGGAAGTC TTGGAATGG CCAGGGCCGA GCAGTTAGCA 60  
CAGCAAGCTC ACAGCAACAG GAAACTCATG GAGATTATTG GGAAATAAAA CGGTGCGTTT 120  
GGCAAAAAAG ANTCTGCATT TAGCACAAA AAAATTTAAA AAAATACAGT ATTCTGTACC 180  
ATAGCGCTGC TCTTATGCCA TTNGTTTATT TNTATATAGC TTGAAACATN GAGGGAGAGA 240  
GGGAGAGAGC CTATACCCCT TACTTAGCAT NCACAAAAGTG TATTCACGNT GCAGCAGCAN 300  
CACANTGTTA TTCGTTTTGG NCTTCGGTTT NGTTNCCGGG GNCAGGTGTT TTTATTAGTG 360  
GNGTTTTTAA AAGGNGGNTN GTNGGGACCC TGTGGAGNA NAANCGGTTT TGN 413

SEQ ID NO:4575

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05428

SEQUENCE DESCRIPTION:

GATCACGCCA CTGCACTCCA GCACCCTGGG CGACAGAGTG AGACCCTGTC TCAAA 55

SEQ ID NO:4576

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05429

SEQUENCE DESCRIPTION:

GATCTGGCGT TGCCAGGCAT TCTGTAAGGG AGGGCTTTTC CAGTTCCTGG AAATGGAACT 60  
GGAAAATNTG GCTGGAAACA TTAATATGGC TGGAAATGGA AA 102

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SEQ ID NO:4577  
SEQUENCE LENGTH:420  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS05430

SEQUENCE DESCRIPTION:

GATCCAAGCT GCTTGAGGGG GTCAACCTTG GACCAAAGTT GCCTTAAGCC TGTGGTAAAA 60  
GGGCTTCAGG GAAGGTAAGT GGGCCANCTG CTGGAAGCTG CCAGCTGCCC GGNTGGCAAT 120  
GGTGTGAGTG TCTTGGCCCT GTCCCTGCCC TGGGGTCCAG CAGGTNATCC CTCCCTTCTT 180  
CTCTCTCCTT TGGCGTTTGT TCCTGTAGTC ACTGGGCTAA TCTCCCCCTA GCTTGAAGCT 240  
GTACATAGGG CCTCCNAGTG CAAATGNTNC TGNCCATACC GTGCACCCTT AGAAGCCTGC 300  
GTGTGCATAG AGCGCCCNNT ACTTNCCAGT TAANTTCCNA GTTCTTGTTN CNTGAGCTTG 360  
GTATTTTGTG ATGTGNCAAA TTCTGACTTT TGAAGGTTGG GNAAGTGAAG GGGAATTNAN 420

SEQ ID NO:4578  
SEQUENCE LENGTH:307  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS05431

SEQUENCE DESCRIPTION:

GATCTGGGAC GTCCACGAGT GAGGGGCTGG CCACCCAGCC CGACAGCCTT GCCTGACCAC 60  
CCTCCAGCAG ATAGACGCCG GCACCCCTTC CTCTTCCTAG GGTGGAAGNG GCCCTGGGCC 120  
GAGCCTGTAG ACCTATCGGN TCTCATCCCT TGGGNTAAGC CCCAGTCCAG GTCCAGGAGG 180  
NTCCCTCCCT GCCCAGCGAG TCTTNCAGAA GGNGTTTAAA AGGGTTGCAG GTNCCNACCA 240  
CTGACCCTTC CCGGNTGGCC TNCTTGNCNA GCTTANAANC TTAAAGTCCA GNACGCAGTA 300  
ACCTNTN 307

SEQ ID NO:4579  
SEQUENCE LENGTH:239  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS05432

SEQUENCE DESCRIPTION:

GATCCCTCTC CAAAGTGGTT GTCTTCTNT ACCTTGTGTC TTCTCTTGTA AAAATGAAAC 60  
TCAAAAATAA AATAAATGTG TCAAATTTTG AAAAAAANG AAAACTGAAA AAGCTAACAT 120  
GANTTGTGTG AAATTGCATA ATGCTGTANT GCTAATCTAC AATATGTAAT GCTATCTTGT 180  
ATGTNGNATT TGTTAATGCA CCACACAAGT GCAANGTAAA GACTGATTCA CNTTGNNNN 239

SEQ ID NO:4580  
SEQUENCE LENGTH:51  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS05433

SEQUENCE DESCRIPTION:

GATCTGACTG TACTAAATAT GAAAAATAAA GCAGCACATA CTTTCTCTAA A 51

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SEQ ID NO:4581

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05434

SEQUENCE DESCRIPTION:

GATCCATATA ACTGTTGGGT GCATCAGTGC TTTTNAAGG GGCTGCTTAC TATAGGGTTA 60  
 ACTATGTATA TNCATTGTTA AGAGTTAACT TGTGGTTTGG CTGTTTCCTG GATTTNATAA 120  
 CATACATGTG CAGAAATGTA TTCAAATGAA AGGNAGCATA CCTTTATCAN GATGCTATTA 180  
 AANTTGANCA TCGNGTNTAA A 201

SEQ ID NO:4582

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05435

SEQUENCE DESCRIPTION:

GATCATACAG TGAGGCTACA GTGACTGAGG GGAGAATCCC CTCCTGTTCA CTCTCCCAAC 60  
 CCTGCTCCAG CCCCTCAGCT TCCCAGACCC TCATGCANTT GGTGTGAAAT NCTCCCAGGA 120  
 GCTGTTTTAC TGTCTACTTT TCAGGATTAA AAAAAANNNN AAAACTTAAA 170

SEQ ID NO:4583

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05436

SEQUENCE DESCRIPTION:

GATCGGACTC TGCCCCTGGA CCTGGGAACG ACTGGACTGT CACGGGGTTA CCTCCTAGCT 60  
 CTCCCAGTGA ACTCCTGCCA GGCACACACA GCCCCTATAG CACTGAGCTC ACATGGGACT 120  
 GGGATATGGG GGCATCTCTT CCCCAGAGAG GCACTCAGTG AGCCTCCTGT GCCTGGNCCC 180  
 AGCCTGGGCC ATCTCTTAGG TGAGACAGTT GCCCGAACT AAGCCAGGCC TGGCTGGAGG 240  
 AGCAGCAGCT TGGGGAGAGG GATTTCCCTG CAGACCTCAA GCCATCATGC GGTGGGTGCT 300  
 GCCATGACAG AGGCTGGACC NCTGGGCCAG CGGGGTTGCT CAACCACCTT TTGTGCAAGG 360  
 TGGCCTTTGT GCTTGC GCCTT GCAGGCAGAN GTN 393

SEQ ID NO:4584

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05437

SEQUENCE DESCRIPTION:

GATCCTGCCC GAGGAGGAGG ACGAGGGTGC CGACTCCTAA CCCC GCCAGG CAGCCTCGTT 60  
 CTGCACAGGC ACTTTAGCCC GAGCCAGGNA CACCTGCGAG GGGGCAGGTG TGCTCCGCCG 120  
 CCCTGCTGAT AAGCTGGCTT CATTAACTG ACACTTCTCA AA 162



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5 SEQ ID NO:4585  
SEQUENCE LENGTH:122  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05438  
SEQUENCE DESCRIPTION:  
10 GATCTGTAGG GTCAGGAACA CAGCACCTAA CACAGTGCCT TATGGATAGT AGTTTTATAA 60  
TACAGATGTG TTGGAAGAAT AAATGAATGG GTCCTTTTCA AACAAATTCA CCAGAAGTTA 120  
AA 122

15 SEQ ID NO:4586  
SEQUENCE LENGTH:288  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05439  
SEQUENCE DESCRIPTION:  
20 GATCTGTCAC CTTCAGCGAG ACCTATTTCC TCCCCACCCC CAGAAACCTC TTGTGTTCTT 60  
GCCTAGGCCC AGGTGTTTCT GGCAGCCAAA TCGAGTCTCT CATTTTCTCT TGTGGACCAG 120  
TTAGTTTTGC CCATAACGCA GTATTCTGAG TTTGCAACTG TCTCTCTGAT GTGTGCCTTT 180  
TGTTCAACAC AGTAACCCCT GCATTCTGCT CTGCTCTAAT ACACTACCTG GAGAAAGTCT 240  
25 TTTCTTATT TTCAATAAAT GTCAGACATT ATTGNAAAGA AAAAAANTN 288

30 SEQ ID NO:4587  
SEQUENCE LENGTH:188  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05440  
SEQUENCE DESCRIPTION:  
35 GATCCCTATG TGGCTAACAG AATTAATGNT TCCAAAAATG TTGNAAATTA TATAGTNCTC 60  
TTAATTCCCC ACCTCTAACT ATATTTTGGG GTTATTTCTT TAGGAACAGA TGCCAGGAG 120  
TCATATTACT GAGAATCTAG AAATCTTTTG CAAAGTTCTT GTTATNTTGN CAAATTGCTT 180  
CCCNNTNN 188

40 SEQ ID NO:4588  
SEQUENCE LENGTH:287  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05441  
45 SEQUENCE DESCRIPTION:  
GATCTGCCCC CCTCGGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCAC CAGTGCCCAG 60  
TCCTGCCACA TCTTTTTTGT TAGTTGCAGT AGCAATACAA CCTTATCTAG AAAAGCTGGC 120  
CAAAAAAGAA AATACCATGA TAATAGGGTA CCTAATTTAT TGCTTTATTT AAGAAAAATG 180  
50 TAATATTTCA TTCGAATAAG TACTTTTGGG CTGGGATGNT ATTTCAATTA GCTACTTGGC 240  
ATGCCACCCA TCTTAGGGAA TTATATGAGG GTTTATACTT TAAAGTN 287

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SEQ ID NO:4589

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05442

SEQUENCE DESCRIPTION:

GATCAAAATT TCAAGTTGAC AAATTTGGAT TTGAAAAC TC ATTCACTTTT TCAATTTTTT 60  
TAATGAGGCA TAACATGCAT ATGGTTAAGT GCACAAATCT TAAGTG TACA GTCAGTGAAT 120  
TTTTGCATGT ATGTATGTAC CTGANGCAAG ATATAGAACT TATTACTTG TAAATAACAG 180  
CTATATTGAT ATGTCACATA CCAAANANTT TACCCTTTAA NTTATACAAT TCAGTGGTTT 240  
TTNGTATATT TGCAAAATTG TGCAACCNTC CCNACCATCT AATTCTAGN 289

SEQ ID NO:4590

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05443

SEQUENCE DESCRIPTION:

GATCCTCAAA GAAAGATTTG TTAGAGATAG ACAGGTTTAC AATTTGTGGA AACCGAATTG 60  
ACTGAATCTG TGGCTTCATG CGCTGAAGAA GCTGGGTCCT GGGGCAACAA GTGCTGTGTT 120  
GCCAGGACAA ATAGATGCTA AACATGGCAC TTAAATATTT ATTAAAAAC TTAAATTATT 180  
ATTGGCAAGC AAATCTTAGT ATCTTTCTTC CAGTAATATG GCCTGGCTGA GGGTCAGACC 240  
ACAGGACAGG NGCGACCTCC GGCCTTGACT GTCTGGGAAG CTTGATGGAT TTN 293

SEQ ID NO:4591

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05444

SEQUENCE DESCRIPTION:

GATCCACTTA GAGCAATAAC CACTTTTTTAA ATGTAAAATA AAAAGACAAA TGNAAAGGCA 60  
AA 62

SEQ ID NO:4592

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05445

SEQUENCE DESCRIPTION:

GATCTTCCCA CTGCACTCCA GCCTGGCCAA TAAGACCTGT CTCCAGCAAG ACCCGNGTCT 60  
CAAA 64

SEQ ID NO:4593

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05446

SEQUENCE DESCRIPTION:

GATCTAGATT CATTAGGAAT GTNTTCTTGT CAGCCAGGCC AGGACCCGGG CTTGCCAAGA 60  
GCAGAGGCCC TCCCAGCAAC CAGGATACCA CCACTTTGGG GGCTTTGTGT ACAGAGGTCC 120  
GGGTCTGAGA CCTCATAGGC TGCAGAAATC TGGGGCAGCC ACCATCAAGA AGCCCCTCTC 180  
AGGGGCCAGA ACTCCTTTGC CAGCGTGGAT TTCTCAAGTC GGGACTGCAT AATTAAAGCA 240  
GTTGCAGTTT TATTTTTTTT ACAGCTTTT TCCCAAAAAT GATTGTAGT TGTGTGTGCA 300  
GCACTTCGG CCTGATATGT GTN 323

SEQ ID NO:4594

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05447

SEQUENCE DESCRIPTION:

GATCAAAAAG ATAAGTTTAC AAAGTTGAGA CCTCTCATAA AACAAATGAA TAAAAATTC 60  
CTCTTGTA 70

SEQ ID NO:4595

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05448

SEQUENCE DESCRIPTION:

GATCACCTGT GCCTCCCCTC CCCCTTTGTT TGCCCTGTG TGGTTGGTCA AGGAGGGATG 60  
TGAGGGNAAT AGGGACCCCC CGACTTGCCC TCCTGCCTCA GTCTTTCCCC CACCCTGTCT 120  
CTTCTTGTC CTTCTCTGGA AAATGCCAAA ATACACGATG TGAATAAAAG TACAACGGCT 180  
AAA 183

SEQ ID NO:4596

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05451

SEQUENCE DESCRIPTION:

GATCTATAAT TATGCCAATA CCACACTGTC TTGATTACTG TAACTTTAGA ATAAATCTTG 60  
AAAGTAGAAA 70

SEQ ID NO:4597

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05452

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## SEQUENCE DESCRIPTION:

GATCTGCCTG TCAGAGTCCA CGTGTCTCTGG TCACTGGTCT TTATAATTGT TGTGCAATAA 60  
 CTAAAGGCTA AGGACTAGAT GCACTATCGT GTAAAGAGAT TACACATGAC TGTACCATGT 120  
 TGCACCTAAT CAAATAGTAT GTGGGGNTTT AAAATCGCTT GCATTGTTTC ACAAATAAA 180  
 TATCTCAATG TCAAATACTA AA 202

SEQ ID NO:4598

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05453

## SEQUENCE DESCRIPTION:

GATCCTGGNG CCTGGACCGG GCTGGANGAC AGCTGAGNAT GGGCCTAGCA GATGAAGCTT 60  
 GCCAGCAAGG CCAAAGCAAA CGGTTTCTNC TGTGGATAGT GGACAGAGAC CTTTGTAACC 120  
 AATGGAATTA TTCATTTTNC TCTATCINN 149

SEQ ID NO:4599

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05454

## SEQUENCE DESCRIPTION:

GATCAAGCAA TGGAAAAATT TGCACCACCG TGTCCCATGA AATTGTTTCA ATGTTTAGTT 60  
 TAGATATTGC TAAGTTGTGC TATTAACCTT TTGACAAGCG TGTAAGTATTG TTTGTTTTGG 120  
 GTTCTTTTT GATTTATAAC TATTTAGTAG TCCCCAGCTA GCTACCAGTA CAGATTTTAC 180  
 CCCATGGGTA GGATTCTATT GTTAAGCCAC ATAACAAAGC AACTAATTC TGACANCACT 240  
 GCAATGGAA AATACGAACC AAAAAAAGT TACACCGATA AGTTCANCA ACTGTCCATT 300  
 TTTGGATATT N 311

SEQ ID NO:4600

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05455

## SEQUENCE DESCRIPTION:

GATCCTGCCT TTTCTTTTC CCCACAACCT CACGCCAGNA GTTCGTTTAC ATCAGGTAAA 60  
 TCTTGAGAAA GCCTTGGTGC CCTCCTCCCC ACCCCCCACT CAGTAACCAC GTGCGTGCAC 120  
 CCCCAGTATC TTTCTCAGTA GTTAAGACGT TCTAGGCAAT ACCATAGACA CATCTGACTG 180  
 TGTCTCTNTC TTTGAGTGCA AGAAACTCAA GTNATCTTAA A 221

SEQ ID NO:4601

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05456

## SEQUENCE DESCRIPTION:

GATCAGAGCA GCTACACTGA AGCAAAAACC CCAGCGCCCA ACGCTAAATA TATTGCAATG 60  
GAGAAACCGT CCACAATGGG GTGTCTCTGT CCTTAGCAGA GCCTTGGGGC TGCCGTTTAA 120  
GACCCTCTG CTACTCCAC CCTTTTAGCA TCTAGTAAAC CACGCGCTGT AACAAA 176

SEQ ID NO:4602

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05458

## SEQUENCE DESCRIPTION:

GATCTCTATC ACTTTGCCAC CTGTTTGATG TGCAGTGGA ACTGGTTAAG CCAGTTGTTC 60  
ATACTTCGTT TACAAATATA AAGATAGCTG TTTAGGATAT TTTGTTACAT ATTNGTAAAT 120  
TTTNGAAATG CTAGTAATGT GTTTTACCA GCAAGTATTT GTTGCAAACT TAATGTCATT 180  
TTCCTTAAGA TGGTTACAGC TATGTAACCT GGTATTATTN CTGGGNCGGG CTTNTTTAAA 240  
ATACNAGNCC NGGCCAANAN AAANTAGGAN CAAAAACCTN GGGGGTTCTG AAA 293

SEQ ID NO:4603

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05459

## SEQUENCE DESCRIPTION:

GATCAGGGAT GGGGATGAGG TGAGGGGATT TGCTAGAAAG GGGTGCAAAG GAATTTAGCG 60  
GGTGATGGAG CTGTTCTGTG TCTTGATTGT GGAGTTATTA CAAGACGGTT ATTACAGTTT 120  
TGTNGTATTG AATTTTACTG TATGAAAATC ATACCGCAAT AAACCTCACT CACATACGCA 180  
CAAA 184

SEQ ID NO:4604

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05460

## SEQUENCE DESCRIPTION:

GATCAAGGAA TCTTTCATGA AGGAAATTTA AATACAGAAT GAAACATTAA NGGTAAAAGT 60  
GGAGTAATTA TTAAATTAT GTGTATAAAA GGAATCAAAT TTTGAGTAAA CATGATGTAT 120  
TACATCATCT TCGGAAATAG ATATGATGGA TTCTAGTGAA GACCAAANTT ACTTCTGTTT 180  
ACTTTCTATC AGGAAGCATC TCCATTGTAA ATATGTATTT NCATGTTTAT TACAAAGACC 240  
CAAATGANAA NTTTTNNGTC CATTTTTNGC ATAGCCTAAT GGTAGACTNG GAATAANAGT 300  
TCTGTATTTN TGGGATTTCC NGNGTATAAN NCTGGTTTCT AGNTGGGGCG TTAAGTCCCN 360  
TTTGGGTAAA NN 372

SEQ ID NO:4605

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05461

SEQUENCE DESCRIPTION:

5 GATCATGTAG GACGCGGCAT CCTGCCCTG GTAGAGAGGA CGAATGTNCC ACACCATGGT 60  
 GTCTACGAAA AANAAATAGT TAGTCACCTT CTNACCTTCT CCTCTTTCTC AAAGCCTTCT 120  
 GTCCCTGGTT TTTGCAAGTN CTGCATTTC GCGGAGAATC CGCGTTGCCT ACTGCTGCCA 180  
 CCTCCTGTNC ATTTAGAACT ATGCAAAGAC TCCGNTTCCG TTTTCCTGAG CTCCTNGGGC 240  
 10 CCCAGAGTCT CTGTTTGATT ATTTATTTAT TTATTNAGN 279

SEQ ID NO:4606

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS05462

SEQUENCE DESCRIPTION:

20 GATCGAATTT CACATTGTAG AGATGTATAG CTGTGATTAA GCTGCATATG TATGCTGGGA 60  
 AACGGCTTGA GTGGATGGCT AATATAAAAG TTGTTGGCCA TAATGCCACA CCTCTCATCT 120  
 GCTTGAAATA TGGACCAGTA TTCTAAAGTA TCAGCTACTG GGGTCTCATT CACTACAAGA 180  
 TAANTTCAA CTTACAGNA CTTTGCAGCA GTTCACCACC AGGCGGGACT GTGTCTGCAA 240  
 ACTCNCTTGT CTTACAGAC GNCTGATTAA NGCNANNNCT CTGGNNTCTC AAAGATNTAT 300  
 25 TGGGGAGTGN NGGTTTTNTG GGNN 324

SEQ ID NO:4607

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS05464

SEQUENCE DESCRIPTION:

35 GATCACAGAC CTAAGGCCCA GGCCACCTNT CCANACCTGG AATCTATGCA NAANTAATTT 60  
 CCCCTTAACC TGGGAGGCAG CGACACGTGT NACTTCTGTA AGAAACGTGT GTACGTAATG 120  
 GAACGGCTGA GCGCCGAGGG CCACTTNTTC CACCGGNAGT NTTCCGATG CAGCATCTGT 180  
 GCCACCACCT TGCGCCTGGC CGTCTACACC TTTNANTGCN ATGAN 225

SEQ ID NO:4608

40 SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05465

SEQUENCE DESCRIPTION:

45 GATCTAAATN CAGACTNNGG AGTTGGGAGG AGGNACCAA GTGAACCATC CTTCATTTAT 60  
 TCAGTCATTC GTTCATCTGT CAAACACGTA TTTGGACATC AAGGTTGCAG AGATGAACAA 120  
 TGCATGGNTT TCATCTTTNA GGAGTTCAAA ACCTAGTGGA GAGANCACAT GGTACAATCG 180  
 TAACACATGA AGGTCAAGTA AGTNTGTCAG TAAAGGTACT AATAACATGT TCCTTGNNC 240  
 50 AGNAGGATGN N 251

EP 0 679 716 A1

SEQ ID NO:4609

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05466

SEQUENCE DESCRIPTION:

GATCCAAGTG TTGCCTGTCA GCAGAGATAG GAGTGAAGTT GATGATGATG GTTAGATGGC 60  
CTCACAAGGG ACTCTAGTGA TAGTAAAGGT TCCAGTGGCA AACACACAAG TGAAAAGTTT 120  
GAATATAGTT TCATAATGTT TGAGAGTGTA AAAAATGCAT TTTTAAATTA ATACATTACT 180  
TTCTGTACTA TTTTAAATAA GTGTGTATCT AAATAAACAC ATAANATGTT ATGAGTAAA 239

SEQ ID NO:4610

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05467

SEQUENCE DESCRIPTION:

GATCATCCTG GCTGGGAGAA GTGGGACCGA GCCACCCAGC TNCACATATCC CCAAGCNGCG 60  
CTACAGCCGG GATGGGAGGC ACGTGGCCTC TCTTTTATCC GTCTATTTAT NTTGTAAGTG 120  
TATTCGTGTG GAGGAGGTTG TTGCTTTATT TTTTAAAGGC TCTGGAGTNT TGTGTATGGT 180  
TTCTTTTCAC ATCNGGGCNT CCCATGGGCA CTTCTAAGAA GAGAGGGGAT TTCTTTGAAA 240  
AGGAGAGAGG AATCCCCTAG AGCAGGGGAA GCANTGCCTG CCAGCTNTTG TGCACCTTNC 300  
GGGNGAANTT AAATATNCNN NAAATTTTCA AACCAGNGAA AANN 344

SEQ ID NO:4611

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05468

SEQUENCE DESCRIPTION:

GATCTCTCTC TCTCTCTCCC TTTCTCTCT CTCTGTTGGA TGCTTCTGTA TCTTTTCCA 60  
CAGCATAATG TCTGGTGTGA TGGGGAGCTA TTTATTGAAA TNAAAGATTA TNTATTTGTG 120  
CCATGAAA 128

SEQ ID NO:4612

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05469

SEQUENCE DESCRIPTION:

GATCCATTTT TGGGATAGAA TTGTATTTTT TAAGTCATTT TTTTTTCTTG AAATGGATAT 60  
GTACAAATAA AATAAATGGA AGACAGGATA AA 92

SEQ ID NO:4613

SEQUENCE LENGTH:130

## EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05470

SEQUENCE DESCRIPTION:

GATCCAACAC ATTCAAGTCA GTAGAANCAA ACCAAAACAT GCAAGCTTCA GCCTGNTCGA 60  
GTTCTATAGT TGTACCTAA ATCGTATGTT GTATGATACA TANGGTTATG TATTAGCNCG 120  
TAGCCGNGGN 130

SEQ ID NO:4614

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05471

SEQUENCE DESCRIPTION:

GATCACAGCT NCCCTGAAT CTCATTGCCT CAGAGAAGAC TAGAGGGCTC TTGGACTATC 60  
CCTAGGGCTA CACAAGAATA GTTCAGCCTT CTGCCATGCC ACACAGCCTC AGCTTGAATC 120  
TGGTTCATTG CGTCCTCGTG TTCTTCTCTC ATCCTTGCCT TANACCAGGG ATTCTGATAC 180  
CGAAGAAGAG GGGCCAATGA AAACCATGGA GTCTGTTCTG GACTCCCAGG GCTGGGACAT 240  
TATGTAGGAG CCACTTCATA AACATTCTCT TACTCAAA 279

SEQ ID NO:4615

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05472

SEQUENCE DESCRIPTION:

GATCAGTCAT GTGTCCGTAA CCTCGTTCCA TGACATCAGG ATAGCTGTGT TTGCACACCA 60  
TGCTCCATGT NCATTCCGAG CCAGGAGGGG TTCTNAGTGG AGCCTGGCTT AGGGAACAGG 120  
GAGCGATGGA AGAATGCCAA CATTAGCGTT GGTCTTCTCT TGTNAGGAAT NAAGGATGCT 180  
TGCACACATG CACCCCCTCA CTCTCACACT TGCACACATA CACACACACA CACACGAANA 240  
TGTTTGGTTT GTCAAANCTC ACTGTAGTAC ATAAAGNTTG CACTCTGNGT NNNNATATCT 300  
AGCNGNATGG GGGGTACGNT TTGGGCNGGT GTN 333

SEQ ID NO:4616

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05474

SEQUENCE DESCRIPTION:

GATCTCTTCC CACCTACCCT ACCTACTCCT ACCCAANACC CCCCTTCCCC ATTAATGTGA 60  
GTAATGAATT AGCCTGACCA CAGGTGGTCA CTGTAGGCTA ATGGAAAATA CCCAAGGGNG 120  
GGCAAAGCCC CCCATCAGAT GCATGAAGGT TTGCNAATGT TGAAGGCCAC TGCCCCACAC 180  
ACTGTGTCTT TATAGANTTN CCCTTTGCCN CACCCTCTTC CTGTNTCCAA CCTGGGACAC 240  
ANCTTNGCTC AAAGNGCTGG TGGNTTGTGG GGCATTAAATC TACAACCANA GTCCTGAATG 300  
GAGGCAAAGA GGGCCCCACN GGNTTTGNGG GGNTN 335



SEQ ID NO:4617

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05475

SEQUENCE DESCRIPTION:

GATCCATTCA CATTGCAAAC TTATCCTACT GTATAGCCAT CCATTGTAAG AATACATTTT 60  
 TCNATTTATA TTGTGTACAT TACTCCAGTG AACATTCTNN ANCTCCTCTT TTNGTATCCT 120  
 GTGCAAGANT N 131

SEQ ID NO:4618

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05476

SEQUENCE DESCRIPTION:

GATCTCAGCT ACGTGGGAGG CTGAGGCAGG AGAATCTCTT GAACCTAGGA GGCAGAGGTT 60  
 GCAGTGAGCC AAGATTGTNC CAGCCTGGGC GACAGGGTGA GGCTCTTGTC TCAAAAAAAA 120  
 AAGTCCACAT CTTCATGANC CCTCAGACTC TGGAGTTGGG TGTCGGCTTT TTTAGCCAGN 180  
 TTTTGTGGGA ATTGCCTTTN NCCTATTAAA GANGGAANGT GGGTAATGGA GTCCCAGCCA 240  
 CTCANGAGNC TGGNTATCCC CCGAGANTGG CTTGGGTTAC CAGCTATGGA CCCTTGGAAG 300  
 ATGANTCTAN ATCCTTCTCA CNN 323

SEQ ID NO:4619

SEQUENCE LENGTH:346

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05477

SEQUENCE DESCRIPTION:

GATCACCTCT CTGTATCCCC CACCCACTAT CCCATTTNCC CTCCTCCTCA GCTAGGGCCA 60  
 CGCGGGCCCA CATTGCACTT CTGGGGGGTG ACCGACTTCG TACACGGGTT TAAAGTTTAT 120  
 TTTNATGGTT TAGTCATTGC AGAGTTCCTTA TTTTGGGGGG AGGGAAAGGG GGCTAGTCCC 180  
 CTTCTTTTGG CCCTCCGCCC CCGCAGGCTT CTGTGTGCTG CTAAGTGTAT TTATTGTNAT 240  
 GCCTTGGTCA GGGCCCTCT ACCCACTTCT CCCAGTAAGT TGTGGCCCA AGCCCNATC 300  
 CNTGTGCTGT GTGGAGTGGN CAACCTGACC CCCGNAAGNG GGNNAN 346

SEQ ID NO:4620

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05478

SEQUENCE DESCRIPTION:

GATCTTTTAA AGGATAGACG TGGTCTCATG CTTCTTTGT NCGACTCCGT TTAAAGGAG 60  
 CATTGTAACC ACTATCCTCA TCCCTACAAA AATCCAGTGG ATGCACTTCC AAATTACTTC 120

# EP 0 679 716 A1

TGTCATTTTG TATGTGTTGT GTTTAGGGNT GCGTAATTTT CACTGGATGN TGAGATACAT 180  
GGTGATACTA TGTCAGTTTA TTCTCTGTGA ATATGTCTGT ACATAGNCAG GAAGCTCTAC 240  
TTATTTGTNC ATAGGCTGTC TGANGTATGT ACTTCTGTCA CATGGNCTTC ATTCTGATAA 300  
AGGGTGTTTC TCCCTTGNTT CACTGTCCAT ACCTTGTGN NGN 343

SEQ ID NO:4621

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05479

SEQUENCE DESCRIPTION:

GATCCTTCTG TGCTTGCTTG CATCTTAAAT AAAGACATGT TCCCGGCAAA 50

SEQ ID NO:4622

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05480

SEQUENCE DESCRIPTION:

GATCCAGCTA GGCTGGGACA CTCCCTAAAT CAGCTGCGTG TTGTTAGCAT CAGGCAGAAT 60  
GAATGGCAGA GAGTGATTCT GTCTTCATAG AGGGTGGGGT ACTTCTCCAT AAGGCATCTC 120  
AGTCAAAATCC CCATCACTGT CATAAATNCA GNGGNAATNG NCTGNACAAA 170

SEQ ID NO:4623

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05481

SEQUENCE DESCRIPTION:

GATCCTCTCT GTGTAAATCC TGCCCGGTGC TGTNAAGGCT GGACGGTGGA GGACCTGCTG 60  
GGGTCTCCTG GNACCCGCCT GTTGCTTCTN CCCTCCCTG TGGAAAGGTC TATATNACGG 120  
GCTGCCTGAG GCCCCAGAAC TCGTCTGTAA ACCACCTTTT CCAGCCAGAG TTCCCAAAGC 180  
TGGAACGCTA GCTGCCTGCT CTTCTTAAG NTGGCCTCCC CCNGACCCGT CANGGTCCTC 240  
AGTTGCCAGG GCTGGGGCCA NCCACTGTNA CACTGNGGNN TGCANGANAN 290

SEQ ID NO:4624

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05482

SEQUENCE DESCRIPTION:

GATCCAGCTT CAGCTGCACA CCTCTGTCCC CTTGGATGGG GAACTAAGGG AAAACGTCTG 60  
TTGTATCACT GAAGTTTTTT GTTTTGT TATACCGTGT CTGANTAAAA ATNCCCAACNG 120  
TTAAA 125

EP 0 679 716 A1

5 SEQ ID NO:4625  
SEQUENCE LENGTH:252  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05483  
SEQUENCE DESCRIPTION:  
10 GATCCTGACC CCAGCCAACA GCTGAGCTGC CGGGCCTCCT CGAGGCCCTA AGCCAGCCCC 60  
AGAGGTCCCA TCTNAAGCTG GAGTACCCTG GGGTCAGCAG CAAGAGAAAG AAGNGGAGAT 120  
TTTNTGTTN TTTTCCCCT CAGCCCTGCC ACCGTGGGA GTCTGGTTT TNTCTTCATC 180  
CTGTCTCTCT CTCCTTACT CTTGGATAAA TAAACAGCCT GTGAGCACAC AGGCAAGCCC 240  
GGCCCAGTGA AA 252

15 SEQ ID NO:4626  
SEQUENCE LENGTH:334  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS05484  
SEQUENCE DESCRIPTION:  
GATCGTNACA AATCTNCCCT CCTCACCAGC TAGTCTGGGG TTTCCTCTCC CTGCCCCAGG 60  
CCAGAACTGC CTTCTTCATT TCCACCCACG CTCCCAGCCT CTTAGCTGAA AGCACAAATG 120  
25 GTGAAATCAG TAGTCTCGNT CCATCTNNA TAGACTAAAC CTAAATGCCT CTAGGACGGA 180  
CTGTTGCTAT CCAAGNGTTT GGTGTTACCT TCTCCTGGGA GGTCTGCTG CAAACTCAAG 240  
TTCCNCAGGA TGGTCAAGNT GTCANGANAT ACAAGTTTNC ATCAATTGTA ATTATTACCT 300  
GGTCTTTNCA ANTTTGCAAN GGNGTTTTGG GNTN 334

30 SEQ ID NO:4627  
SEQUENCE LENGTH:192  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS05485  
SEQUENCE DESCRIPTION:  
GATCTTCCAT CAGGGCCGGA GTAAATCCCT AAGTGNCTCA ACTGCCCTCT CCCTGGCAGC 60  
CATCTTGTC CCTCTATTCC TCTAGGGAGC ACTGTGCCCA CTCTTTCTGG GTTTTCCANG 120  
GGANTGGGCT TNCAAGGTNG GNGTNTCTGT AAAATCAACA GGTAATAAAA ACTGTGTATG 180  
40 AGNCCNGGCA AA 192

45 SEQ ID NO:4628  
SEQUENCE LENGTH:315  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05486  
SEQUENCE DESCRIPTION:  
50 GATCTACAAT NAGATATCAC TTAACACTCA CTGGAATAGA TATATAATCA AAGTGATAAT 60  
ATCAAGTGTT GGNGAGGATG CAGAGAAATT GGNACCCTCA TGCAGTGTG GTGGATACCC 120  
ACGTGATATN AAAACAAATG TCTACACAAA AACTTGTGCA CAGATGTTCT TTGCAGCATT 180

55

EP 0 679 716 A1

ATTTATAATA GCCCAAAATT GANACAGCCC TANTTTCTAT CAACTNACAG GTGAATAATC 240  
ANAACGTGGC ATATCCATNC ATGGNGTATT ATTCAGCATT ANANNATGGG ATGAAGTACT 300  
GGTATGCACC ACTCN 315

5

SEQ ID NO:4629

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS05488

SEQUENCE DESCRIPTION:

GATCTGAAAT NATGGTTCAA AAAATACATT CATAATAAAA GTCTTAACAA A 51

15

SEQ ID NO:4630

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS05490

SEQUENCE DESCRIPTION:

GATCAATGCC CNTNTNTCAG TCTCATCTGT ACTCACGGCA GCCCTGTGGA GTACGGTGTA 60  
CTGGCCCAGC TTACAGATGC AGAAAGCGAG AC GTTCTGCC ATNAGATAAA GTCACGTGGC 120  
TCTTTAGTAN CACGGACAAG GCTCCTCGCC AAGGAACTCG TGGCAGAAGA GGGCAGCAGT 180  
TGGCAGTAGC TGCCGATGTC TGTCCCCAGC TNCACCATTC CTCCTGTGG CTGTGCCATG 240  
CTCGTGGTTT CAGTNTCCGT GTGTNCATGT GNCTNCCCTT NAAGAGCTCG CANCTGGTGT 300  
GCTTNGGGGG TCCCAGGGCT GTGTAGNGTN TTCTNCN 337

25

30

SEQ ID NO:4631

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35

CLONE:HUMGS05491

SEQUENCE DESCRIPTION:

GATCTGTCTA TTTCTTCAT CCATAGTTGC CTNACTCCCC GTCGTGTAGA TAACTACGAT 60  
ACGGGAGGGC TTACCATTC TTCCCTGAAA 90

40

SEQ ID NO:4632

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45

CLONE:HUMGS05492

SEQUENCE DESCRIPTION:

GATCAAAGGC TCTTTCCTCT TTTGTTTGAG AGTTGGTTGT TTAAAGCTT AATGTATGTT 60  
TCTATTNNAA AATAAATTTT TCTGGCTGTG GCAGAAA 97

50

SEQ ID NO:4633

SEQUENCE LENGTH:320

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05493

SEQUENCE DESCRIPTION:

GATCATCGTA TGCAACAGCT GGGTAATAAG ACTGGCATAG CTCAACTAT CCTGCCAAAC 60  
GCTCTCATCT GATTTTTCCT CCCTTCTCCC CCAACCTCCA ATCACCCTGA GTCACCTGTA 120  
AATTCATTTG TCATTCAAAG CGGAATAACA AGTTGTCCCT AGCAAAACCG CTGAGCGCTT 180  
TATAATTTTG TGGTGTATTT TTGTCAGTAG GTAGCAGAGG CGGAAGTATT TTTTGGTGTA 240  
ATTCTTGAAA TTTTCTGACA GGAAACCGGN TAAAGATAGA TGTGTCTGAG GNTAAAAAAN 300  
GTNNGGNNNG NNNTGNTTTN 320

SEQ ID NO:4634

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05494

SEQUENCE DESCRIPTION:

GATCTATGAA ATAGGTAACA TTTGAGTAGG TGTCATTAA ANATAGTTGG TGAATGTCAC 60  
NTATGCCTTC TATGTTGTTT GCTCTGTAGA CATGAAAATA AACAATATCT CTCGATGATA 120  
ATTGTATTA AGTAATCTAT AAGAAA 146

SEQ ID NO:4635

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05495

SEQUENCE DESCRIPTION:

GATCTATCCA GCTGCTTCCT TGTAGCCAAG AATGTGTTCA ATGAATTGTG ATTCACTGAT 60  
TTTATTGATT TTGTTTTAAA ACAGGGAGAC TGGTATTTTT GAAGCTGCTA TCATTTTCTA 120  
TTTCTNTATT AATNNCTTTG TAATCATCTT ATTAAAGTTT TCTTATTAG TGGGAAA 177

SEQ ID NO:4636

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05496

SEQUENCE DESCRIPTION:

GATCCTCTCC TTGTATGTAA TACCTTTTTT TCCCCTTCT AGCAAGTACT TTCAAAAGAA 60  
CTCTGTACAT TTAAACATAA AAAATAAATT ATGTTGAGCC AAA 103

SEQ ID NO:4637

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05497

## SEQUENCE DESCRIPTION:

GATCCATTTG TAACTACTCT TAATATATGG TACATAGTTT AAAAAATTTN ATTGAGCTTA 60  
 AAGTGTATCT AGTTTTGTGT CCTAATTATC CTGCTTAACC TTCTATTGTA AGGNTTTNCC 120  
 ACGTCAATAA ATATTATAAT GTAAA 145

SEQ ID NO:4638

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05498

## SEQUENCE DESCRIPTION:

GATCANCAAA CTCAACACCA TCTTGCAGGA GCAACGGGNT GGCCTTTAAC ATTGCTGAGG 60  
 CTTTCAAAGA TGTGTCAGAA CCCATTGTAT TTCTGCAACA GATGCAGGAG TTTAGAGAGA 120  
 AAATCAAAGT AATCAAGGAA ACTCCTTTAC CTCCCTCTAA TTTGCCTGCA AGCCCTTTAA 180  
 TGAAGAACTT TGATACCAGT CAGTGGGAAG ACATAAACT AGTCGGTGTG GATAAACTTT 240  
 CTTTGCTCA AGACACTGGC ACATTCATTN GCAAGGNTN 279

SEQ ID NO:4639

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05502

## SEQUENCE DESCRIPTION:

GATCAGAGCA AAGAGAAAAG AAAGCATAAG GACACTTACT CAACAGAAGC ACCTTTAGGC 60  
 GAAGGAACAG AACAATATGT CAATAGTATC TCAGATTGAC CATTTCTGTT ACTTGTCATT 120  
 TCTACTTTCA GAAACTAAAT GACTTTCAAA TTTGGGTATA GACAATAAAG AACTGAAGTG 180  
 CTCCTACTC AGTGATTG AAATTTTGAT GCTTGTATAA ATGTCAGATA ATTAATTCN 240  
 AN 242

SEQ ID NO:4640

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05503

## SEQUENCE DESCRIPTION:

GATCTTGTTA GACACATGAA TGTGTATAAT CATGTAAAT GCAAATAAAA CTAGTTCATA 60  
 GAAA 64

SEQ ID NO:4641

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05504

## SEQUENCE DESCRIPTION:

GATCATNAAG GTAAGGACTG GAGTNATGCA GCCACAAACC AAGGAATATC AGTAGCCATA 60

AA

62

SEQ ID NO:4642

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05505

SEQUENCE DESCRIPTION:

GATCAGTNCT AACCTGAGC TGGCGGCTAT CTTTGAAAGT ATCCNGAAAG ATTCATCATC 60  
TACTAACTTG GAATCAATGG AACTAGTTA GATGTTTGT CACCATGGGG ACCATTACAT 120  
ATGACCATAC AATGCACTGA ATTGACAGGT TAATCATAAG ACATGGAAAG AGAAGTGTCT 180  
AAAAGCTTCA AAATGTTCCA CTTTTTTTTT CCTTCATGGN GACTGTTTGT TTGGCTTTCT 240  
TCCATTGTNG TTTTGTAGC ATTTATTCA GAAATGTGTA TTTCCATAAT CCAGAGGTTG 300  
TAAACCACT AGTGTTTTAG TGGGTACAG CANCEATTN 339

SEQ ID NO:4643

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05506

SEQUENCE DESCRIPTION:

GATCTTCCTC CTTATTTTAA TGCTTCTTTC TCTTTACAAT TAAAAGTTCA TAAAATCTTT 60  
CAACATTAAA 70

SEQ ID NO:4644

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05507

SEQUENCE DESCRIPTION:

GATCAGCCCT AATNATGCTG TGTCCATGAT GCTTTTAATA AAAACAACCC CCACAAA 57

SEQ ID NO:4645

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05508

SEQUENCE DESCRIPTION:

GATCTCTATG CCAATATGC TGCCTCAACT CTGAGCTGTC TGCAAGGCTT AGTAAGTATT 60  
GAGTGGTGTT TTTTTTTTTC NTTTTATACA ATACCATNTT AACCACATGA GTTAAATAAA 120  
TTTGAGAAGT TTTTTTAAAA CAGTGCTTCA AACTGAAA 158

SEQ ID NO:4646

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS05509

SEQUENCE DESCRIPTION:

5 GATCCCCGGG TACNANTNAN CCATGCAGGC ATGTTTTTTT TNATTTTTC ATAGGCAATC 60  
CATTCTGTAC AGGTAGCTAA CTTTGTAAC GCTGTGTATT CCCTCTGCCC CCATGGCTGC 120  
TGGTGTAAT AACTGCATC TCCCGTTGGT AAA 153

SEQ ID NO:4647

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05510

SEQUENCE DESCRIPTION:

15 GATCCAGAAG TCATTAAGG AAACATAAGG CTGGGGAGGC AGGGGGAGTA AGTTCTATTA 60  
GAAAATCCTA ANAGCTTAAC AAAACTAGGG TACTAAATTC AGTTATAACA TGTTACAGAC 120  
TTAAATCATA GAGCTGCCCC AACATCTAGA CAGTCTCTCC TACTGATTAT AAATGAGTGA 180  
20 AACTATCAG TTAGAAAAAT CTAATTTAAG TTGTTAATAC ATGTTTCTTT GGTGAGCACC 240  
TGGATATANT TATCACAAAT NCTTTTATAC ATATGTCGAA AATGCTTTCA ACAAACCTAA 300  
GTGTCCTAAT TACATGCCAC TTTTNNAGG CTCACCTTAT GN 342

SEQ ID NO:4648

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05511

SEQUENCE DESCRIPTION:

30 GATCGCTACG GTTCTAAATA CTGAAGTCAT GATGTGTATT TCCNGGAGAA ATTCCTCTTT 60  
AAATGAACAA GTAACCACAT CTCAGGCGGC AGTGAAGTCC AGATAGTTT GCAGATTGTT 120  
TTGCTACTTN TNCATATGGT ATATGTTTCT GNTTTTAAAT ATTNCTNTTG AGAAATTCTG 180  
AGTNCTGATG TAGGAGCTTT CCTGTNATNN CTGTTTCACG TTCCTTCCTG TCACACCCTC 240  
35 CTTGTGGCGT CTCTGTGTAT ATCCTNGGCT TTATTTTCTN GGANCCTTGN GATTTCACAA 300  
CTGNGGGCCT GGAGACCTCG GCTCCTNCTG GTN 333

SEQ ID NO:4649

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05513

SEQUENCE DESCRIPTION:

45 GATCATGAGA AATTACCAAA ATGTCCACCA ATAGAATGAG TGAATCACCT GTGGTATATT 60  
TATAAATAAA AATATTAANT AGAAGGTAAA ACAAATCAGA CATACACACA TTAGATAGAT 120  
AAATTAGAG GAAAAAAAAA AAACCATGCA AGNTTCAGCT NCNCGNGTNC TNTGGTGNCA 180  
50 CCTAANN 187

SEQ ID NO:4650



SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05514

SEQUENCE DESCRIPTION:

GATCGAGGGG GTATGCGTGG GGGAGTTGTG AGTGAGCTCA GCTCCTTTCA GGCCTGGCCT 60  
CTCCCAGAAC AGAGTGAAGC CCCTGCCCTG GACCCCTGCT CCCTTCTACC CTTGAGGGCC 120  
ACCAATGGAA GAGCCCGCCC TTCATTCTGC AGCTCCTGCG GCCAGGCTGA GCTCTGCCCC 180  
CAACTTTGTT TTCTCTCATG TTCTCAATAC ACTCTGCCTC AAATCAAA 228

SEQ ID NO:4651

SEQUENCE LENGTH:300

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05515

SEQUENCE DESCRIPTION:

GATCTGTAGT TAAGGGAACC AAGGGGTCAT TGGGGCAAAA GCATTGTTTC TCAAAGCTCC 60  
TTGATTAAAG GAAAGAACAG AAATTTGCAC AGAAGATAGT GTCAAGGAGT GAGAAAGTTT 120  
GTTTGAGGGC AGTAGCTCAG TGTGGAAGAA AATCCTGAAG TTTCTGTTGA AGCCATACAA 180  
TGTTCTATGG GGTTACTCTC TAAGACATTC TCTGAGGTGT GTGAGGAAGT CACTACTCCT 240  
AGCCTTTGTT AAGATGTAAT TTAAATATT CAGTTATGGT ACTATGTTTG CAACTCTCTN 300

SEQ ID NO:4652

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05516

SEQUENCE DESCRIPTION:

GATCAGTTTA TATTGCTCTT AAATGATAAT CCTCAGCTTC CAAGTTTTTG TGAAGTCACT 60  
TTGGTTTATG TGTTTGCTAC ACTCACTGAG AAATTAAACA CCTTGCTTGA TTTATTGTAA 120  
AAAGGAAAAA ACAACAGAGC CATACTTAAG CAAA 154

SEQ ID NO:4653

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05518

SEQUENCE DESCRIPTION:

GATCTTTATG CTGTTATNAC AGGAGAAGTG ACATACTTTA TATATGTTTA TATTAGCAAG 60  
GTCTGTTTTT ANTACNATAT ACTTTATATT TCTATACATN TATATTNCTA ATAATACAGN 120  
TATCACTGAT ATATGTAGAC ACTTTTAGAA TTTATTAAAT CCTTGACCTT GNGCATTATA 180  
GCATTCCATT AGCAAGAGTT GTACCCCCNC CCCAGTCTTC GNCTNCCTCG GGNTTAAGCT 240  
GTTTTATGNN 250

SEQ ID NO:4654

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05519

SEQUENCE DESCRIPTION:

GATCCCCACC CCAATTCAAT CCCGGAAGGG ACTTACTTAG GAAACCTTC TTTACTAGAT 60  
 ATCCTGGCCC CCTGGGCTTG TNAACACCTC CTAGCCACAT CACTACAGTA CAGTGAGTGA 120  
 CCCCAGCCTC CTGCCTACCC CAAGATGCCC CTCCCCACCC TGACCGTGCT AACTGTGTGT 180  
 ACATATATAT TCTACATATA TGTATATTAA AACTGCACTG CCATGTCTGC CCTTTTAA 240

SEQ ID NO:4655

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05520

SEQUENCE DESCRIPTION:

GATCCAAATA GTCAGAAAGA AAGGAAGGAA GTGCTGGTAA GAAGGAAGGG AGGAGCGTAT 60  
 CCTAAAGAAC TACTCCCAAC TATACAACCTG TTGTTTTCCT CCCAATTTTC CTAGGGATTTC 120  
 CTCATAATTA TCTCCTTCT CTTCATAAAT TCTACTTACT GACCTGAAAT AAAATTTCTC 180  
 ATTTGGTTGT CCTCAAGGTG CAGAATATGG ACTTAAGGCT CCTCCAGACA ATTCAAATGT 240  
 ATTGTAGACA GTTAAGNTAG AGTAAACTC ACCGTTTTGT CCCACTGAAA 290

SEQ ID NO:4656

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05521

SEQUENCE DESCRIPTION:

GATCGACAGG CATCCACAGT TGAGTATCTC CCAGGCATGC TACATTCAAA TTGCCCTAAA 60  
 GGTCTCCTAC CCAAATTCTC CACGCTGGTC TTNGGTAAA CTAGGCCCTG CTAAGTCTTA 120  
 TAACTTTCAT ACAGGTTTGG ACCAACAGGG CTTTATTCCA GGANCAAATT ATCTTATGCC 180  
 TTGGGACATT GNCATCAGGA CTAGAGCTGN AGATGAAGGA GACTTAGACA CAACTCTTG 240  
 GCCTGCTCCA AATAAAGCTA TTCCTNGNAA GAGNAGTGC GTTGTAATGG NTAAGAGNGN 300  
 AGANCGGCGA GATGACATTG NTCGAGCTTN TNNTGGNCTT TGAATATNGA AGTCN 355

SEQ ID NO:4657

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05522

SEQUENCE DESCRIPTION:

GATCCGCAA CGATTAATTC TGTCAGACAA AGGCAGCTG GATTGGAAGA AGATGTATTT 60  
 CAACTTGTC CGATGTTACC CAAGGAAAGA GCAGTATGGA GATACCTTC AGCTCTGCAA 120  
 AACTGTGAC ATCCTTTCCT GGAAGGGCAC TGACCATCCG TGCACTGCCA ATAACCCAGA 180  
 GAGCTGCTCC GTTCACTTT CACCCNNGN CTTTATCAAC TTGTTCAAGT TCTGGNATCC 240

EP 0 679 716 A1

CAGCACATGA CAACACTTCA GAAGGGTCCC CCGTCTGACT NGAGAGCTNG GGAATATGGC 300  
 ATTTGGACAC TTCATTGTGTT AAATTAGTGT ACATTTTAA ACATTGGGTT CGGNNAACTT 360  
 TCAGNGGTNA GGTCCGNGNN TN 382

SEQ ID NO:4658

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05523

SEQUENCE DESCRIPTION:

GATCATTAAA AACTTAAAAT ATATTTTATT AGAAAACATT TATCTATGAA TGAATATTTTC 60  
 CTTGATGCTG GTCTCTGCAC ACATATGCTT GGTACTTGC ATGCATTCAT TGGTTGTTCA 120  
 ATAAGTGAGA TGATTACAGA TAACTTAATA CTGTATTTNC CTTATATGGA AAACCGTTAT 180  
 AGACCCAATA ACAACTAANC CTTTCAAAG AAANTATTTN CTATTATGAN TGTGATTTT 240  
 CATACCNAAG AAGATGGAGA GTCTAAAATT TGGGNTATGG ATNCTNGATG GNNTTTTAN 300  
 TNGGNAAGCC TTCTNCAAG TTTNAN 326

SEQ ID NO:4659

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05524

SEQUENCE DESCRIPTION:

GATCAGCTTT GCAGTAGATT ATGCTGCATC CTCGTGGCAA AATTCTGTAT TCTTAGTGAT 60  
 TGTTACAAAC CCCTTTATTG CTGTCTGAGA AAGTGAAAGA TTGTGTATTT CTATTAAC 120  
 ATTTACAATC AAA 133

SEQ ID NO:4660

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05525

SEQUENCE DESCRIPTION:

GATCAACATC CGGAGATGGA TTTNCCAAG GCTAAATTCA ACTAGCCCCT GTTTTTTCCT 60  
 CCCTGAACTC TTGGGGCTGA GCTGCAACCA CCCAACTTC TTCCCACTC TTCTCTGGGA 120  
 CTTGTGGGCC TCAGGGCTTG GGGCAGGCAT GGGACTGGCC CAGGCACACA GGTCCTGGGG 180  
 CATCAGGAGA AAGGCTGGGT CTTGGGACCT TGTCTCCCC AGTTGGCCTA CTGTTACACA 240  
 TTAACGAT TTGCCAGNT CAAA 264

SEQ ID NO:4661

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05526

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCACCTNT TCCCTTCAAT CCTTGTGGCT TCTGGGAATC TTCAGAGCCT GGGTCTGAAA 60  
GGTGTTCCT ACATGTCTCA GGGCTGGATG CAAACCTGGC TGGGGACCTG AGCATCAACT 120  
CCCATTTAGA ATCAGACATC TCCCTTCCCT GCAAATTGTC TACAACTACC AAATTGCTCC 180  
5 AGGTTTGAGA TGGTATTGCT AAATTTAAAA TTAAACAAGN GACCCANCAN CAGCTTTTTA 240  
AAGTGTCTNC TATTCATNN GTATTTTNTT NAACCTGGC CCCANTTGNT AGAAAAGTCT 300  
TTTGCNGAAA TGNATTNN 319

SEQ ID NO:4662  
SEQUENCE LENGTH:239  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05528

SEQUENCE DESCRIPTION:  
15 GATCAAAACA GTGTGGTGCT GGCAAAACAA GAGACATAAN TCAGNAGAAG AAAGAGTCCA 60  
GAATTAGACC CACACACATA TGGACAATTG ATTTTCAAT AAGGGCACCA AAGCCATTCA 120  
ATGTATAATA GAGAAGACAG TTTTTTCAA CAAACAGTAT TGGANCAGTT GNNCNNNTAC 180  
20 AAAAAGTAA CTTCANCCCA TACCTCACAC TATATCTAAA ANTTAGCATC AAATGGNTN 239

SEQ ID NO:4663  
SEQUENCE LENGTH:68  
SEQUENCE TYPE:nucleic acid  
25 TOPOLOGY:linear  
CLONE:HUMGS05529  
SEQUENCE DESCRIPTION:  
GATCTATTTA GTCCTACAAA TCAGGAGTGG TGTAGAGACA TCCAAATTTA AAGAAAAAAA 60  
30 AACACAAA 68

SEQ ID NO:4664  
SEQUENCE LENGTH:122  
SEQUENCE TYPE:nucleic acid  
35 TOPOLOGY:linear  
CLONE:HUMGS05531  
SEQUENCE DESCRIPTION:  
GATCGAGTTT TAAATTGATA GGAGGGAACA TGTCCTAATT CTNCTGTCCT GAGAAGCATG 60  
40 TAATGTTAAT GTTATATCAT ATGTATATAT ATATNTNCNC TATGTATATA CATATATNTN 120  
AN 122

SEQ ID NO:4665  
SEQUENCE LENGTH:196  
45 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05532  
SEQUENCE DESCRIPTION:  
50 GATCAGGGAC GGGGCTGAGC-TGGAGAGTGT GCAGGATTGA TTAATGATGT CTGCCACGGT 60  
CAGGCCAACT GCTGTGTTTC TGGGGCCAC AAGCTAAAAA TGGTTGGAAA AAAATCAAAA 120

# EP 0 679 716 A1

CATTAATATT TGTGACATAT GAGAATGCTA TGAAAGTCAA CTTTGCTATC CATAAATAAA 180  
GTTTTATTGA CATAAA 196

5 SEQ ID NO:4666  
SEQUENCE LENGTH:316  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS05533  
SEQUENCE DESCRIPTION:  
GATCAGATTG CTCAACTCCA TTATAATTTG TTTCCAAACT AATCTGTTCA GGCAAGATAA 60  
AGATATAAAT GTGGATTGTT GCTGAGGTTA AGTCTGGTCA GATTTTNCCA NTTATGCTTG 120  
AAAAGTAACC ATATTTCAAT CAAATATATA ATATGTATAT NTCATAATAA TATANGCAAT 180  
15 ATTAGTCTCA TTATTAATTC AAAANTCTCA TCTATATTC ANCACTGTAG AACATTATTA 240  
NNTGANTAAN TGACCTATAA NTATTTGGTG CCTGANGAAG TCACTTTGCT ATTANTNATA 300  
CGGTGTAGNG TGTGGN 316

20 SEQ ID NO:4667  
SEQUENCE LENGTH:168  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS05534  
SEQUENCE DESCRIPTION:  
GATCTCAGGG AAGCCTGGGA GTCCCTTCTC ACCCCTCAAC CTCCGGAGTC CAGGAGAACC 60  
CGTACCCCCA CAGAGCCTTA AGCAACTACT TCTGTGAAGT ATTTTTTGAC TGTTTCATGG 120  
AAAACAAGCC TTGGAAATAA ATCTCTATTA AACCGCTTTG TAACCAAA 168

30 SEQ ID NO:4668  
SEQUENCE LENGTH:311  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS05535  
SEQUENCE DESCRIPTION:  
GATCATCCCA TCCTTGACCA CAGGGACAAG AGGGGCCCCC TCGCCCCAGC CCCACCCCAC 60  
ATGGAGCTCA GGGGGAAGCA GGGAGGGGTT CCCAAAAGAG CCCTGCGGAG GCTAGGAGTG 120  
40 GTTCTTGATG CTCACCTGAA GCCCCTAGAC GCTGCTAGGA GGGGGGGCCC TCCTGGGCCC 180  
NAAATACCN TCCGCTTGCC GCTGCTAGCG NACCCCTGCA GTCCAGCGTG CATCCACCCC 240  
ACGNACGTCC CGTGCTGTGT TCCTGGGCCN TGTCCATGGC CTNAATAAAC TCTCTGCTTG 300  
GGTGTGACAA A 311

45 SEQ ID NO:4669  
SEQUENCE LENGTH:167  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
50 CLONE:HUMGS05536  
SEQUENCE DESCRIPTION:

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GATCGCAAGC TGTGTGATGCA CAGGCGTCTT GTTGGCAAGC CCAGCTTCAG TTTATGTTAG 60  
ACAATCAGTA CACATGCTGG TGTGTTTTCC AATGGCCAGT NATAAGAAAT TAAATAAGTA 120  
TTTGTGAGAT TTGCTATTTT TTAATAAAGT AATTNTTTTA AATTAAA 167

SEQ ID NO:4670

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05538

SEQUENCE DESCRIPTION:

GATCTCATAC TTGTATAGAG TAATAACAAC AGTTGTACTT CCACCAAAGG CATGTGGCAT 60  
ATTTACCAAT GTCATGTATT CTGAACAAAG GCAAAAAATA CAAATTCCTA CCATTAAA 118

SEQ ID NO:4671

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05539

SEQUENCE DESCRIPTION:

GATCCTTCAA ATAGGCCCTG AGATGTGAGG TCTGCTGCTT CACTGGGGCC CGATGACTTT 60  
GGCTGGGGGA GGGGGCCTAG GGCTCTNCTC ATTGAAAGCT CTGCTTTATA CAGACCCAAG 120  
CATACACACC AGGCCGTCAC TTTGGGTTCT GGCATAAGTT CAGAACAATT CAAGTCCATG 180  
TGTCCCATGG CTGGTCAGAG CCCTGGGTCA AAACCACTCA GCCCAGGGGA GGGGATGAGG 240  
CATTGTCACC CTAGACCCCT CTTCTCTCTT CCCNCACCAT AGTGTGCAAT AAAGTGTCTG 300  
TTCTTACCAA A 311

SEQ ID NO:4672

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05540

SEQUENCE DESCRIPTION:

GATCTTGTC A GAGCTGCACC TCTCTGTGAA CTGGCCATTC CTTTCGGTGC TGCTGTCCTT 60  
TTTGGGGGGG TTCCTGATTT CTGTATACAT GTAGCTTTGC CAGATATGTA CTTAGTAATA 120  
TAAACTGTAT TAATAAAATC CATTTACTGT GTAATACACG AGTTTAAAAA TTAAGAGCGA 180  
TTAGCTGTTT ACTTTGGTAA CAGGTAGTTA AGTGTACAC AAGGTGTTGT TGCAATGGCA 240  
TGACGGTGAC CTGTTGGNGG NACTAAGCCT TACAGCAAGG CATGTGCCGN ACGTGCTCCG 300  
TGGTACTTAG AGCCCTGGGG GCCCGNTCG GACTCCGN 338

SEQ ID NO:4673

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05541

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTGTTTA CAAGGTTTGT AGATACTTTT TTTGTTCTG TTCATAGATG GGAAGCTTCC 60  
TTATAACTGA TGCAGAGAAA AATTAGTCCT TCAAATACTG CTGTATTTTC AGGAAAN 117

5 SEQ ID NO:4674  
SEQUENCE LENGTH:279  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS05544

SEQUENCE DESCRIPTION:  
GATCAGTGTT GCTAGTAGCT TGGCAGCTCT TCATAAAAGC ATATTGGGTT GGNAAGGTGT 60  
NTGCNTATTT TTCAAATNAT TTAATAGATG TNTGGTACCA TTAAAAAGTG GTTGTGTCTG 120  
AATTTACTGT GGGGATAACA TACACTGTAA TGGGGAAAAA TTACCTAAAA CCAATTTCAA 180  
15 AANGGCTTTC TNTGTATTTT AGTTTAAAAA CCCAGTGCAT GATNCGCCCT CTGGAGATGC 240  
AATAAACNCC TTNGTGCCAA AGGNGATTGC CNGNGGAGN 279

20 SEQ ID NO:4675  
SEQUENCE LENGTH:137  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05545

SEQUENCE DESCRIPTION:  
25 GATCTGTAAT AAAATAGTAT ACTGGACTGT GCATCAAAGG GATGTAAAAT TACAGTATTC 60  
CAAAGGTTGA AGTTCTGCTG TTTTGTATA ATGCCTGATA CACATCTTGA ATAAAGTCTT 120  
AACATTTTNC TTATAAA 137

30 SEQ ID NO:4676  
SEQUENCE LENGTH:259  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05547

SEQUENCE DESCRIPTION:  
GATCATAAAA ATAAAAATGT GAATGTCAAC AATAAAAAGC AAGACTATGA AAGGCTCAGA 60  
TTTCTTGAG TTTAAAAATGG TGTCTGAGGT TGTNCTATTT TGGCCAAGTC TGTAGAAAGC 120  
TGTCATTTGA TTTTNATTAT GTAGTTCATC CAGCCCTTGG GCATTGTTAT ACACCAGTAA 180  
40 AGAAGGCTGT ACTCAAGAGG AGGAGCTGAC ACATTTCACT TGGCTGCGTC TTAATAAACA 240  
TGANTGCAAG CATTGGAAA 259

45 SEQ ID NO:4677  
SEQUENCE LENGTH:261  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05548

SEQUENCE DESCRIPTION:  
50 GATCATCATG ATGAGTTTTG CCTTATGCCT TGAATCTTNA GGTTAATAGT CATAAAATCC 60  
CTGCTTTCTA AATTCGCATT TTTCTGGTG TACCNTTAAT GTGAACNTT TGGCATTCTT 120

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EP 0 679 716 A1

CTGCAATNTT CTGATTGGAG ATTGCATTTT GACCTAGTCT GTAAGTTTTT CTGTCAGAAG 180  
AGGACTTTCA TCAACTTTCA NGGNAAGATT GTTTATTGGC AACTGTAAA GTTAAGTNAN 240  
GCANTTTNAA AGTNGTCTAA A 261

SEQ ID NO:4678

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05551

SEQUENCE DESCRIPTION:

GATCCGATTT TACCTTGGAC CCCTGCGTCT TGCCCTGGG AACCCANATG GGGACTGCTC 60  
TGAACCTTTG GATGACATNT GTGGCCCCGG AGATGTTCTC AACCCAGGGG TGCCCTTCGT 120  
AAATGTTNCT CCATCCTCAC TGTACCAGGA GTGTGTGAAT AAACACAGAC CCCCTCTGTG 180  
AAA 183

SEQ ID NO:4679

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05552

SEQUENCE DESCRIPTION:

GATCCAGTG ACGTGGAAGT CATCAGAAACC CCACGGTACT TTGAGTACCT CTCTGCACCA 60  
AGATAGCTGA CTGNTTTTCT GCTCAGTCAC AATTTTACTT GNAAGCAAGN ATTGTCCTAG 120  
NTCCTNTTCC ATTATTCCAA AACGTTTAAC GTTCAAAGCA GGGTCTCATT AAAANCCCAA 180  
CTACTGGTTG ATATAATTGA GATATTACAA TTTCAGAATA AACATTTGAT TAAA 234

SEQ ID NO:4680

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05553

SEQUENCE DESCRIPTION:

GATCAGAATC TTCAAGAATC AGTTAGGTTT CTCCTGCAA GAAATAAAAT GTCAGGCAGT 60  
GAATGAATTA TATTTTCAGA AGTAAAGCAA AGAAGCTATA ACATGTTATG TACAGTACAC 120  
TCTGAAAAGA AATCTGAAAC AAGTTATTGT AATGATAAAA ATAATGCACA GGCATGGNTA 180  
CTTAATATTT NCTANCAGGA NAAGTCATCC CTATTTCTT GTNTTACTGC ACTTANTATT 240  
ATTNGGTTGA ATTTGTNCAG TATAAGCTCG TNCTGTGCA AAATTAANTA NATATTNCTC 300  
TTACCTNATA NCANAN 316

SEQ ID NO:4681

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05555

SEQUENCE DESCRIPTION:



EP 0 679 716 A1

GATCATCCTG GAATCCGACT CTGTCTCAGC TCAAGGGGGT TCNGAGATTT CCTAAGCTAG 60  
 CCCTCTCATT TTACAGCTGC AAAAACGGAG GCCTGTTAAT TCAGTCATTT TATGAAATCC 120  
 TTTGAAATTT TTATTGAGCT CTAATTGTGT GTGAAGTATT ATGGAATGCT TCTGTACTGG 180  
 AATGCATAGG TTGAACAAGA CAGAAAGGCC CAGATGGCAG AAGTTCAAGA NCTTTCACCA 240  
 ACCCATATAG NGAACCTAGT AATATTAATG ACTAATGTTA ATGGANTCCA TGCTTTGTTA 300  
 CGAN 304

SEQ ID NO:4682  
 SEQUENCE LENGTH:287  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05556

SEQUENCE DESCRIPTION:  
 GATCAAATCG GAGTACTTAG CATATCTATC ATCTCGTGCA TTTATCATTT CTTTGTGGCG 60  
 AGAACATTTA AAAATCCTAT TTTCTAGCTA TTTTGTAATA TACACTACCT TACTGTGGCG 120  
 AACCATAGTC ACCCTACTGT GCAATAGAAC ACCTGAACTT ATTCCNCCTA TCTAGTTGTA 180  
 ACTTNGTACC CATTGNCCCC CCNTCCCTNC CTTCCACTCT CCCCTCCCCA GNCTCTGGTA 240  
 ACCACTGTTC TGTTCCTAT GAGATAAAAC TTTTTTGN CTTCCAAA 287

SEQ ID NO:4683  
 SEQUENCE LENGTH:298  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05558

SEQUENCE DESCRIPTION:  
 GATCTTTTGA AGATTGCTGG AATACTGGTG TCTGTTAGAA TGCTTCAGAC TACAGATGTA 60  
 ATTAAAGGCT TTTCTTAATA TGTTTTAACC AAAGATGTGG AGCAATCCAA GCCACATATC 120  
 TTCTACATCA AATTTTCCA TTTTGGTTAT TTTCATAATC NGGTATTGCA TTTTGCCTTC 180  
 CCTGTTTATA CCTCAAATTG ATTCATACCT CAGTTTAATT CAGAGAGGTC AGTTAAGTGA 240  
 CGGATTCTGT TGTGGTTTGA ATGCAGTACC AGGNTTCTCT TCGAGCAAAG TAGACCTN 298

SEQ ID NO:4684  
 SEQUENCE LENGTH:297  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05559

SEQUENCE DESCRIPTION:  
 GATCCATCTT CCTTACACTC CTTCCAAAAT AATGTTAATA CTCTGTCTAT CAAATGCTTA 60  
 CAGTGTTCCT TAGCACATAT AGGGTAAAGT CAAAGCTCAT TAGCAGGGCA TAGGAGGCCC 120  
 TTCATGACCA GCCTNACCNG CACCTCTAGC TACATCTCCT ACTGNGNCA CCTCCACATT 180  
 TACCCTTCGG CATGCCAACC TGCTTATGGT TACGGGGCAC AGCTTGCTGT TTTGGNTNNT 240  
 GTGCCTCCCN TTGTTTGTCT TCCTGNTGNT GAANTNATGN TGGGACCATT CTTGTGN 297

SEQ ID NO:4685  
 SEQUENCE LENGTH:120

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05560

SEQUENCE DESCRIPTION:

GATCAGATTC ACTGTTTCAT CATATTTATT GTAATATATT TTTTGTTTG TAAATATGTT 60  
ACAACAAAAT GTGATTGGTC TAAAATATTT GTAATGTATA TTAAAAGGTT CAAAAATAAA 120

SEQ ID NO:4686

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05561

SEQUENCE DESCRIPTION:

GATCAGAGGA GTTCAGGGAG ACATACATAA AAATGTTAAT CACGGTTTTTC AAA 53

SEQ ID NO:4687

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05562

SEQUENCE DESCRIPTION:

GATCGCCAAG TGCAGGCACG GCATCGCATC CCCAGGTGTC ATCCTGTGAC CCAGGAGGGG 60  
AAGATGACAC ACCCAATTTA GGTAATGCTG CACTTCTNGT TATAATTGGT TATTGGAAAA 120  
TGTGCCTTTA TTATCAGAAC AGTGGTGTGC GCATTTCTGA TTATGGAGCT AACTTTTGGA 180  
TATCTGACTT AGATACTAAA AACATTGGG TGTTCAGTT TTGCACTTGT AGATACAACT 240  
TAAAAGCATG AAACGTGGTGA TTTAATTAGA TGTTTCTAT AAAATGCACC TTGTTACATT 300  
TCTGTGAAAG GGGTCTTACC AGCGTGAAT AACNTGGCTC AAGGGTTTGA GGGGANCANC 360  
NGN 363

SEQ ID NO:4688

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05563

SEQUENCE DESCRIPTION:

GATCCACGTG TACTGGCACC TCAGAAGACC AAATCATGGN CTGTACAAGT CTCTATACAA 60  
TGTCTTTATC CCTGTGGGCA GNANGCAATG ATGATAATGN CAANCAGGN 109

SEQ ID NO:4689

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05564

SEQUENCE DESCRIPTION:

GATCAGAAAAG CATTCACTCC AGTCAGAATT CAAGGTGGGA AAAGTAGGTG TATTTCTGAN 60

EP 0 679 716 A1

CCATTTGGGA AGGAAAATCA TTTTCTGAA CANCACTACC TGCATTTCTG TTTCTGCAGA 120  
 CAATCAAAAA ACAAAACCANT AAAANTAAGT AAGTGAANGA AAGGCCANTT AGCATTATTC 180  
 ATTTGCCTTA GGTTTACAGG GTCACAGATT CATTAGCTTA ATTACATCCT CATTTTGGNT 240  
 GCCAAAGAAT GGAGCAAGAG CANTCAGTAT TGCTANCTGG CTCTTGCTTC TTCTTCCTGG 300  
 GTTTGTTTTG GTTTTNCAGA GAAACAGGGA AGNGAGGGCA TTNGCNNAGT ATAATTGGTN 360  
 TATAGGAGN 369

SEQ ID NO:4690  
 SEQUENCE LENGTH:70  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05565

SEQUENCE DESCRIPTION:  
 GATCATAAAT GTACTTGCTG AATTCAATCA TTTTAAACAA GCCAATAAAG TTTGATAATT 60  
 CATCTCCAAA 70

SEQ ID NO:4691  
 SEQUENCE LENGTH:293  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05566

SEQUENCE DESCRIPTION:  
 GATCCTCAAG GCCTTGCTCT NCCCCGTGGA GACGCTTGCT CGGATGAGCT CAGGAAACAG 60  
 TACCGGCTGC GTGGCAGGTC TGGGTGTTGT GTGCGAGGAC GTGGCCTTTG CACACCGCTG 120  
 TGTTCTCAGA GGTCTTAGG AGATATTTTT TTTTGTCTTA GGGGGACTGT NTAAAGTTCA 180  
 GACAAATCAN GCTGGGTGTG GAGAGAGTCT GAAATACGTC AGTGAAGTAA GTAGCAGTGA 240  
 GCGATTGTGA ATTTGNANTN TAAATGGAAA ACCGGGTTTT TACCGNGTT TTN 293

SEQ ID NO:4692  
 SEQUENCE LENGTH:251  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05567

SEQUENCE DESCRIPTION:  
 GATCAAATC TTCATTGAAG TACTCATNAG GCGTGATGGC TGTGGGGTTG TTTGCAGTAG 60  
 CACATTNCGT GGTGAGGTCC TGCTGAGCCA GNACTCAGGA GAGTCAGAAA TGCCAAANN 120  
 TGTTACAAG TGAAGGCCTG TGGCACTCAG TGTCTGAGGT GGACGTGTTA ACCAGCTAAA 180  
 GACCGGGAAG TTCTATTCAC TAACTTTTT GCATGGAACA AGAAAATCTA TGAGGATATC 240  
 ACCAAACTAA A 251

SEQ ID NO:4693  
 SEQUENCE LENGTH:97  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05568

## SEQUENCE DESCRIPTION:

GATCCATCTT GCTTTTGCCT TATATAAAGA CTACAGTTAT GGAAGTNTGG AAAACTGTGG 60  
CTTCTCAATA AATATTCAGA TGCCTAAGA NTATAAA 97

SEQ ID NO:4694

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05570

## SEQUENCE DESCRIPTION:

GATCTCACAA AGTACAAAAC GAATGCCTTT CTTTCTTGT TTATAATGGT CACTCACTGT 60  
GTTTGGTTAC TGTCAAGAAA TCAATAAATG TGTTTAACAA GTTAAA 106

SEQ ID NO:4695

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05571

## SEQUENCE DESCRIPTION:

GATCAGTNGA TATTAAGATG AGATTACAAA TTTTNTTAAG TTCAGCCATT ATTACTTTTG 60  
GTATCCCAGA ACATGACAAA TTATGAATAA AACAAGTATA CATAAA 106

SEQ ID NO:4696

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05572

## SEQUENCE DESCRIPTION:

GATCCATAAA ATTTTATTAA TCAAGATATC ATATTAAAGT ATTATTATAT TAATTTATGA 60  
CACCAAATTT TTAAACCAAT TTTATGTTTT TCCTTATGTA TCATTATAAA CCCTATTGCA 120  
TTTTATAAGT AATANANTAT TTTNAGAAA 149

SEQ ID NO:4697

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05573

## SEQUENCE DESCRIPTION:

GATCGCGACG GCTGGTTTGC ATCGCCAGCT TCTATATATT ACGGCCTTTT TTTTGCTGG 60  
ATATTATCTT GTAAAACGTG AAGACTACCT GTATGCTGTG AGGGACCGTG AAATGTTTGG 120  
ATATATGAAA TTACATCCAG AGGATTTTCC TGANGAAGAT AAGAAAACAT ATGGTGAAAT 180  
TTTTGAAAAA TNCCATCCAA TACGTTGAAG TCTTCAAAAT GCTTGCTCCA GTTCACTGA 240  
TACCTGCTGT TTCTGAATTT GNTGGGGCAT GTTCTTATG GCANTTGGAG GCTNATTGNT 300  
AATNTGTATG TTGGCACCTT GTNATTAAAA TACGGGGCCA TGNNANAAAA AAAAAA 356

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SEQ ID NO:4698

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05574

SEQUENCE DESCRIPTION:

GATCCACCTG CTTTGGCCTC CCAAATGTTG TGTCTTTTAA AAGTATCTAC AGTAACCTTG 60  
TATCAACTTA GTTGTGTCAGT CTATTAATAC TAAATTTAGC TCCTTCAAAG CAGTTGGAAC 120  
TATGTGCTAC ATAAATTTCA GTTTCACCCA AGGGAAGAAG TGAAATTAGT GAATAGACAG 180  
TTACAGCAAA 190

SEQ ID NO:4699

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05575

SEQUENCE DESCRIPTION:

GATCCGNTCC CAGACGGCCT TGGACTGCTT GCATTTCCCC GGAGAAAAAG GGGTTAATAA 60  
ATGGGCCATC CTTTCTGAA A 81

SEQ ID NO:4700

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05576

SEQUENCE DESCRIPTION:

GATCACTGTG GGGTCAAGAA TGTCTTACAT GTTTTATTCA TCATTCTTGA NGGAAGAAAT 60  
AATTCAAACC TTGAATTAA AAAGTCAAA 89

SEQ ID NO:4701

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05577

SEQUENCE DESCRIPTION:

GATCTTGGCA AGAAACCCTA ATCTCCCTCC AGAAACAGTG GACTCTCTAA AAAATATCCT 60  
GACTTCTAAT AACATTGATG TNANGAAAAT GACGGTCACA GACCAGGTGA ACTGCCCCAA 120  
GCTCTCGTAA CCAGGTTCTA CAGGGAGGCT GCNNNNACTC CATGTTACTT CTGCTTCGCT 180  
TTCCCTACC CCACCCNCCG GCATAANGNC ANACCAATCA ACCACGACAA AGGNAGTTGA 240  
CCTAAACATG TAACCATGCC CTACCTGTT ACCTTGNTAG CTGCAAAGTA AACTTGTTNGC 300  
TGNCCTGCAA A 311

SEQ ID NO:4702

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS05578

SEQUENCE DESCRIPTION:

5 GATCTCTCTT GCACGGGCCT TGCCAAGGCC CAGGAGGGAC TTGGGCAGTA TGTTCATGTG 60  
GTCATATGTT TTTGTAAAAA ATTGTGAAAG TAAA 94

SEQ ID NO:4703

SEQUENCE LENGTH:248

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05579

SEQUENCE DESCRIPTION:

15 GATCCGAATC CGACTGTGGG GGGCGGGCTG GGAGGTGGGA GCCGCGTCTC AGGCCCCGGCC 60  
GTTATCAAGG CCCCTCCGCC CCCGAACCCT GGGGAGCTGG ACCAGGAGGT GGAGGCTCAG 120  
GGGACCCCAT GGGGACAGGC AGAGCTGGTC TCCTCCAGC AGACGGAGCC AGGACGGGCA 180  
CAAGAGTCTT GGAGGTTTGC GTGTTTCTGC TAGAATTAAG AAGTTAAAT TAAAAATGAA 240  
20 AATGNAAA 248

SEQ ID NO:4704

SEQUENCE LENGTH:66

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05580

SEQUENCE DESCRIPTION:

30 GATCAGCAAA GTGAGACAAA AGAAGATACT TCCCCAAAGA AGAAAAAGAA AAAATTGAGG 60  
CAGAAA 66

SEQ ID NO:4705

SEQUENCE LENGTH:65

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05581

SEQUENCE DESCRIPTION:

40 GATCGGGTCT CGGAAGGGAA GTAGCCATCA CACCATTAA AAGCCTGTGG ACCTTTAAAG 60  
GNAAA 65

SEQ ID NO:4706

SEQUENCE LENGTH:308

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05582

SEQUENCE DESCRIPTION:

50 GATCTTCTTA GGACATCTTT TTTAAAAAGC TGTTAGTAT CATTTTGTGT ATATTGTTGA 60  
AATGCTTTT CATCAATAGC AGTCANCATT TTATCCTTTC TTTTATATT CATAATGTTA 120  
TTTAAGTGTC ATTGATGTAC TGTATTGACT TGGGGTTTGC TTATTGTTA CTTAACATGT 180

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GTACATGCAT GAAAGCATTT TTNGTTGTTT CCTGATAGTT ACATTTCAAC CTTGGGATTT 240  
 TNCCAAATNA CTTAAGANGT TTAATGTCAG TNAAAGATTT TNTTACCCTC NTTTTGGGAA 300  
 CATCAATN 308

SEQ ID NO:4707  
 SEQUENCE LENGTH:323  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05583

SEQUENCE DESCRIPTION:  
 GATCCGGAAG ACCACGGCCA GCCAGGTGTA CGAGACATTG CTCACCTACA GTGACGTCGT 60  
 GGGCGCGGAT GTGCTGGACG AGGTGGTGAC TGTGCTCAGT GACACTGCGT GGGACGCAGA 120  
 GCTTGACGTG GTGAGAGAGC AGCGCAACCG TCTGTGTGAC CTTCTGGGCG TACCCAGGCC 180  
 CCAGCTGGTG CCCCAGCCTG GTGCNTGCTG AAGCCAGTCC TTGGAGCCCA TANCTACCCC 240  
 CTGCCTGGTG AGGATGTCTT GTTTCCTGAG GGTAGGCCGG TTGTGGAAAA GCCTCANNAC 300  
 NAGTGNTGCC TNNAGGCTGN GAN 323

SEQ ID NO:4708  
 SEQUENCE LENGTH:302  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05585

SEQUENCE DESCRIPTION:  
 GATCTTCCTT TGGAACCAGG CACATTTGGC CCCTTCTCAG TGACTGCACT GTGGAACCTCT 60  
 TCTTAAGAAA ATATTGAAAA CAGCTTAATG CTTTCATATA GTGACCGACA TTTAGTTGAA 120  
 AACTACTGCT GCATAGCAAA TATTGTGACT CTTTCATGTT CCACAGGAGC TCTTGTGTGG 180  
 GTTTAAAGCT ATGAAGTGTA TTCACATTGT GAAGTTTAA TTATCTTTAT TGAAATTAAT 240  
 TGTGTAAGAAA TGGTATGTGC TCTATTAGGT ATTCAGTTTG TATGTGAATT CTATAAAGAA 300  
 TN 302

SEQ ID NO:4709  
 SEQUENCE LENGTH:302  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05586

SEQUENCE DESCRIPTION:  
 GATCCCTCTC AGCTACTGGG AGCTGCTTTG TGCCTTGGA GCCTCAAGCT GAAATGGATG 60  
 TCAGCCTCAA GTTTAACTCC AAGAGGGTTC ACCTTGTTTC TTTGAACAAA ATGTGCTGCC 120  
 TGTGCTTCC CTTTGCCAGG AGTGGTGTTC CCTTTCCAC AGGTCTGGAC CACAGTGTCT 180  
 CTAGCTCCCG CTCCTGGATA CTTGGTTACT GTGTGTTTCG GGAAAAAAGG ATNCACAACA 240  
 TGAATATNCA CTAAGCTGTA ACAGGGGCCT GCTGCANCTA TAGTATTTCC TGAAAAAGTA 300  
 TN 302

SEQ ID NO:4710  
 SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05587

SEQUENCE DESCRIPTION:

GATCTTGCCT CTTTCCTCCT TCATGAAAGC AGCACACATT GTGTAACTT ATGTCTCTTG 60  
TTAAATNAGC TTAATGTCTT TGTGTTTTGT CCAAACTGT ATTGNNNNAA TATTGTTTAA 120  
TGCAAATNAA GGAATGCAAT AAAGAGTAA TATACTTGAA A 161

SEQ ID NO:4711

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05588

SEQUENCE DESCRIPTION:

GATCAGAGCG TGGGAGGAGG TGGGGGTGGA CGTCCATCCG GTGAACAGTG AAGGCGTTTG 60  
TGAGGTCTTT CTGGTCCCAG CATGAAATAA AGCCTTGCC TGGGGGCCGC TTCATTCAA 120

SEQ ID NO:4712

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05589

SEQUENCE DESCRIPTION:

GATCTGGCAG TACCCAGCCC TTGTGTGTGT GCGTTANTCA GCACCTGCCC AACTGCGAG 60  
CCCCCGTAGG ATGTGCCTTG TCCTTCCCTG TTTCAGCACT TAACACACTA CCTGGTACAG 120  
AGTATGTAGT GGGCATCTGT TGAATGAATG CTTTCCCAG TAGCAGTGTA TTCATACAAT 180  
ATTAATATAA TTGTCCCCTG GCTTACAGAT ANAAATGAAA GCATCAAGTG CCCAGTTGAG 240  
TGAGACCCAG GTGTTCTTCC TNCACCCCTT AGTGGTTCCC CTGGGGGCAG NTCTTN 297

SEQ ID NO:4713

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05590

SEQUENCE DESCRIPTION:

GATCTCTGCG CTAGGTCGTT TACCGCTATT TATTTTATG GGGAAAATAA AACTCTCAA 60  
AATGAAA 67

SEQ ID NO:4714

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05591

SEQUENCE DESCRIPTION:

GATCACTAGA TGATTCTAAC ATCGAAATAA ACCTCTTTT ATATGGCAA 50



SEQ ID NO:4715

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05593

SEQUENCE DESCRIPTION:

GATCTGGTGC GTGTGGCCCT GTGGGAGTCC ACTTTCCTCT CTCTCTCTCT CTCTGTNCCA 60  
AGTGTGTGTG CAATGTTCCG TTCATCTGAG GAGTCCAAAA TATCGAGTGA ATTCAAAATC 120  
ATTTTNTTTT TCCTCCTTNT CAATGTGATG GAATGAACAA AAAGGAAAAA ATTCAAAAAA 180  
CCCAGTTTGT TTTAAAAATA AATAAATANA GCAAATGTGC CANTTAGCGT AAA 233

SEQ ID NO:4716

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05595

SEQUENCE DESCRIPTION:

GATCTTGCCT TGAGGAAGAC CCAGGCCATG TTCCCAAAGG NCAGCGGGGG CCCTGGATTG 60  
TAATGCAGCC TCGGGACAGG GCTGAGGCCT GCGGGGGAAG ACCTATACCC CACGACTGGG 120  
CCTGGNTTCA CCTCACCCTA ATCCCCGGG AGGAGCTGAC TGATGCAAAA AGCTGAGGNN 180  
GCCTGCTGGG NNGTGGCTGT TTTNATGNCC CAGCCCCGNN AAGTTGGGGA GTGTTTGTGG 240  
GGGTNCAGAG CCCTNCCCCA GNCAGGAGAG AACCTTCCTN TN 282

SEQ ID NO:4717

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05598

SEQUENCE DESCRIPTION:

GATCTAGGAC TAATTCAAGG GTCTAGATTT ACCTCCAAAC TTTGTTTATC TACAAAAAAT 60  
AAAACCTCTAT CTTCTTTAAA 80

SEQ ID NO:4718

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05599

SEQUENCE DESCRIPTION:

GATCCTTCCC CTCTCAGACA CCCCTCTTTC AGCTTAGAAT TTGGGGAACC TATAGAGAAG 60  
TCACAGAATC CCATGAAAGG GAATGGGGCA GGAGCCAGGG GTGTTTTTNC CCAGTGCAGG 120  
GTTGTGTCTT TGTGTCTCTG TCTCTGTGAC TGAAATCCT GCCCTGCCCC ACTCCCAATA 180  
AAAGCTTTGG TGTATAGGCT CAAA 204

SEQ ID NO:4719

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SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05600

SEQUENCE DESCRIPTION:

GATCAGTTTG TTTCTTTCTG TGCTGGTAAC AATAAGCGTC GCACAGACAT GGTTCAGGT 60  
AANTAAATCT ATTCTATGAT AAA 83

SEQ ID NO:4720

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05601

SEQUENCE DESCRIPTION:

GATCTCTGGA TTGTGTTATG TCAGTGTTGG TAGGTTAGGA ACTAGATTTC CCAGAATCCA 60  
TTCCATTTGT NATTCATGA TACAATTGAC CAGTAACCTA TCTTACATGA GATTCGGAAG 120  
TAAGTTAAGA AGGCATTAGT CATGGTTTGG AAGCACCATA CAGGGAGACA GCTGTGTGAA 180  
TACAGGCTGT ATGGACACTT GCTTCCATCC CATTNNCCTG CTTCTTTGGG TTGCCAATCA 240  
AGTGTATCCT CAAAACGACT TGACTTTAAT TTTCTCGGAG GTGATAGTN 289

SEQ ID NO:4721

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05602

SEQUENCE DESCRIPTION:

GATCAAGTCT TACATGCCCA TTCAGCTTCT AGGCCCCCT CACCTCCCTG CCCTCATTCA 60  
CAAGTGGCCC TGAGACACGT GAACACCTCC CTNCTATGCA TCACAAACCT TCTCCACCGA 120  
GCTTTGGTGC TTTNGCCTCT GGNACACCTA ACTAGCATTG GCAGAGGAGA GTCTACACTC 180  
TNTNCTNAT TCAGGGTNGA TGCTTTAAGA AATNCTGNCT CTTGTGNANG CAGAN 235

SEQ ID NO:4722

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05603

SEQUENCE DESCRIPTION:

GATCGTCAGC ATCATCGGAG GCATCAGTTC CTTCTTCATC TTCATCTTCC CAGGTTTGTG 60  
CCTCATCTGT GCAATGGGTG TCGAGCCTAT AGGACCAAGA GTCAAGTGCT GCCTGGAGGT 120  
CTGGGGAGTG GTCTCTGTGC TGGTCGGCAC CTTNATCTTT GGGCAGAGCA CGGCGGCAGG 180  
GTCTGGGAGA TGTTCTGATG GGCAGCCAGT GCCGGGCAGG AAGGGGCCCT CCGGGGGCTG 240  
ACCCTACGTG GCTGCTGTAT GCAGNNGGGA GANCAN 276

SEQ ID NO:4723

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05604

SEQUENCE DESCRIPTION:

GATCAAGGTC ATAGAAAGTG AAGATTATGG CCAACAGTTA GAAATCGTAT GTCTGATTGA 60  
 CCCGGGCTGC TTCCGAGAAA TTGATGAGCT AATAAAAAAG GAAACTAAAG GCAAAGGTTTC 120  
 TTTGGAAGTA CTCAATCTGA AAGATGTAGA AGAAGGAGAT GAGAAATTTG AATGACACCC 180  
 ATCAATCTCT TCACCTCTAA AACACTAAAG TGTTTCCGTT TCCGACGGCA CTGTTTCATG 240  
 TCTGTGGTCT GCCAAATACT TGCTTAANCT ATTTGGAN 278

SEQ ID NO:4724

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05606

SEQUENCE DESCRIPTION:

GATCTGGAAT GCNACCGGAG CACTTGCTCT GAGGAATCCC AGGGTGACTC TGTCGGGGAA 60  
 GAATCCGGTC ACAGCCTCCC CTCAGAGACA GGCCTCANTT CGAGGGCAGC CCATTATCTG 120  
 TCGCAGCATC TGCCATGTCC CTNAGACTGC GGGAGGCAGG GNATGCATGG GTGTCCCAT 180  
 CTGTCCCTGG TGAGAAGCAA GGCTAGCTCT GCCTTCCACA TGCTTNTNAG GATGCCAAGA 240  
 GGCCTAGGAA CCCAGNAACC CCCTTGNGAG GAGCTGTGNN 280

SEQ ID NO:4725

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05607

SEQUENCE DESCRIPTION:

GATCTGCATT CACCTTAGGG CTTAGCCTCT NATTTTATGA ATTTTCAGGC TGTGATTNGT 60  
 GTTGGATGGC TAAGNTCTAA GATAATGCAA ATAGCCCCAA TCTTTAAATA TAGCGGTGCT 120  
 AAGTTGAACA NGTAACACAN TACAGAAAAT GCTGATATGA ATACTTAGTA ATAATACAAA 180  
 AGTTCCTGCT AAATTATATA TGTGTATCAC TGCCTGNCNN GANACCCAC TTNNCTTTTC 240  
 TAATCCAGCN CAN 253

SEQ ID NO:4726

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05608

SEQUENCE DESCRIPTION:

GATCCAGATA GCCTAGGGTG AGGGTGACAG AGGGACAGTG GGCTATGCCA CTAGGCCCTG 60  
 GTCTGGCTTT GGAAAGACCT NTGAGGGGAA ACCTTCACCC AGCACCCATG CCCCCTCTG 120  
 CTGAGGCCAG AGGAAGGGAG GCCTGAGGGG CAGATTNGTT CATGCCTGGG GTGGAGGCTA 180  
 AGCCTGGACA CAGTCAGGGC GGGGCTGGCC AGCTGTGCGA GAACACAAGC CACGCCTGCN 240  
 ATGGTGCTGC ACCCCTGGGT GTCCCTGCCT TGGCCCTGCT CTGGTCACTT CAAACATNGT 300

N

301

SEQ ID NO:4727

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05610

SEQUENCE DESCRIPTION:

5 GATCATAAAA CAATAAAAGT AGTTTCTAA TGTGCTCAT AAAC TGGGAC TGAAAATCAT 60  
 TTCAATCCA GGAGACAGTC CAAAAATGGT TATTGAGCAN TGGCCACATA TTGGAATAAA 120  
 AATTTTNATT TTCAGTCTGT GTTTGGGAA AACAGCATT CATTGCATAG GTGGATAAGT 180  
 15 NCTAGAATAT TGGCTAANCA TATNGTCATT TGCTATAATG CATATGCATT NCAGAAAGTTT 240  
 TCTNGCTCCT GANGTATNAT GGGGGGTTTT CTAGCTCCCN TATNGCNAAA ANTTN 295

SEQ ID NO:4728

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05612

SEQUENCE DESCRIPTION:

20 GATCACTGA GCCAGAGGTT AAGTCTGCAG TGAGCTGTGN TTGTACCACT GCTCTCCAGC 60  
 25 ATGNGCAACA GAGCCGGACC CTGTCTCACC AAAGNCAA 99

SEQ ID NO:4729

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05613

SEQUENCE DESCRIPTION:

30 GATCCATTGT CGGGAGCTTG TGGCACATCA CCTTCTACT CTGCAGTCTT CCCTGCCTCT 60  
 NAATTCCGTT TATGTCTACC GTCCCCTCAA GCACACCCTG GTGACCTGTG ACAAAGGAGT 120  
 GTTCAGATTA CATCCCTCCT CTGTCCCAGG CCCAGACTTC TCCAAGGACA ACAGCAAGCC 180  
 AGAAGTGCCA GTCAGAGGTT NAGTAGCCTT TTACCATCAT CTCCCAGNTG CCAGTGGGTG 240  
 CAAGCAGACC TCTACTAAAC GNAAAGTAGA GGGAAATGGN AGTGGATGAC TTNTGTGATG 300  
 40 GANTCAAACG GCTCTATAAT GGANGGTTN 329

SEQ ID NO:4730

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05614

SEQUENCE DESCRIPTION:

45 GATCCTGCCC TTCCTGGGT NGGTGGGNGG TATAAGCACT GCCACCAGAA CTGTTGGGTG 60  
 50 CTAGCTTCAA AGCCCAACAC AAGAAATACT ACCAATTATG AAATTACAAC AACAANTNTA 120  
 AATGACATAA TTTTTTGAAA 140

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SEQ ID NO:4731

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05615

SEQUENCE DESCRIPTION:

GATCCATAGG ACTACCGCAG CCCGGACTCA CCAACTTGCC ACATGTTCTA GGTTTCAGCA 60  
 ACAAGACTGC CAGGTGGTTG GGTTCGCTT TTAGCCTGGA CCAAAGGGAA GTGAGGCCCA 120  
 AGGAGCTTAC CCAAGCTGTG GCAGCCGTCC CAGGCCACCC CCATGGAAGC AATAAAGCTC 180  
 TTCCCTGAAA 190

SEQ ID NO:4732

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05616

SEQUENCE DESCRIPTION:

GATCCCAGCC AGGAAGGCTG GGGGCCCTAC TGTTTGTCCC CTCTGGGCTG GGGTGGGGGN 60  
 AGGGAGGAGG TTCCGTCAGC AGCTGGCAGT AGCCCTCCTC TCTGGCTGCC CCACTGGCCA 120  
 CATCTCTGGC CTGCTAGATT AAAGCTGTAA AGACATAAA 159

SEQ ID NO:4733

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05618

SEQUENCE DESCRIPTION:

GATCACAGAC AAGCTGGGCC TGCATTCCCT TCGTCACCGT AACTGGTACA TTCAGGCCAN 60  
 CTGTGCCACC AGCGGGGACG GGCTGTACGA AGGCCTGGAC TGGCTGGCCA ATCAGCTCAA 120  
 AAACAAGAAG TGAAAGCCAG ACAGCCCTAA CAAAGCACCC CACCCACCCC TGACATACCT 180  
 ACTGTNACCC TGCCCCAGTC CTACCCCTTC CTCTCCATGC AAGTNTGGCC AGGGCCCTGG 240  
 GTATCATGTC CACATGCCCA GCAAGAGCCT TGCCTNCCNT TGCCTGCNCT GCTTN 295

SEQ ID NO:4734

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05619

SEQUENCE DESCRIPTION:

GATCCACCCA CCTNGGCCTC CCAAAGTGCT AGTATTATGG GCGTGAACCA CCATGCCCAG 60  
 CCGAAAAGCT TTTGAGGGGC TGAATTCAAT CCATGTAGGA AAGTAAAATG GAAGGAAATT 120  
 GGGTGCAATTT CTAGGACTTT NCTAACATAT GTCTATAATA TAGTGTTTAG GTTCTTTTTT 180  
 TTTTCAGGAN TNCATTTGGA AATTCAAANC ANTTGGCAAN CTTNGTATTA ATGTGTTAGG 240  
 TGCAGGNGGN CATTGGTATT CTGGGCACCT TCCTAATATG GCTTTACAAT CTNNN 295

SEQ ID NO:4735

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05621

SEQUENCE DESCRIPTION:

GATCTCAGCA ACAGCTGGGT AATAAGACTA GCATAGCTCA AACTATCCTG CCAAACGCTC 60  
TCATCTGATT TTNCCTCCCT TCTCCCCAA CCTCCAATCA CCCTGAGTCA CCTGTAAATN 120  
CATTTGTNAT TCAAAGCGGA ATAACANGTT GTCCCTAGCA NNNCCGCTGA GCGCTTTATA 180  
ATTTTNTGGT GTATTTTGT NAGTAGGTAG CAGAGGCGGA NGTATTTTNN GGTGTAATTC 240  
TTGANATTTT CTGACAGGN 259

SEQ ID NO:4736

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05622

SEQUENCE DESCRIPTION:

GATCACTGCA TGTTATGATG GCTTGTAAGT GCGTTGTAA GACTTTTNTT TCAGTGTTTG 60  
TNTCCAGTA TTTGAACCTA ATTTAAAGAA AAAGACGTTT CCAAGTTGTA TTTATTAAAT 120  
GTNTTTNCC TTACCTTTTG TNCTGCTACT TTNCTAATCT CATTAGCTTA GCTGTGTTTG 180  
TNCATAGGTT ATATNTGGTA ATAAATNTAT AGAGTGTTNG TTGTCATCGA AA 232

SEQ ID NO:4737

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05623

SEQUENCE DESCRIPTION:

GATCTGTAAG TTTATTTGCT CAATGTACGA CAGCTACATA ATGACTCACA TTCATGATAT 60  
TCCATCACTG AGGAAACTGC TAAAGATGGT CCGTGTGTGA AATAATTCCT TAGAGAAACA 120  
CGGAGCTGGA AAAATAAA 138

SEQ ID NO:4738

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05624

SEQUENCE DESCRIPTION:

GATCCAAC TGACAACGTGT GGGATGGACC TGGAAACAAG CACCTCCCCA AACACATCAC 60  
CACTCCCTAG GCGGGGGCCT GTGCATGCTC TCGCATGACA TCTCCATGCT GGTTCCTGCA 120  
TAGCATAAAT GGAAA 135

SEQ ID NO:4739

# EP 0 679 716 A1

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05625

SEQUENCE DESCRIPTION:

GATCGATGTT AAACGTCACA GCAGTACTTT GCTCAATAAA GGTCATATTG GAAACATAGT 60  
CAAA 64

SEQ ID NO:4740

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05627

SEQUENCE DESCRIPTION:

GATCTGTGGT AGGGTATTGA GGGATGAGGG AGAAAAACGA CCTAATTCAN GTAGGACTNG 60  
CAACGGCTCC CACCCTCCCT GGGGACANGG NTTAATAAAA ATTGACATCA CAAGAAA 117

SEQ ID NO:4741

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05628

SEQUENCE DESCRIPTION:

GATCAGAAGG GCTGCGTGTA GCACCCCTTAT GGTCTTGCAG AACACACCAA GAAACCCGAC 60  
GGCTTCCATA TTTNCTGACC CTACAAACAG GTGCCTAATA CTGATGTGGA GAAAGCTCAA 120  
GAGGGAATCA TCTGGCCTGA GCCTACCATG AGGCTGTTTG TGGTNCTGGC AGAAAAGCAA 180  
CAACTCGCTC CCCTTCCCAT GTATCAGTGA AAACCATTAT GCAAATAAAG AGCTGGGCCC 240  
CAAA 244

SEQ ID NO:4742

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05629

SEQUENCE DESCRIPTION:

GATCTTTTTT CCTCCTTCTG TTTATNTTTT TGTTTGTTTT ATTTATAGTC TGATTTAAAA 60  
CAATCAGATT CAAGTTGGTT AATTTTAGTT ATGTAACAAC CTGACATGAT GGNGGAAAAC 120  
AACCTTTAAA GGGATTGTNT CTATGGTTTG ATTCACTTAG AAATTTTATT TNCTTATAAC 180  
TTAAGTGCAA TNGAANGNGT TTTTNCAAA 209

SEQ ID NO:4743

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05630

## SEQUENCE DESCRIPTION:

GATCATATAC TGTATATATA AAANNNTTGA GATGGTAGAA ACATGTATGA NTGTACTAAG 60  
TAGTATTCCA CTGTACTCAT TCATAAGGTA GGTTTTCTTA CAAAACTCAC ACCAGGTACT 120  
TAAAGATGTG CTCTGCTTTT TTCCAACCTAC GGAGTGTAC TGCTTTCTAG GTCAGTCCCT 180  
GCAGACTCTT CTCAACTCTT TCCCTATAGG AAACCTACTC CGCGTCCTGC CCCCACCTCC 240  
TAAATAAATA ANGGAATCGG CGAAA 265

SEQ ID NO:4744

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05631

## SEQUENCE DESCRIPTION:

GATCCCTAAC ATACTGTACT ACTTGCTTNT ACAATGTGTT AGCAGAAACC AGTGGGTTAT 60  
AATGTAGAAT GATGTGCTTT CTGCCCCAAGT GGTAATTCAT CTNGGTTTGC TATGTTAAAA 120  
CTGTAAATAC AACAGAACAT TAATAAATAT CTCTGGTGTA GCACCTTTTA CTGTAAA 177

SEQ ID NO:4745

SEQUENCE LENGTH:377

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05632

## SEQUENCE DESCRIPTION:

GATCAGCCGA AGAAAGCAGA AGCTCTGGAG GCTGCCATCG AGAACCTCAA TNAAGCCAAG 60  
AACTATTTTG CAAAGNTTGA CTGCAAAGAG CGCATCAGGG NCGTCGTTTA CTTCCAGGCC 120  
AGACTCTACC ATACCTGGG GAAGACCCAG GAGAGGAACC GGTGTGCGAT GCTCTTCCGG 180  
CAGCTGCATC AGGAGCTGCC CTCTCATGGG GTACCCTTGA TAAACCATCT CTAGAGAGGA 240  
CATCCCTGCT GGGCTGCTGT GCAGAGTATA AGATTTTGA CTTGTTTCATG TCCCCTCTCT 300  
CCCTATAAGG GGTGTATTTG TGACACCCTA TCTNGTCANT AAACAGCATT TCTGATTAAT 360  
AANAANAAAA AANAAN 377

SEQ ID NO:4746

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05634

## SEQUENCE DESCRIPTION:

GATCCTGAAG TTTTGGTCA ATAGGCTCTG TCTTCGTGAG AGACGGGCTG AGAGTCAGAA 60  
ATAAATCAAC CATTNTGGT TTATTCAA 89

SEQ ID NO:4747

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05635



## SEQUENCE DESCRIPTION:

GATCTTTCTT CTCCCAGCTA AGAGTTCTTC AATAAATTTA AGAAATACCT GGAAA 55

5 SEQ ID NO:4748  
SEQUENCE LENGTH:244  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS05636

## SEQUENCE DESCRIPTION:

GATCAGCAGG GACCAAACCA TTGCCACATC CCAAGGNTGA ACAAGCATGG CTGAGCACCA 60  
GAGTNTGCAC CAAGTNTGAN TTTAGGCCTG CCAAGTGGAT TTACACCCAG CACGTCCCAA 120  
ATTTGGGTGA GTGCATGCCA ACCCTGTAAA CATGTAGGGG TGGACAGGTC AACAGACAAG 180  
15 GTGACCCAG CNTCCCGGCA AACTTGATTA ACACATACTG GNCACAGCAA TTANNNGAN 240  
NTGN 244

20 SEQ ID NO:4749  
SEQUENCE LENGTH:184  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05637

## SEQUENCE DESCRIPTION:

25 GATCGCAGGG CCNTAGGTGC CTGGACCCAG GGTGTGCCAG CCCGTCTCTN TGCAGTCCCT 60  
GGAAGGGCGC TGAGAAAGGC ACCAGCTCCT TGGACCCAC CTCCCATGCT CTCACTCTCA 120  
TCCCCGTTCT CTTGTCCACA CAGCTCTTCC AATAAAGGTG TTTCTNTTCC TCCTTCTCCT 180  
CAAA 184

30 SEQ ID NO:4750  
SEQUENCE LENGTH:282  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS05639

## SEQUENCE DESCRIPTION:

GATCCTAGTT GCCTTTGTGT ATATTTACTG CCTGCTTGAG TGTTTCTATG TGTGGGTTTT 60  
CCCTGTATCT TGTAGAAATG TTGGGGTGTT TTCCTCTGCC ATATGGCTCG TGGCCTGCGA 120  
40 GCCAACTATT TCAGNTGTGT TTNACCTTCA TTTTGTATGA GGTGATTTAA ANNTNGTTTC 180  
ACTTTGTGTA GTGAATTCCA CAGTAGTTTT CTGANTGTNG TTAAAAATGA CTTAACATAT 240  
TACACAGATA TTCAATAAAA ANGTTTATT TCCTGTTGNA AA 282

45 SEQ ID NO:4751  
SEQUENCE LENGTH:65  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05640

## SEQUENCE DESCRIPTION:

50 GATCCCATTTG TGTATAAGTT AATATGTGAT AACTATTGAA TCTTGTACAA AAACAAAAAT 60

55

TGAAA

65

SEQ ID NO:4752

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05642

SEQUENCE DESCRIPTION:

GATCCATCCG CGGTGTTGCC TGAATCAACC GCTCATCCCT CGGATTGCTG AGCAGGATTC 60  
ACAGGGTGGA GGCACCACAA TGTATCTGTG TCCCCAGAAA GAATACTTGC AGTTTCCAGT 120  
TGGACACTTT ATCAATAAAA TCACTATAAA CATCTGAAA 159

SEQ ID NO:4753

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05643

SEQUENCE DESCRIPTION:

GATCTTGAGT TGCAGTCCAC AGCATTCAACA TTCTCAGGAT AAACATGCTT GTCTCCATAT 60  
ATACTATCTG TGCCTGTAAT GAATGAAAAA TCCATCCACT CTGCTGCCAT TCACAGCCTA 120  
ATCTTCTGGA GTAGTCCAAA CAATGTTTGG AAAACATGG GACTGTATGT CATTACTATG 180  
ACTGATAGCA GAATAATAAT GCATCTNACT TCTATATAGN GATAGNCTTA CATAGGTTAC 240  
CCTTGANATT CATTAGTNTG TCAATANGTTT TAGGAAAGGT AGGACCCGGN AAGNNGTTCT 300  
ANTTAGTTGT CTAAATNTTT TNCAGTGNGC CAAGNNATTC ACCATGANAN AN 352

SEQ ID NO:4754

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05644

SEQUENCE DESCRIPTION:

GATCGGCTCA AAGCCTGTCA GCAGAGGGAA GGACAGAACT ACCAGCAGAA CTGTATCAAG 60  
GAAGTGGAGC AGTTCACCCA GGTGGCCAAG GCCTACCAGG ACCGCTATCA GGACCTGGGG 120  
GCCTACAGTT CTGCCAGGAA GTGCCTGGCC AAACAGAGGC AGAGGATGCT GCAAGAGAGA 180  
AAAGCTGCAA AAGAGGCCGN CGCTGCCACC TNCTGAGGCA GCTGTGGGTG CCCCTGCTGT 240  
GTGGCTCTGT ATNACTTGTT TGCTTGAAAT NTAAGAGGCC TNGCAAACCC TGGGAAA 297

SEQ ID NO:4755

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05645

SEQUENCE DESCRIPTION:

GATCCCAGGC CTGTGGCTAG CAGCACTGGG GACAGGAATG GCTGGTCCCT TGAGGAGGTC 60  
GTGACAGGCT CAGCCTNGTN GTCTNGAGGG GACTCGGAAA TAAATTGTAG CAGCTTTCCT 120

GCCAAA

126

SEQ ID NO:4756

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05646

SEQUENCE DESCRIPTION:

5 GATCTAAAAA GTCAAAAATC TGAAATTTAA TAATATGAGA CTTACACTGA NTATAATGTT 60  
 CATTTAGAAG TTGCTGTGGT CCACTTCATT TATANGGAAC AAATATTTTT ACAGTACACT 120  
 ATAGCAACAG CAAAAGCCCT CTCTCACCCT GATAGGAATG GGTTTGCTGG GTGTCTAGAA 180  
 10 GTTAGATTCC TGCTGAATAG ANTTAGCCAT CCTTAAAAGA TNTTAATCCA ATACTGAACT 240  
 15 GGTTTATAAA ANGCTTTCTC TATTGTANTG NACTGTAAGT AGTGAAATTC TGTATATACT 300  
 GCTATTNGCT GNCTGTN 317

SEQ ID NO:4757

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05647

SEQUENCE DESCRIPTION:

20 GATCAGTAAT CCTATTAAAG AAGCGGAAGA AGATACCTCA GAAAGGTCGG AAGAAAAAAG 60  
 GTTTTCGGAG GCGGCGGTGA TTATGGGTGT ACATATTTGT ATATTTTTTG TCATCCTGAG 120  
 ATACTTCTAA TTTCATTGTA TATAGGTGGT TTTCCCTGGA ATTCATTAAT TGTTTGCTTT 180  
 25 GGACATGTGG AAAGAGCCTT ACTAATAAAA TTGATTTTAC TTATGAAA 228

SEQ ID NO:4758

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05648

SEQUENCE DESCRIPTION:

30 GATCAGTTCT GAAACAGTTT CTTTCTGAAA CAGAGAAAAT GTCCCCTGAA GACAGAGCAA 60  
 AATGCTTTGA AAAGAATGAG GCCATACAGG CAGCCCATGA TGCCGTGGCA CAGGAAGGCC 120  
 35 AATGTCGGGT AGATGACAAG GTGAATTTCC ATTTTATTCT GTTTAACAAC GTGGATGGCC 180  
 40 ACCTCTATGA ACTTGATGGA CGAATGCCTT TTCCGGTGAA CCATGGCGCC AGTTCAGAGG 240  
 ACACCTGCT GAAGGACGCT GCCAAGGTCT GCAGAGAATT CACCGAGCGT GAGCAAGGAG 300  
 AAGTCCGCTT TN 312

SEQ ID NO:4759

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05649

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCAAGGTA AGAAACATTG TAAAAAATAA TTACAAAAGT GCTATTTGTT TCCTAAAAAC 60  
AGTGATTTCT ATTAAAAAGG TGTCAGANCT GGAAA 95

SEQ ID NO:4760  
SEQUENCE LENGTH:336  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05650

SEQUENCE DESCRIPTION:  
GATCCTNTTT CCANTNAAA GGAAGTGTAA GCTTTTATCT TTTAACCAAC TGAACAATAC 60  
ACCAAAAGCA GCCTAGGGAT GAGCATTCTT TTGAAAGCAA TTAGGTTATT CACCTGGTAT 120  
TAAAACTATT TACTGTATAA AAATCTGTGA CTTTCATGAAG TTGATTNTA AAGGCAGCAT 180  
CANAACTGA NANGGAAGGG AAANANTAGG CAGCTTCTCT GCACTTGTTT GGAGCTCCCC 240  
AAANCAGGGT GCCATGGGGN AGTGGGCATC AAGNCCGGGC TGCCCTTCG NGGTCANCCT 300  
GTGGCAGTTC AGAGTCANGG TTTTCTCNC GCTGGN 336

SEQ ID NO:4761  
SEQUENCE LENGTH:310  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05651

SEQUENCE DESCRIPTION:  
GATCCAAATT CCCAGGTCGG CGCCTGCATC GTGAATTCAG AAAACAAGAT TGTCGGGATT 60  
GGGTACAATG GGATGCCAAA TGGGTGCAGT GATGACGTGT TGCCTTGGAG AAGGACAGCA 120  
GAGAATAAGC TGGACACCAA ATACCCGTAC GTGTGCCATG CGGAGCTGAA TGCCATCATG 180  
AACAAAAATT CGACCGATGT GAAAGGCTGT AGTATGTATG TTGCCTTGTT CCCTTGTAAT 240  
GAATGCGCTA AGTCATCAT CCAGGCAGGT ATAAAAGAAG TGATTTTCAT GTCTNGATAA 300  
ATACCATNTN 310

SEQ ID NO:4762  
SEQUENCE LENGTH:364  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05652

SEQUENCE DESCRIPTION:  
GATCCCCTCC AAGGAGCACC CATATNACGC CGCCAAGGAC TCCATCCTGC GCAGGGCCAG 60  
GGGCATGTTT ACTGCCGAAG ACCTGCGCTA GGGGACTCCT CATAGCCCTC AGCCCTTCCC 120  
TCGTTTCCAG GCCTCTCCCC AGGCTTGCCA TCAGCCTTCT TTACTTTTGT AGCCTCTGAT 180  
TTCCAATTCC CTGCTNCCNN CCACTCCATT AAGAGGCTAG GTGAGGCGCT TCTAGGTTGC 240  
TGGGGCTCTG CTGGTTAAGG AACAGGAAGC CTGACCATCT CCCTCCACTA CCTCTTCCCT 300  
GTGCTGTTAC ACAGTGTCAT TGTTGATGTT AAATTAAAGT CATATTCTTG CTTCTTTCCG 360  
NAAA 364

SEQ ID NO:4763  
SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05653

SEQUENCE DESCRIPTION:

GATCGTCTGG AAGCAGCAGA GATGTACAGA AAAGCTGCTT GGGAAGCGTA TTTGAGTAGA 60  
CTTGGTGTTT GAGTGCTTCA GATACATTTT TCAGATACAA TNTGAAGACA TTGAAGATAT 120  
GTGGTCTCTCC TGAAAGTCAC TGGCTGGAAA TAATCCAATN ATTCCTGCTT GGATTCTTCC 180  
ACAGGGCCTG TGTAAGAATG GGTCTGGAG TTCTCATGGG NCTTTTAGGA AATATTGAGT 240  
AATTTGGTAA NTCACCGNAT TGGTACTAT ANATAAGGTC CCANTNCNTT AAGGCTTGAT 300  
AAGGTGAATN GNGGTGNGNN NTNTGGGGGG AGN 333

SEQ ID NO:4764

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05654

SEQUENCE DESCRIPTION:

GATCCTCCAA AATCAAACA AGGAAAAATC TCTCCCAATC TCTCCTTTCC TCCATCCCTT 60  
TTCTTTACTT CTCATCCCAT ATATAATATT ATATAANGCA TACGTAATAA AAGACATTCA 120  
CTATTATTAA A 131

SEQ ID NO:4765

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05655

SEQUENCE DESCRIPTION:

GATCTCTTTT GCTATGGCTC ACATTATTTT CATAAAGTTG CTGGCCAGCT TTTACCTCTT 60  
GCATATAATC TGTTGAAGAG GAATCTGTTT GCAGAAATTA TTGAGGAGCA TCTGGCAAAC 120  
AGAAGTCAAG AGAACATAGA CCAACTTGCT GCATGAGTAA GGTGGCTTTG NTTGGTGTA 180  
AGTATTTCAA AGGACTAGTA TTAANCTTGT GATTNGGTT TTGTTTTTAA GGGGTACANN 240  
NNGTAAGCCA TTNCTTAAN AACCGTTGAA A 271

SEQ ID NO:4766

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05656

SEQUENCE DESCRIPTION:

GATCTTTCTC TTGAGTCATT TTATTTTAT CATGGACTAG TCGTGCTCC GTGTCCACCC 60  
CAATAAAAGG GTCTTTCCTA CTTGAAA 87

SEQ ID NO:4767

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05657

SEQUENCE DESCRIPTION:

5 GATCTGGGCA ATTTTGGCCT TGACTCTTTC CTGGCTCCAG AGCTCAAGCT TAGANGCCAG 60  
 CCCTGCTATT TCCAGCCTCC TGAAGGCTCA GCACGGTGAG GCCTGACATC CTGGGGAAGG 120  
 GCAACAGGGA GACCTACAGG ATGNTGGCTG CTTGCAGACT GGTCAATGGG GGATGACGGT 180  
 GGGGAGGTTG NCAGATGTGA GACTTNNGTA GCATTTNGTA CACATGGCCC TGTA GTTGTGTC 240  
 10 CTTTNGAAGA ACATCANTNA AAATATANGG GTNNTTAAAT TNTGGGNAAA AAN 293

SEQ ID NO:4768

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS05658

SEQUENCE DESCRIPTION:

20 GATCTTGCTA GGGAAGGCCA CCTTGATATGC CGTGCTGGTC AGTGCCCTCG TGCTGATGGC 60  
 CATGGTCAAG AGAAAGGATT CCAGAGGCTA GCTCCAAAAC CATCCCAGGT CATTCTTCAT 120  
 CCTCACCCAG GATTCTCCTG TACCTGCTCC CAATCTGTGT TCCTAAAAGT GATTCTNACT 180  
 CTGCTTCTCA TCTCCTACTT ACATGAATAC TTNTNTCNGT TTTTNTGTTT CCCTGAAGAT 240  
 TGAGCTCCCA ACCCCCAAGT ACGAAATAGG CTAAACCAAT AAAAAANTGT GTGGTTGGGG 300  
 25 CCTGGGGNGC AAA 313

SEQ ID NO:4769

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS05659

SEQUENCE DESCRIPTION:

35 GATCCCCTCA TCACCCTGT GCCCACTTCG GAGAACCNT TCCGGGAGAA GAAGTTCTTC 60  
 TGTGCTCTCC TCTGAGCTCC CCTGTCCCTT CTCACAACTN CTCCCTTTTC CCTCTCCTGG 120  
 GCCCTTCCTT AGGTCAGTAA TTGTTGTGAG CCCCTTAGGC TCCTTGCATC CCATCCCTAA 180  
 CCCTTGCCCTG ACCATGTGAG GTTATCTGAA GCACAAGNNC CACCCTNANG NNGNNTNTCG 240  
 ACCCGATTTC CTACCACCTT TTTTGGGCCG ANCCNAAGN 279

40 SEQ ID NO:4770

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS05660

SEQUENCE DESCRIPTION:

50 GATCCATGTA ATCTGACGTC ATCTTGTCTC GAAGTCTCTT TTTTGGCCC AGGCCTTGAA 60  
 GAATACACTG TGA CTTAAGA AGCCTTACCA CGCAGTAACT AAAGCTTTAG GATGACTGTN 120  
 TTCGAGGAGT GCCGTGTGTT GCATGCAGCT ACCCGTAGGA AGACTTCGCG CATATCACTA 180  
 ATAAACCTGA AGTCGTGATG AAA 203

# EP 0 679 716 A1

SEQ ID NO:4771

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05661

SEQUENCE DESCRIPTION:

GATCGTTGTG CTTTNTTNC TGTGTTGGT GCCAGTTTAT AGTGCCAACA CGTGGCGCGC 60  
CTTTAATGGC CCGNGTGCAC ACCNAGCACT CTCGGGTGCT CCNATCTCCT TN 112

SEQ ID NO:4772

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05662

SEQUENCE DESCRIPTION:

GATCTGGGAG GTGGAAGCCA GGCCAGAGGA CTTGGGGAAA ATNAGATGGA GGAAGGAAAA 60  
AGGGAGAAGC TGAGCCACAG CTTAACTCCT ACAGAGTGAA ATNAAAACGG GCTGAAAATA 120  
CCACCCAGG AGAGGACCTC GNCCCANGCA AGCCAGTGAG CAGCCCTGCC AGACTACTGN 180  
CAGNCTGNGA AACCCAGANG CTGGGTAGTC ATGTGGGGCT TGCCTTCTTT TGCCAAAACG 240  
NCTGGGGGAA NCCAAAAATN GGGCCCCACC CTTNNTGTTT CTTTCCTTNG N 291

SEQ ID NO:4773

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05665

SEQUENCE DESCRIPTION:

GATCCCAGGC CTNTGGCTAG CAGCACTGAG GACAAGGAAA TGGNTGGTCC CCTTGAGTAG 60  
GTCGTTACAA GGCTCAATGC CTGGTNGTCT TGGAGGGTAC TCGGAAATAA ATTGTAGCAG 120  
CTTTCCTGCC AAA 133

SEQ ID NO:4774

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05667

SEQUENCE DESCRIPTION:

GATCACCCAG CAGGAGTCGT GGCAGAACGG AGCATCAGCC AGACCCTGTT GTGGGCGTTG 60  
TCATCAAGGG AGCTTGAATG GAGGGTCTGG TGTCAGATAC AGCCGACTCC AGCCCCAGCT 120  
CATCCCCAT GATGCTGTGT GACCCACTGG GCACTCTGGT GAGGGAGCTT TCCAGACATC 180  
AACAGCCCAC TCTGCTTCCC TTTCTGAGTC CCCTGTCCAG CACTGCCTAG TGTTGGAGGG 240  
TAGACCAAGG CTGTGCATGA TTCACCCNT CTTCCATCC TGGAGCTGGC AGTGAATAAA 300  
AGCCCGTATT TACAAA 316

SEQ ID NO:4775

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05668

SEQUENCE DESCRIPTION:

GATCTCCAGA GACCCAAGTT TAGGTTCTCA TAGTGTATTT GAAGTAGTTA TACTCCTGGC 60  
TTAAGTAGTT TAGTGCCTGG GAGAATCCAT TACTGAAAAG CATTTAACCT AAA 113

SEQ ID NO:4776

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05669

SEQUENCE DESCRIPTION:

GATCTAACAA AAATGAAACA TGAAATGCAG TAGCAACCAC TAAAAAAAAA AATTCAAGGN 60  
CATCTAACTN TTTCTCTCAC TTTNGCCCTT TGTTTATCCT TCCCTGTGAT TAGATAANCA 120  
NAATAAAAN CAAATGCTG TATTTCTCTN CTTACGN 157

SEQ ID NO:4777

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05671

SEQUENCE DESCRIPTION:

GATCACTTAG AGAAACAGGC CGTTAGGAAT CCATTCTCAC TGTGTTTCGCT CTAAACAAAA 60  
CAGTGGTAGG TTANTGTGTT CAGAAATCGC TGTCTTACT ACTNTTGC GG AAGTATGGAA 120  
GTCACANCTA CACAGNGANT TCTCAGCCTA CAAATTGTGN CTATACATNT CTAAGCCTTG 180  
TTTGCAGNAT AAACAGGGCA TTTNGCAAAC TAAA 214

SEQ ID NO:4778

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05673

SEQUENCE DESCRIPTION:

GATCAGTTN CAGCAGCAAG TACAAAAGGA GAAGAGGAAC ATCCGTTGAA TNAGTGTGTT 60  
TTGTACATAA CTTCAGATAC TTGTNAACAT GCCTTATATT TGTCCAACAA CTGTCAGANT 120  
AAAGAACATT CTAAATNAA A 141

SEQ ID NO:4779

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05674

SEQUENCE DESCRIPTION:



# EP 0 679 716 A1

GATCTTGTGA AAACACNGTN TTNTCGACTA AAAATTCCAC TNTCTTCATC TNGTTGTGAA 60  
GCTAAAAAGA GGGACTGTGA AATACAATGT ATGATACCAT GGCAAAAATC TTTCTGAAT 120  
TGTCTTTNGT AAAAGTATTA TTGAATTTN CAAN 154

SEQ ID NO:4780

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05676

SEQUENCE DESCRIPTION:

GATCAAAATA GCTATTGCTA CAACATTTTC GAAAACAAAG TTGGGGCTGT ATTTCTTTAA 60  
AAAGATAAGC CTCTAAAAAT GCTTGGCAAA AAAAATATAG TGTTAAAATA GGCCAGTGAT 120  
ATTAATGAGA AAATGAAAGT ATGTATCAGG ANTAANGTGA TATTGCATAG GNGTATTGTA 180  
TTTTNATGAA TTTNATGCCA GTTGTTTACA TGTACTATAT ATGTNAANTT ANNNNN 236

SEQ ID NO:4781

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05679

SEQUENCE DESCRIPTION:

GATCTCAGTT GCACGTGCAA ACAAATCCAA ATTCGAACAT TCTTAGGAGG TTTTNTTAA 60  
GGCATGACAG ATGATNTAAA CAAATAAATA GCATGCAACA AAANGTCTTT ATTGNAAGAA 120  
GTGGAAGTTA TCTTAATGCC ACGGNTCACC ANCAATTNAA AAGTANAN 168

SEQ ID NO:4782

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05680

SEQUENCE DESCRIPTION:

GATCAGTGAA CACTAACATT TTGGGGACAA CTTAGTCAAT TGGTTTTCCT TACAACAAAA 60  
TAAAGTAAAA TGTAGCAAA 79

SEQ ID NO:4783

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05681

SEQUENCE DESCRIPTION:

GATCACCATT CAATTTGAGT TTCCAGGGGG AAGTGCATGT ATAATGNAAT GATAATGGAC 60  
TTCAATGANG GATGTCATCA ATNATGNACA TATAGATNGC CTTATAN 107

SEQ ID NO:4784

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05682

SEQUENCE DESCRIPTION:

GATCTAATAA GACACGTAAT AGATTAGAAG TAGGGAAATT AATGAAAAAG CAGAATTAAG 60  
 GATGACTTCT CACTGGCTTG AAATNCTAAA TGGATGACGG TGCTGTTTAG TGAGTTGGGG 120  
 AAGACTGGGC GTGGTGATGG GTGTAGAAAT TGAGAAAGGA AAATCAAGAN TTTCCAGAAC 180  
 TTTCAAGACA ATGTTAAATA CTTTCCTTGA TAGTGGGTCA GTCATCATTT ATAAGTGCAT 240  
 TTCTAAAAAT NTTGCTTAAT TTTNTTTTGG AGCTTTGTAT AAGTGGAATT TTGTGTGTAC 300  
 TGATTATNTT GCTCAATAN 319

SEQ ID NO:4785

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05683

SEQUENCE DESCRIPTION:

GATCTTTCAT CTGTGATTCT TATAAGAGCT TTGTCTTCAG AAAAACTAAA AATAAAAGGC 60  
 ATTGACTTAA ACAGCAAA 78

SEQ ID NO:4786

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05684

SEQUENCE DESCRIPTION:

GATCAGTTGT AAGTTCATTT CTTTACAAAT AAAAGCCTCT TCCATTTGAA A 51

SEQ ID NO:4787

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05685

SEQUENCE DESCRIPTION:

GATCTTTTCC ATCTGAGGGT ACAGGAAGTA CCAGGACCTG TTTCAAGTTT TNAATCCTGC 60  
 AAGCACATTC CAAGACTGGC CTGAACTGC ATGAGCAACA TCACTCGAAA TAATTTTTTT 120  
 TTTCAAANGC ACCTTAACAA CCANTTGCGA TGCTGTCTGT TTCCTTTTTC CTCACACCCT 180  
 TCTNTCCTTT CTCGTCCNA TGCTCCACCA NCTCAGTGCT NTGTGCTGTA TGCCTGTGCT 240  
 CTCTGTTNTN GTATACTCAA TATANGTGNA ATAACTGGT GTTTTGTN 288

SEQ ID NO:4788

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05686

## SEQUENCE DESCRIPTION:

GATCATGCAT GCAGTCATGT CTCCAGTATT CTGTGAAAAG CCAGGATACG TTAGGATGTG 60  
 AGTTTAGAAA CTGAGTCCAT TCGGTGCATG GAAATNCACC GCGGAGTTAC ACAANGCTCC 120  
 TCACTGTAGT CCAGGCGATT GGTNGGCCGC CANCACCCTG CGGGCTTCAC AGGGACGCGT 180  
 GCTTGTNCTC CAAGNCCCGN AACCCTTACT GTGCACACAN CATCNNACAC ACCTTTGTTT 240  
 TTGAAATTAA AATGTTNATT AGTTNAAAAA AGGGNGGN 278

SEQ ID NO:4789

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05687

## SEQUENCE DESCRIPTION:

GATCCCGGTG TGTGGCCAG CTTGTNCAGG CCCTGGNATG CTGCATCTCC AGGCAACTAT 60  
 GCACCTTTCCC GGGGAGAGAA CCAGTATGAG AAGTGGGGC AGGGCACACA TTCATCTTTG 120  
 TAGGAAGGTC TGGCCTGGGG TCGGGTGAAG GAGGGCCCAG GTCAGTNCAG GGGTCCCAGT 180  
 GACCTGCTTT GCCATTNTCC TGGTGCCGNT GCTGCTCCCT GTTCTGGAG CTGGATGTTN 240  
 CCNAGCTGGC AGTTGAGCTG CCTGAGCCAA TNTAGTCTAG NCTTTGGTAA CTTGNGTGAA 300  
 CCATAATAAN GGGGAACCAT TNTNGGCCTT GTGNAAA 337

SEQ ID NO:4790

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05688

## SEQUENCE DESCRIPTION:

GATCACAAGG CTGCCTGCCT CAGTCTTGGA GTCCTGTTGG GTGAATNAGG CAGATGGGAA 60  
 ANAGCCTCAC CAGCAGCTGC TTTTGGAGCA GGGGTCCAAG GAAGAGAGGG TGGCCTCGAC 120  
 ATCAAAGTGC CTGGATTTT CTACCACCCT GTTACATCAT AACAAGTCTT GAAACACACA 180  
 CCAGCCCTGA GTTCTGGGCT CATTTGAAGC CTGGAATAGC AATAAATCTT TTAACTTGC 240  
 GGACAGTTAA A 251

SEQ ID NO:4791

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05689

## SEQUENCE DESCRIPTION:

GATCGAAGAT GTACAATGTT AAATGTNCAT ACCAGTTAAA CTGCACTTTC CCAAGGGGNC 60  
 AGCTGGNATC TACTTGAAAT GGGNATCAAG AGACCACCAA ATGTTTACAG TTTCTGTGGC 120  
 CCGTTTAAAGT GTAAAATGCA GAAGTGGCTC TGTCCCCCA GAGTTAAGGN TTTGCTACAC 180  
 TGGTCTCTG GAAGCATTTA NGTAGAAGAA AAGGCTTATA GTCAGNNTCA CTTTGTAGTA 240  
 TCGTCTNCTG GTCCTTGNC TNTTCTGGTT CTGTNANTGC TTGTAACCAA TGANTGATGG 300  
 TGTTGCCAAT CTNAGN 316

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SEQ ID NO:4792

SEQUENCE LENGTH:346

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05690

SEQUENCE DESCRIPTION:

GATCAGTCCT GTCATCCAGC TGCAGCCCAC CTTACACCCC ATGCGGGTCG CACTNGCTGG 60  
CACATTCCAC TACTACAGCT GCGAGAGAGC CAAAAAGGCC ATGGGCTACC AGCCACTAGT 120  
GACCATGGAT GATGCTATGG AGAGGACCGT GCAGAGCTTT NGCCACCTGC GGAGGGTCAA 180  
GTGAGGGNCA CTNGNGGCTG GGCTCTCTNG ACACGTTGCT CAGCCAGTCA CTNCTTCCCC 240  
TGNTGGATTG ATGAGNTAAC ATCCTTTNGA ATGGAGTTN GCTCTTTGCC TGTGACTCCT 300  
TCTGCTAGGC AGNGGAGCGC ACCNTACTNT TTNCGTNGCG GTGNGN 346

SEQ ID NO:4793

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05692

SEQUENCE DESCRIPTION:

GATCCCAGGG ACTCATCCTG TGACTTTGTA ACCACACTCA TTCCTTTCAA ACACAGAGGA 60  
GGAATTATTG CTTTACTCTGA CTTTATTCAA ATCTAGTTAT GTATTGGCCT AAATTATTTG 120  
TGCAAAATTT GAANNNNNT TTNATTTAAA TATTAGAAAT AGCACAAAGT CATGGNGTTT 180  
TTAANAN 187

SEQ ID NO:4794

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05693

SEQUENCE DESCRIPTION:

GATCTCAAGA GCCCTGTCAG TAGAGTAGAA GTCTCTTCCA GTTTGCTTTG CCCTTCTTTC 60  
TACCCTGCTG GGGAAAGTAC AACCTGAATA CCCTTTTCTN ACCAAAGAGA AGCAAAATCT 120  
ACCAGGTCAG AATAGTGCCA CTAACGGTTG AGTTTGTACT GCTTGGAAC TGAATCCTTT 180  
CAGCAAGACT TCTCTTTGCC TCAAATAAAA AGTGCTTTTG TGAGCAA 228

SEQ ID NO:4795

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05694

SEQUENCE DESCRIPTION:

GATCTGCTTA AAGTTTAACT TTTTATACCT ATCTGAGTGA ATTACAGACA ACCTATCATT 60  
NATNCTGCTN CGAGGGTCCC CAGGGGCCCT GTACAACCGA CAGNTCTTAC TTTTAAATGC 120  
AATCTCTTGT CTACATACAT NATTTTCTTA ATTNCTTAGC TATTTATAGA AAGCTGCAAT 180  
AGAACTGTNT CAACTGTATA ACTATTTACN ATTCANAATA NAANTATTN 230

SEQ ID NO:4796

SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05695

SEQUENCE DESCRIPTION:

GATCTCATT TCTGAATGAT TGATTAAAGA GTAAAATTNG CCACTGCGTG CTTTTTGTAT 60  
AGTAACCGGT TTTGTTGCAC TNGTCTGTGG CTGAAACACT TACCTGCAGT GGAANGCCGA 120  
GCAAGGAGGA GGTAAACATT GGAGATGTTT GTGAAAATAT TACTCTTGCT GTGAGGTTTT 180  
AGTTTGT TTTT GAATGAGAAA GGGGCTAAGT AACTTAATCC ATCTCAATGT AGTGTTTTAA 240  
TAAAAANGGN GCCTAATATT TGAAATGGGG TCTCAGGNCA TGNTCTACAA ATNTGGGGNA 300  
NCTATTTTNN ATGCCCCGTG TAATTTTNNCA CCATTTTGNN NATGAGTTNA TTGTAGGGGT 360  
CANNATN 367

SEQ ID NO:4797

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05696

SEQUENCE DESCRIPTION:

GATCTTTTCT CAGAGCGTCT CCATGCTATG GTTGCATTTT CGTTTTCTAT GAATNAATTT 60  
GCATTCAATA AACAACCAGA CTCAGAAA 88

SEQ ID NO:4798

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05697

SEQUENCE DESCRIPTION:

GATCACAAGT GCAGCATTCCT TTAATTCCTT CTGCTATATG TCACACAGTT GTTATTTGGA 60  
GAACCAAGTA TGTATTGCAT GAAAACATTA TGACTTTTTT CTCTTAGTTT AAATAAACTC 120  
CAAGGTAAGT GGACTTCTAA AGCACCTTTC TGTTTGCCCTG ATATCTACTT TAGCAATAAT 180  
TTTTTTTACA ACCCTCTGAC TCAACAAAGT AAATAAAAGT ATATTTTATC ACTATTAAA 239

SEQ ID NO:4799

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05701

SEQUENCE DESCRIPTION:

GATCTGGCCT TATGCCCAGG CCTGGGCCCT CAGAAAGCCC GGAGGCTGTT TGATGTCCTG 60  
CACGAGCCCT TCTTGAAAGT ACCCTGATGA CCCAGCTGN CAAGGAAACC CCCAGTGTA 120  
TANTAAATCG TCCTCCCAGG CCAGGAAA 148

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SEQ ID NO:4800

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05704

SEQUENCE DESCRIPTION:

GATCCTCAAC AGACACCTTC CTTGACTGAA AGTTTAAATC GTGATGCAGA GNCAGTCAGT 60  
NATNTNCCGC CATCCACAGG AAATTCAGCA TCTTTATCTC TNCCACTTN 109

SEQ ID NO:4801

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05707

SEQUENCE DESCRIPTION:

GATCAATTCA ATTAGATTAA AATNAAGAAC CTTGGGGCAG AGTTTGGGTT TTGTAAAATN 60  
AAAAGAGTTC TGGAGTTAAG CATCGTGAAC ATGCTTAACA CTACTGAACT GTACACTCAT 120  
TTTATAATAA AACTATTAAA TTGTAAA 147

SEQ ID NO:4802

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05708

SEQUENCE DESCRIPTION:

GATCTAATTT AAAATTCATT GGATTGAAAT NTATTGAATA TAATTCANCT TTTGTAACTA 60  
GGTAGACTTT NCTNATAGTT TAGTTTAAAT ATAGTTTAGG GTATTACTGG CTTTTCCCCA 120  
GGTGACACAC TAAGGNCCTGT TTACATGGCA ATTCCAGCAG CAACAGGNGG CTGGAATTNA 180  
GACAAGGAAA GCTCATTGT TTCTTTTATG AAGGTAAAG AAGTCTACAG CTTGGGCTGG 240  
CCGGTATTTA TTNATTCTGT GGCCAGAGGA TTTTAAATTT NNCNCNAATN TTNTN 295

SEQ ID NO:4803

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05709

SEQUENCE DESCRIPTION:

GATCATGCCA CTGTCCTCCA GCGTGGCAAC AGAGTGAGAT TCTGTCTCCA AA 52

SEQ ID NO:4804

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05710

SEQUENCE DESCRIPTION:

GATCAGATGG GGACACACAA CCCCTGGATA TGTTTCATTG TCAGATTTTG TGCTGNNATT 60  
 TTAAGAATGG AATGGTGGGT ATCTTTCCTT TTTTAAATG TATCTTAACT GTTGCCTGTC 120  
 AGTGNNNACA AACTAGTGCG TTGACGGCAC CGTGTCCAAG TTTTAGAAC CCTTGTTAGC 180  
 CAGACCGAGG TGTCTGGTC ACCGTTTCAC CATCATGCTT TGATGTTCCC CTGTCTTTCC 240  
 CTCTTCTGCT CTCAAGAGCA AAGGTTAATT TAAGGACAAA GATGAAGTCA CTGTAAACTA 300  
 ATCTGTCATN GTTTTACCT NCCTTTTCTT NTTTNAGNGC AGAGGTAAA AGTAAGTATN 360  
 AAGCACCCGT GAAA 374

SEQ ID NO:4805  
 SEQUENCE LENGTH:123  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05711

SEQUENCE DESCRIPTION:  
 GATCTGACTG TGGAACATC CTCTCACTTG CATTCTTTTA ACTTAAACT ATTTAAGAAC 60  
 TGATGTTCCG ATTATTGTAT ATATTNNCT AAAANCCAAA TAAAGCTACC TATGAAATG 120  
 AAA 123

SEQ ID NO:4806  
 SEQUENCE LENGTH:299  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05714

SEQUENCE DESCRIPTION:  
 GATCAAACAG GAAATTGAAA GCCACTGNAA CTATGCAGCA TTTCAGTTTT CATTAAACA 60  
 CTTAGTTCAG AAACCTTAAA GGATTTGANT ATTTCAAATT GCACACGTCA CTCCAGCATC 120  
 TCTGTAANAT AATTGGAATG AANATACTTC TTGCACTTAA AACTGCACA TGCCGTNCTT 180  
 TGCGGTTNGT CTGCATCTTG AACTTTAATA CCAANTNNT TTTGCATGCT TTTGTTTCTT 240  
 ACGNGATAAT GGATGGTTT CATATGTNAC TACTTTGGAC CAGTGTTC ANNATGGNN 299

SEQ ID NO:4807  
 SEQUENCE LENGTH:204  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05715

SEQUENCE DESCRIPTION:  
 GATCTGGACA AATGACAGTA ACTGTTTCTA ACCTTGATTT TCTCATCTNT AAGATGCCAA 60  
 TTGTAAGTCC TAAGGNTACT GAGGATTTT TAAATGCGT GTACAGTTCC TGACCAAGTGG 120  
 TTTGTGCTA ATAAGTATT ACAAATNATT ACCNAGTAAA ANCCTTGCAG CANGTGTGAN 180  
 AACGTAAAGC TANTTAATCC ATNN 204

SEQ ID NO:4808  
 SEQUENCE LENGTH:348  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS05716

SEQUENCE DESCRIPTION:

5 GATCAAGCGA CCTTGAGAGC AGAGNACAAA TCCCAGTGTT GCTGATATAT GGCTTCTNCT 60  
 TCTCTTGTGT GTGCCTCAGC TCTGAAGNAG TTCCTGAGAA TGGGTACAG ATGTCATGTT 120  
 AGCTGGGAGT CTTCCACAT GTGGCACTTC AAAAGGCAGC ACCACTGGGC GCCTGCACTT 180  
 ATTTGAAAAT GGNACTTTGG GNGAAGTATC CCTGCTAGTG GCTCTGTAAC TTAACAGATG 240  
 TCANTTAGGC TTTTGTCAAT GTTGCCATCA TATNNANGCT AATGTNTACA TCCTTTTAAA 300  
 10 CANNTTGNGT ATGACAATTN CCTCAGGATT TNGGGTAAGN CTTCCCAN 348

SEQ ID NO:4809

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05718

SEQUENCE DESCRIPTION:

20 GATCCTCCTG CAGACCACGC CCGTCCTGCC TGTGGCGCCG TCTCCAGGGG CTGCTTCCTC 60  
 CTGGAAATTG ACGAGGGGTG TCTTGGGCAG AGCTGGCTCT GAGCGCTCC ATCCAAGGCC 120  
 AGGTTCTCCG TTAGCTCCTA TGGCCCCACC CTGGGCCCTG GGCTGGAATC AGGAATATTT 180  
 TCCAAAGAGT GATAGTCTTT TGCTTTTGGC AAAACTCTAC TTAATCCAAT GGGTTTTTCC 240  
 CTGTACAGTA GATTTTCCAA ATGTAATAAA CTTTANTATA NAGTAAA 287

SEQ ID NO:4810

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05719

SEQUENCE DESCRIPTION:

30 GATCACCACC CCGAGCCCTC TNATCCTCTA TGGNTTCACT CCCATCATGA TTTGGAATTA 60  
 TTTATTTGTG AACTTGATTA GCCGAGATTG TAAATNACAT GAGGTCAGGG ACTGGACTGG 120  
 35 GTATGTTTTT TTTCTGTTG CTTTCTGGC ATGAAGTACA GTAAATACAG CACCTGATAC 180  
 ATTATACATG GCCACAAATA TTTGTTGAAT GAATGANTAA AAGCACATTG GGTCTGACC 240  
 ATTCAGTGTC CCTGNAANGA ATGCAGTTTT TCAAACCTGT GCNTCACCAT CCATTAGCGG 300  
 GNGTGTGAAT CCAATTTAGG TNGGTGATGT CTAGCATTNN AN 342

SEQ ID NO:4811

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05720

SEQUENCE DESCRIPTION:

45 GATCATTAAAC CAGAGTACCT CTACTCTTAG CAAACTCTAG TTTATGACAA GTATTTAAAA 60  
 TATTTAAAAC AAGCTTATGC AGTTCTTAAG GNCGNAGGTA AATGAGATGT ANCTTAAAAA 120  
 TAGTATTGGG AAAATGTTGA TAGTTAACAT TAGTGGATTT AGACTAGCCA AATGACATAG 180  
 50 TAGGCTCTGA AACATCTTGT CAAGTNTATG TTTTTGTGC ATGANTTTTT GCTGGAAAGC 240  
 TGTCTTTCTC TGAAAAACAC ANCGTTCTTA GACTGNNANG CCANTTATAA CNTAANN CN 299



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SEQ ID NO:4812

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05721

SEQUENCE DESCRIPTION:

GATCTTNATG CCCAACATTG GTTATGGAAG CAACAAAAA ACAAAGCACA TGCTGCCAG 60  
TGGCTTCCGG AAGTNCCTGG TCCACAACGT CAAGGAGCTG GAAGTGCTGC TGATGTGCAA 120  
CAAATCTTAC TGTGCCGAGA TTGCTCACA TNTTNNGNTC CAAGANCCGC AAAGCCATCG 180  
TGGAAAGAGC TGCCCAACTG GCCATCAGAG TCACCAACCC CAATGCCAGG CTGCGCAGTG 240  
AAGAAAATGA GTAGGCAGCT CATGTGCACG TTTTCTGTTT AANTAANTGT AAAANCTGCC 300  
ANANAAANTN 310

SEQ ID NO:4813

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05722

SEQUENCE DESCRIPTION:

GATCCCTTTT CTTTGTATGG ACCAGAAATN ATGGGTGTA CAGGGTGCCA GATAGATTGG 60  
AAA 63

SEQ ID NO:4814

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05723

SEQUENCE DESCRIPTION:

GATCCAGTG CTCTACTGGG GGATGAGAGA AAGGCATTTT ATAGCCTGGG CATAAGTGAA 60  
ATCAGCAGAG CTCTGGGTGG ATGTGTAGAA GGCACCTCAA AATGCATAAN CCTGTTACAA 120  
TGTTAAA 127

SEQ ID NO:4815

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05724

SEQUENCE DESCRIPTION:

GATCGAATAC AGATGACCCT GCTGTCGTGT CTTTATTTGT AAAATNCTCC TACAAATGGA 60  
GACATTGAAG GATTATGTGT ATGAAAATNT TTACAAAATT CCTTTCTGTA CCTATTCTGT 120  
AGATGCCTGT ATAATCGGNC TGGATGTACA GCTATAAATG TGTTGTGAGA GCAAGAGAGA 180  
GAGAATGGGT AGAGCCTGCT GTACCTTTT CCTTTTAAAT TCTTCGAGTT GGTAAATGAG 240  
TAAGATATTG GAAACCTTAA TGNAAAGCTG CTGTTTCATGN TTTGTGTGTA TAGTGAGCTG 300  
CCTGTAGTAT TTNCTATTG TCTGNTAAAA AAAGNAAANC CTGTAAACN 350

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SEQ ID NO:4816

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05725

SEQUENCE DESCRIPTION:

GATCTTGAAC AAAGNCACTT AGTTNCCCTG GGCCTTGGTG TCTTTCGTCT ATAAAATATT 60  
GTACCAGATT ATCTCTGAAA TCACTNCAAG GTTTAATATA TATANTTATC AATATTTTAA 120  
AATTCAAGCA ATATTCACCT TAGANATTAT TATAACATTC TATANTNGTN GGGGGGGN 178

SEQ ID NO:4817

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05726

SEQUENCE DESCRIPTION:

GATCGAATCG GGACATNATG GGAGCTGACA AATTTATATT CTNTTCAAT NATTTTAATC 60  
CCACTTCACT GTGAGGGGAA GGCCTTTTCA CGGGAACCTCT CCAAATATTA TTCAAGTGCC 120  
AAA 123

SEQ ID NO:4818

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05727

SEQUENCE DESCRIPTION:

GATCCCAAAT TTGTCCATAG CTGAAGTCCA CCATAAAGTG GATTTACTTT TTTTCTTTAA 60  
A 61

SEQ ID NO:4819

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05729

SEQUENCE DESCRIPTION:

GATCTATAGA ATTAGATTN NTTATATCTA AAGAAATATA TATAAATACA TAAACGTAGG 60  
TATGTATAGC ATGANCAGAA TACAGTGCTA TTTGACCATT GTCACAAGAC TTATTTATAA 120  
AACCTCCTCA AGCTCTTGCC AATATCTTAG TTAAGNTTGC ATCTAAGGTG GCGGGNGGAT 180  
GNNGATTGAG GCACTGTCAG GTCATGNTTG ATTACCTGGG TGACAAANATT ATGTTTACAC 240  
CAAACCCCA TGNCACACAG TTTACCCATG TGACANNACN TNCACATGTC CN 292

SEQ ID NO:4820

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS05730

SEQUENCE DESCRIPTION:

5 GATCCCCCAT ATACTCTGCT ACAGCTCCTA TCATGAAAAA TAAAATGTTT GTCTTTGCAA 60  
A 61

SEQ ID NO:4821

10 SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05731

SEQUENCE DESCRIPTION:

15 GATCCGNTGG GGTGAAAGCA GCCAGCTCAT CCCAGTAACT CACAGGACAC AGCCATCCAG 60  
CGGCATCTTT CCTTGTGCGAA TGATACTGTA ATNACCTTCC AAAGTNAAGA GTAGCACATT 120  
AAAGTNATTT TATTGTTAAA 140

20 SEQ ID NO:4822

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05732

25 SEQUENCE DESCRIPTION:  
GATCTCAATG CTGTCTGGGG ACCCTAAGAG TTNCTNACC TGTNCAGTCT CATCTAACCT 60  
TCCAATGTCT GATGTTCTCTG CCAAATTCCT GCCTGATTCT GGGTCCGTCC TGACCTCCAA 120  
AGGTCAGCTT GGTGCTTGAG GTCTCCCTGC TCTTGGTGGC AGTGGTAGCA GCAACAGCAG 180  
30 CAGCAGCAGC AGCAGCAGCA GCAGCGNCCT CTCCACTTTN CCTTNGCCCN TCTNCTGGGT 240  
AGAGAGGCAC TTTCAGGGAC TTTCTCCAG GNTGGNTCNT CAATATGGGA ATGNGCTNTG 300  
NAAGGNTTN 309

35 SEQ ID NO:4823

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05733

40 SEQUENCE DESCRIPTION:  
GATCCTCCTG GCGGCAGTAG CCTTGACAAG GGCCACCTCT TCACAGGATG CAGTCTGTCT 60  
GTGCACCAAA CTCTTCACCA AATAGAACAC TTGTGTCTCT CTGTGGAAA 109

45 SEQ ID NO:4824

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05734

50 SEQUENCE DESCRIPTION:  
GATCCATTG GNAGGAAATG AGAGGGCTGT NATCAGCTCT NATTAAGAAA GGAGATTCT 60

55

TCATGCTTTC GATTCTGCAT GGGGTACAGC CAGTCACCTC ACCAGAGANT GACGGCTGGA 120  
GAAGTNAACT CTGTAATACC ATAAATAAGA GTGCTTGTA TAAAAGNCTG TGCACANGGA 180  
TTAATATTTT CCNTCTTAAG TATCAAACGA CCTCTGGANC AAATTNTACC NTN 233

SEQ ID NO:4825

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05735

SEQUENCE DESCRIPTION:

GATCTGACGT TTTCTACGTA GCTTTTGTAT TTNTTTTTTT TTAAANTTG AAGGACCACT 60  
GATGAAGCCC TNCCANACCC CTCCGGGTC TAANAAAACG TN 102

SEQ ID NO:4826

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05736

SEQUENCE DESCRIPTION:

GATCAAGAAA TNTCTCTNCT CCTACATCCA GCTCCTCTAG GGGCAGCCTC CGTCATCCAT 60  
GCCCTCCAG GACCTCCAC TCACTGCTGT GAGTGCCT CACCAGAACC AGTTAAGAGA 120  
CAACTATCAA TTNNGGGGAC CCAAATTATA AGGGCCCTGN CCTGTACTGA AGNAAAGGGG 180  
NGCACAAGGC CTTAATGGAC ATTGNCTTGT GAAAACGCAN ACATGAATAT GGTGGAGAG 240  
CNTGGCTTAG GAGGGTGTCA TGGGNAGNA GNGGCTN 277

SEQ ID NO:4827

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05738

SEQUENCE DESCRIPTION:

GATCCCCTCT CCTGCCAAG CACTTCACAG CTGGACCCTG CTCACCCTC ACCCCCCTCC 60  
TGGCAATCAA TACAGCTTCA TTATCTGAGT TGCATAAA 98

SEQ ID NO:4828

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05741

SEQUENCE DESCRIPTION:

GATCTGGGAT TTTNTTTT TTTTGAAATG GGAGCTTTTT TGTTTACAAG TTCATTAAAA 60  
ACTAAAAACT GTTCTGTAA A 81

SEQ ID NO:4829

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05742

SEQUENCE DESCRIPTION:

GATCGATTC TTTCTCCAG GTAGAGTTT CTTTGCTTAT GTTGAATTCC ATTGCCTCTT 60  
TTCTCATCAC AGAAGTGATG TTGGAATCGT TTCTTTTGT TGTCTGATTT ATGGTTTTTT 120  
TTAAGTATAA ACAAAGTTT TTAATTAGCA TTCTGAAAGA NGGAAAGTAA AATGTACANG 180  
TTTANTAAAA NGGGGCCTTC CCCTTTAGAC TAANTTTCAG CATGTGCTTT CAAA 234

SEQ ID NO:4830

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05743

SEQUENCE DESCRIPTION:

GATCCACCCA CCTCAGCCTC CCAAAGTNCT GGGATTACAG NCATGAGCCA CCATGCTCAG 60  
NCGTGTGTGT NTGTGTGTAT TATTTATATG TATATGCATA CTATATACAT NTATATATAC 120  
ACTATATAAA 130

SEQ ID NO:4831

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05747

SEQUENCE DESCRIPTION:

GATCTTTAAT CAAGCACTAT GTTAATACTG TAATATCAGA ATACTATGTT GCATTATTTA 60  
AAATGTTCAA ATTGAATAGN TTAAAANGTT TTAAATNCT AAA 103

SEQ ID NO:4832

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05748

SEQUENCE DESCRIPTION:

GATCCTTGGT GCTGTGTGCC CCACTCCAGT CTGGGGACCC CACTTCANAA GGTAGGGGCC 60  
GTGTCCCGCG GTGCTGACTG AGGCCTGCTT CCCCTCCCC CTNCTGCTGT GCTGGAATTC 120  
CACAGGGACC AGGGCCACCG CAGNGGACTG TNTCAGAAGA CTTGATTTT CCGTCCCTTT 180  
TTCTCCACAC TCCACTGACA AACGTCCCCA GCGGTTTCCA CTTGTGGGCT TNAGGTGTTT 240  
TCAAGCACAA CCNACCACAA CAAGCAAGTG NATTTTAAGG GGGTTGTGCT TTTTGTGTTN 300  
GTGCTAACGT CTNACTAATT TTAAN 325

SEQ ID NO:4833

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05749

SEQUENCE DESCRIPTION:

GATCTGAAGA GAAGCCAGAG TATAATTNC TACTATTTTC AATACAAAGN TGTGTTTTCA 60  
 TTACAATTAG NGGAATATAG GCTTCTGTGA GCTAGCCTGG AAGCAAACAT AATCATTATT 120  
 GTNCATTGTT TCTGTNGAN ACTGTAATGC TGTTTCTAAA TATTGACCTA ACANTAAACT 180  
 CTGNNGGAATT CATGCTTGTN ACTGGNTGGA AN 212

SEQ ID NO:4834

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05751

SEQUENCE DESCRIPTION:

GATCTGGCCT TATGCCCAGG CCTGGGCCCT CAGAAAGTAA GAGCTCTGGG AAAGAACCCA 60  
 AGGAGTTGGG GGAAGGAGAG AGCCCCAAAT AAACACAACC TGAGACCCA AAGTTTTAAG 120  
 GTGNAAAANG NACCAAAGAC CAGNCACAGT GGCTTCCGCC TGTAATCCA NCATTTTGGG 180  
 NGGCCAAGGC GGGAGGACTG CTTGAGGCCA GAAGTTGGNG ACCATGCCTG GGCANCGTGG 240  
 NCACCTCATT TTTACTACAA ATNAAANAAN CTTGCTGNG TAAA 284

SEQ ID NO:4835

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05752

SEQUENCE DESCRIPTION:

GATCCTACTG ATGAAATCC CACTAAAAAG TCAAAGAAGC ATAAAAAGCA CAAAAACAAA 60

SEQ ID NO:4836

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05754

SEQUENCE DESCRIPTION:

GATCAAAAAA TTGAATGATA AATATGAATG GCTTTTCAAT TCTGTGGACT TTGTACCATT 60  
 TGGCTTCACC TTGTACTGCA AGATGAATTT GTAAACAAAA CAAAATTGGN CTGTCTGGAA 120  
 AGCTAAAGTN CTGAAATATG GAAA 144

SEQ ID NO:4837

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05755

SEQUENCE DESCRIPTION:

GATCACAATG ANGGCCAAGC TTGCNCGCNT AGAGGCCAG GAGCAGGCCT TCCTGGCTCG 60  
 TTTCAAAGGC CAGGACCCTG GGGCCCCTCA ACTGCAGTCA GAGAGCAAAG CCCTTAATAA 120

ATATTTNACA TCCTTAAA

138

SEQ ID NO:4838

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05756

SEQUENCE DESCRIPTION:

GATCTTGTTT ACATCTTGCT CACTGCTATA TTCTCATTGC TGAGCACACA GTTGCAGCTC 60  
 AATAAATTTT GAATGAACTC CAAA 84

SEQ ID NO:4839

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05757

SEQUENCE DESCRIPTION:

GATCACCTNA TGGATGTCGC AATAATACAA ACCAGTGTAC CNCTGACCTN NTCATCAAGA 60  
 GAGCTGGGGT GCTTTGAAGA TAATCCCTAC CCCNCTCCCC CAAATGCAGC TGAN 114

SEQ ID NO:4840

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05758

SEQUENCE DESCRIPTION:

GATCTGCACT ATNAACITTTG TGAAGAGTTT CTCCTAAAAA CTTTAAGTAA AATGTTAATG 60  
 GTAGCTTTGA TAACATCAAA TTCTAAGGGA GAAAAAACA ATATTAAACC GCCCAAGCAG 120  
 TGTGCCCTAG CAGAGGAAAA TGCAACATCT CGCAAGCGCT GCTGTAACGC CTTCAGGAGT 180  
 CACTGATTCA GCACTAGTTT CCGGCTGTGA AAATCATCT TTCATTTTNN CCGTGGNTNG 240  
 GCGCTTTTNT TANTNGTNGT CCTAATGANA TTTCTGNCAT TGTCATATAC AANCNTGAA 300  
 TATCATTAAT ANTTTTTNAN TNN 323

SEQ ID NO:4841

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05759

SEQUENCE DESCRIPTION:

GATCAAAAAA ACGTTCTTTG AAGAGCTGGC AGTAGAAGAT AAACAGGCTG GGGAAGAAGA 60  
 GAAAGTNCTC AAGNGGANGG AGCAGCAGCA GCAGCAACAG CAACAGCAGC AGCAANANAN 120  
 N 121

SEQ ID NO:4842

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05763

SEQUENCE DESCRIPTION:

GATCTTCACC AGCTGCTCGT GGTGGCTCGG TGTCTGTCTC TCAGTGCTGG TCAGACAACG 60  
 CTGTCAAGAG ANCGATGGCT GAGAGCAAAG CAGCTAGAGT CTTTAAGAAG AACGAGGCTT 120  
 CAGCAGCAAA AATGTGTGAA TGGAAATNAA CTTTAAAGAT GTAATACCTA TGAAGAGTAA 180  
 TGGGCAAACT GTAGCCACAT AATTGTAAAA TTCAGATATT CATTTATACC ACATTGTTTT 240  
 ATAGGTAATT TCTATCACA ACCAGTGACA TTCCTGAAA TCANGCCTGG TAACACCTGA 300  
 TGTTTATATG ATATTCAGTA AGGACTTTTA CCTTACTGAT TTCATGGNGN N 351

SEQ ID NO:4843

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05765

SEQUENCE DESCRIPTION:

GATCTGAATT TCCCCATGCT TCCTGGTTTT NATATGTTTC TTGACAAATA AAGCTGATTT 60  
 AAATCTCTAA A 71

SEQ ID NO:4844

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05767

SEQUENCE DESCRIPTION:

GATCTTTTTT TTTATCTCCC TTCCCCTTCC TAAGTCCCAT TTCTTGGTCA TAAATATTGC 60  
 ATTATTCACA CTTTCAAAC GTGTATTTTC TTACAATAAA AAATGATGAA A 111

SEQ ID NO:4845

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05768

SEQUENCE DESCRIPTION:

GATCTCACCA CCCACCTGGC CTCGCAGGGC GTTCATCTCC TCCTCGTGGT TCTTCTTCAG 60  
 GTAGGCCAGC TCCTCCTTGA GGTTCCTCAAT CTGCATCTCC AGGTCGGCTC TGGCCAGGGT 120  
 CAGCTCATCC AGCACCTGC TTCAGTCCCT TCCCATGCT TCCTTGCCTG ATGACAATAA 180  
 AGCTTGTTGA CTCAGCTATA AA 202

SEQ ID NO:4846

SEQUENCE LENGTH:262

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05769



## SEQUENCE DESCRIPTION:

GATCANAACC CTAGCGCCTT TGGTCCTAAG AATGGNAGGC TGCCTTCNT CCCAATCTCC 60  
 CTGCCAGGGC CCACAGCGTG GCCCTAGCCC TCCCCTCCCC GGAATGTAGA ACGGGGACCC 120  
 TCGCAGGGTT GGGGCGGGG CTGATACTCC TNGGNCCCTC CCTACCCTGC CCTGTGTGTT 180  
 GGCTTTNTGG CCGTCCAAGT GCCAATTGGG TTTTNGCCCA AATAAGGGCT GGTATTTNTN 240  
 CTNTGTNCTT GGAGGTGNGN TN 262

SEQ ID NO:4847

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05770

## SEQUENCE DESCRIPTION:

GATCTGTATG TNAGGCACCC ATAACAGTAG TTTCCCTGT NAGTCGTCTT CACACATGCT 60  
 GTTTTCTCTG CCTGGCTCTC TCTTCCCCTC CTTACCTGGC CAGTCCTGTT TATCATCAGG 120  
 CCTTGTNTTG GATATNACGT CCTCTGGGAA GTCTTCTGGG NCCCTCTAAC CTAGGACCCT 180  
 CATTACCGGN TCTCATAGNA CAGTCTACTG NTTTGTACGG AATTCTAAGT ATTCNNGTG 240  
 GNACTNAAATN 250

SEQ ID NO:4848

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05772

## SEQUENCE DESCRIPTION:

GATCATTCTT CAATTAGGAC ACAAACCAGA CAGGTTTAAT AGCGAATCTA ATTTTNAATT 60  
 CTGACCATGG ATACCCATCA CTTTGGCATT CAGTGCTACA TGTGTATTTN ATATAAAANT 120  
 CCCATTTCTT GANGATAAAA AAATTGTNAT TCAAATTGTT ATGCACAGAA TGTTTTTGGT 180  
 AATATTAATT TCCACTAAAA ANTAAANTGT NTTTTAAGGG ANNNGAN 227

SEQ ID NO:4849

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05773

## SEQUENCE DESCRIPTION:

GATCTAAATA TAAGAGCAAA AACCATAAAG CATCTAAAAG TAATTGAAGG AGAAAATCTT 60  
 AGTGCCTTTT GTNCTGGCCA AGATTTTTTA AAGAGGACAT AGAAGTCAGG AACTATAAAA 120  
 GAAACAATTT TAAATTTTNC TTTATCAAAA TAAAAGCCA TAGACCGGGA TAANNCATTT 180  
 GCAANATATA TNTCTGACAA AGTTCTTGAN TCAAGANTAT GTAANANCNG N 231

SEQ ID NO:4850

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS05774

SEQUENCE DESCRIPTION:

GATCAGCCTG AACAAACATAA TAAGACCCTG TCTCAACAAA AAATACAAAA ATTAGCTGGG 60  
TGTGGTGGCA TATGCCTGTA GTCCCAGCTA TTCAGGAAGC TCCATTGCAA TCTAGCCCGG 120  
GTGACAAA 128

SEQ ID NO:4851

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05775

SEQUENCE DESCRIPTION:

GATCCTTCCT TCAACCCCAA GGCCAGCTCC CATCTCATTT CCAGAAAGGC TCATACCTGG 60  
CTTGCAAGGA AGCATCTGTC TTGTCAATCC AGGTGCCAGA ATCCTCTCAG AGTCATTGAA 120  
GGGTGTTTAC CCATCCCACC CAAGGCTTGG CACACTGCCA GTNTCTTAGC AGGGTCTTGT 180  
GAGGGCTGGG GGCATCCAGG CACTCAGAAG GCAAAGGAAC CACCCTACCC ATTTGGCCTC 240  
TGGAGGGGGC AGAAGAAAGA AAGAAACCTC ATCCTATATT TTNCAAAGCA TGGGGGTTCT 300  
NGCATTTAGC TCTGGNGGGT GANCCANTGT GCTTNTTGN TTAAGTGTGN 350

SEQ ID NO:4852

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05776

SEQUENCE DESCRIPTION:

GATCTCAGTT TCCCTCACTC AGGAACTCTG TTTCTAAAGT CTTCAAGTTAA GTTNAGTTT 60  
ATNACTGAGT GGCCTGTACT GTCAGACGTG AATGGGCCTG ACGGGCAAAT CCATCCCTCT 120  
CTCCCTCACA GTTCCAGGAG CGGCTTCCCT CGTCTCCCCT TACTCCACAG GGAGCCTCCC 180  
TTGCCAGGAC CAGGGCTGCG ACGGCCATGC TGGGGCAGGT GAGTGCTCTG TTAGTGCTC 240  
CCAGTGCTGT CCNCAAGGCTG CAGTTCTGGT CCNNGGGGTG TNAGGGTAGG GAAGGGTGCA 300  
CTTGAAGGAN GGTGGTTCAA TTTGGGNTN CCTTAACGTT TATAGTCTNN ACAAN 355

SEQ ID NO:4853

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05777

SEQUENCE DESCRIPTION:

GATCCAGGAG TTTAAGGTGA CAGTGAGCTA TGACCGCTAC TNCACCTCCAG CCCAGNCAAC 60  
AGAACAAGAC CCTGTTTCAA A 81

SEQ ID NO:4854

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS05778

SEQUENCE DESCRIPTION:

GATCCTCCGT AACATTNCNA GACCAGANAG AACATCCAGA AATCCCTGGN TGGAAGCTCA 60  
GGCCCCGGGG CCTCCAGCGG CACCAGCGGA GACCACGGTN AGCTCGTCGT CCGGATTGCN 120  
ACGATTAAAG ACTGAN 136

SEQ ID NO:4855

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05779

SEQUENCE DESCRIPTION:

GATCAAATAT TTTTNATTAA CCTATATAAA GAATTTGACT GCTTATGATT CAATACATAT 60  
GATTTAATAA AATAGATTGC ATTTTNNAAA ATAAAGAATG ATTNGAAA 108

SEQ ID NO:4856

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05780

SEQUENCE DESCRIPTION:

GATCAACCTC TGATTTTACA TCATGATGTA ATCACCCTG GAGCTTCACT GTTACTAAAT 60  
NATTAATTC TTGCCTCCAG TGTCTATCT CTGAGGCTGA GCATTATAAG AAAATNACCT 120  
CTGCTCCTTT NCATTGCAGA AAATTGCCAG GGGCTTATTT CAGAACAAC TCCACTTACT 180  
TNCCACTGGC TCTNAACTC TCTAACTTAT ANGTTGTTGGT GAACCCNCAC CCAGGCAGTT 240  
ATCCATGAAA GNACAAGTGG ACTAGTNCTA TGNNGTACAA AGGCCTGTAT CNTCTTGTTG 300  
ATGGATTTCC TGGTGCTCTT NGCTTGTTTG CAAGTTGCTT AANTTAAAGG CAGNTNTTTN 360  
TN 362

SEQ ID NO:4857

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05781

SEQUENCE DESCRIPTION:

GATCCTACCG GAAACCAACC TGTTTACTGT ACTGTTGTAA ATATCATGCC CTTTATATCC 60  
TGTATATTGG CTTCTTTTAA ATAAAGTGAA ATGTCTTAGA AA 102

SEQ ID NO:4858

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05782

SEQUENCE DESCRIPTION:

GATCTAAACT TTATGCTGCA TAAATCACTT ATCGGAAATN CACATTTTAT AGTGTGAAGC 60

ACTCAANNNTN TAAACCTTAT TATCTAAGGT AATATATGCA CCTTTCAGAA ATTTNTTTTC 120  
GAGTAAGTAA AGCATATTAG AATAATTGTG GGTTGACAGA TTTTAAAAAT AGANTTTAGA 180  
GTATTTGGGG TTTTN 195

SEQ ID NO:4859

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05783

SEQUENCE DESCRIPTION:

GATCCCTTTG AAATNTTTT TTTGTTTGT TGTTTAAATC AAGCCTGAGG CTGGTGAACA 60  
GTAGCTACAC ACCCATATTG TGTGTTCTGT GAATGCTAGC TCTCTNGAAT TTGGATATTG 120  
GTTATTTTTT ATAGAGTGTA AACCAAGTTT TATATTCTGC AATGCGANCA GGTACCTATC 180  
TGTTTCTAAA TAAANCTGTT TACATTCAAA 210

SEQ ID NO:4860

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05784

SEQUENCE DESCRIPTION:

GATCTTTGTT TGTCTGAACA GGTATTTTAA TACATGCTTT TTGTAAACCA AAAACTTTTA 60  
AATTTCTTCA GGTTTTCTAA CATGCTTACC ACTGGGCTAC TGTAATGNG AAAAGNATAA 120  
ANTTATTAA TGTTTAAA 139

SEQ ID NO:4861

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05785

SEQUENCE DESCRIPTION:

GATCCTGAAA GAATAATTGG TGCCACAGAC AGCAGTGGAG AATTGATGTT TCTCATGAAA 60  
TGGAAGNTT CAGATGNNGC AGACTTGGTG CTGGCGAAAG AGGCAAATAT GANGTGCCT 120  
CAAATTGTAA TTGCTTTTAA TGNNNGNGNGN 150

SEQ ID NO:4862

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05787

SEQUENCE DESCRIPTION:

GATCGCAGAT TTNTNTAGAA ACACGGATGT NCATGTCCAG ATTCCCTTTT NCAGGTATTA 60  
AAAATAATTA AAAATAGTCC TGCCTGAGGT TGCAGTGAGC CGAGCTTGCA-CTACTGCACT 120  
CCAGCCTGGG TGACAGAGTA AGACTCCATG TCAA 155

SEQ ID NO:4863

SEQUENCE LENGTH:262

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05789

SEQUENCE DESCRIPTION:

GATCTGTACA ACTGATTTTA AAAAAATGCT AAAAAAGCC CCAAAGCATA TAATCTCTAC 60  
TCCTTACAGT CTCTAGAATT AAATGTACTC ATTTAGACAA CATATTAAAT GCATATTNA 120  
GCCACTTAG AGAAACCTCA TAGGCACAGA GTTCCAAGN TTAATTTTAA GNATATCTTC 180  
ACGAACTGA CCCTCCTACT CCACATTGCA NCATTTCCNT CAGNCAGCAT TTNAATTCCN 240  
GTATTATGTN TNTNGCAANT NN 262

SEQ ID NO:4864

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05790

SEQUENCE DESCRIPTION:

GATCAAGAAG GCCACTGGTG TGCAGGTGTN AGGCTCCTAC AGGCCCACTC TCTTCAGCAG 60  
CCACCCGGCC CTCCTCCAG CACCCGTTTT AATCCACAG AACAACGGGA ACGTTACTGA 120  
CTCTGGTGCC TTATCTCGAA GGGACCAGAA GTGCTGCGTG TTCAGGCCAT CNNTGGCTGT 180  
NTTCTGTCT CTCCTGTCTG TCCACCTACT ACTNNTNCT NTACTTTANC NN 232

SEQ ID NO:4865

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05792

SEQUENCE DESCRIPTION:

GATCAGAGCC GACACCAGAC GTGATTAGCA GCGGCACAA ATTC AATTTG TTAAATGAAA 60  
TTGTATTTTG CCCAAA 76

SEQ ID NO:4866

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05793

SEQUENCE DESCRIPTION:

GATCTCTTGG GCCCAGGACT GTTGATGCCT TTNAGTTTTG TATTCAATAA ACTTTTTTTG 60  
TCTGTTGATA ATATTTTAAA 80

SEQ ID NO:4867

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05794

SEQUENCE DESCRIPTION:

5 GATCCATGCA TTATTTTCCT AGCTTCCTGC CTTGCTCCCT ATTCACTTTA CACTGTGAAA 60  
GGTGGGGGGT GAGTCCCACT TGAGCGCTTC CTGTTGAATA AAGCAGGCAC TTGACCTGGC 120  
TGTAGCCTAG GTCTTGAGTG AACCCCAA 149

SEQ ID NO:4868

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05795

SEQUENCE DESCRIPTION:

15 GATCATGTCT GTACATTGTG TAATGAATGA AAAGCACATA AATNTAATCT ACTTTGAACT 60  
TTGTAAAAAT AATGTGTGGA GGCTATTCTT GTTTCTCCAT CTCAAGTCCT GTGTGTGCAC 120  
GTGTGTGCAA GTGCACATGT GTGTGTGTAA TAACACATTG TAAAGANCAG AAATNACTTT 180  
AAAAAATAAA CAGAAATGGA GACCTGAAA 209

SEQ ID NO:4869

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05796

SEQUENCE DESCRIPTION:

30 GATCCGNCCA CCTTGACCTC TCAAAGTGCT GGGATTACAG GCATGAGCCA TCACGCCCGG 60  
CCACGCTGTT GGTTCCTAAT GACACAGCTT ANCTTTATTG TGAAAAGATT GCAGCAACAA 120  
ATGAGATTTT ACCTGTATTT GTTAAAAATG CTTATCCTTG TCTAAGACTG GCAACATAAG 180  
CAGTTCTTNG GCTTCTATGC CAATGGNCAC TAGGCAGTAA TACATGTGCA GTGCTANATA 240  
GAAAATATTG GAGTNAGGGT GTACTNAGGG AAGTTCTCAA TCTTNNCCCT NTCANTNTCT 300  
TCTGTAATAG TAACCTTNAA TAACATGNNG ATTEN 335

SEQ ID NO:4870

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05797

SEQUENCE DESCRIPTION:

45 GATCTTTCTG CAGGAAATAG TCACTCATCC CACTCCACAT AAGGGGTTTA GTAAGAGAAG 60  
TCTGTCTGTC TGATGATGGA TAGGGGGCAA ATCTTTTCC CTTTCTGTT AATAGTCATC 120  
ACATTTCTAT GCCAAACAGG AACAATCCAT AACTTTAGTC TTAATGTACA CATTGCATTT 180  
TGATAAAATT AATTTTGTG TTTCAAA 207

SEQ ID NO:4871

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05798

SEQUENCE DESCRIPTION:

GATCTGTCAC GGAAGGCGTC CTTTTTCCTT GTAGCTAACG TTAGGCCTGA GTAGCTCCCC 60  
 TCCATCCTTG TAGACGCTNC AGTCCCTACT ACTGTGACGG CATTTCCATC CCTCCCCTGC 120  
 CCGGGAAGGG ACCTTGACAGG GACCTCTCCC TCCAAAAAAA GAAAAAAGA AAAAGANAGA 180  
 AAAANTAAAT GAGGAAACGT GTTNCAAA 208

SEQ ID NO:4872

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05799

SEQUENCE DESCRIPTION:

GATCAGACCA TAATGTTACA TTATTATCAA CAATAGTGAT TGATAGAGTG TTATCAGTCA 60  
 TAACTAAATA AAGCTTGCAA CAAA 84

SEQ ID NO:4873

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05801

SEQUENCE DESCRIPTION:

GATCCTGGCC GAGGTGAGGA ACAGACAGGG GGGGTCTAGA TTCTAAGGGG GTTGGTGGAT 60  
 ATGGGGCAAG GCAGGAAACC TCTGGAGACC TCATTTTCTC CATGGGGAAG ACAGCCATGC 120  
 TCTTCAGGAG GAGACTCCAA GGGCAAAGNA GGGTGTCTTG GCTGTNCTTG AAGGCGAAAC 180  
 CCTGCCATAT CCCAGTGCC AGTCCCCTCA GNCTGTGGTG GCCTTGCATC CTGACTGGAT 240  
 GTTCTCAGCC CNTTGTCTG GGCAAGAACC CAGAGCTCCC CAGTNTGGAT ACTTATTA 300  
 CCTNTTTGGA GNCNCAAATA NAAAAAANA AANNAGN 337

SEQ ID NO:4874

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05804

SEQUENCE DESCRIPTION:

GATCCAGGGG CTGATTGGCA GCGTGGAGGA GCAGCTGGCC CAGCTTCGCT GCGAGATGGA 60  
 GCAGCAGAAC CAGGAATACA AAATCCTGCT GGATGTGAAG ACGCGGCTGG AGCAGGAGAT 120  
 TGCCACCTAC CGCCGGCTGC TGGAGGGAGA GGATGCCAC CTGANTCAGT ACAAGAAAGA 180  
 ACCGGTGACC ACCCGTNAAG TCGTACCAT TGTGGGAAGA GGTCCAGGAT GGNAAAGGTN 240  
 AATCTTCTTC CGTGNAGCAN GGTNCAACCA GACCAACCGT TTGAGGGACT TANGTTACCN 300  
 NGNGCCGGGC CAACCNAAGG AGGGNNTTN 329

SEQ ID NO:4875

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05807

SEQUENCE DESCRIPTION:

5 GATCACTTGC TTTTATGTCC ACTTTTNNAG TGGTACTTAA ATGTAAAGTA ACAACCTGAA 60  
TTGAGTCATT GCTTTCTGAA GGAATCATTG TCCTTTCTCC AGTTTTTGTN CCAGAATAAA 120  
AGGAAATATT TTTAAAGCCA AA 142

SEQ ID NO:4876

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05808

SEQUENCE DESCRIPTION:

10 GATCCTNCAG CACAGGAATT CTCAAGACCT GAGTATTTTT AATAATAGGA ATGTCCACCA 60  
TGAACCTNAT ACGTCCGTGT GTCCCAGATG CTGTCATTAG TCTATATGGT TCTCCAAGAA 120  
ACTGAATGAA TCCATTGGAG NAGCGGTGGG GNACTAGCCA GACAAAATTT NAGANTACAT 180  
20 AANCAACGCA TTGCCACGGN AACATACAGN GGATGCCCTT TCTGTGATTG GGTGGGATTT 240  
TTTCCCTTTT TATGTGGGAT ATAGTNGTTA CTTGTGACAN GTATAATTTT GGAATAATTN 300  
CTATTAAATA TCANCTCTGA NGTACTNGT N 331

SEQ ID NO:4877

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05810

SEQUENCE DESCRIPTION:

25 GATCATGCCA TTGCACCCCA GCCTGGGCAA CAACTTAACT TTTTGAAC TCTGTCTCAA 60  
A 61

SEQ ID NO:4878

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05813

SEQUENCE DESCRIPTION:

35 GATCCTCTGG ACACGTAACC TATGTCAGNC ACTACATGAT GACTCAAGGC CAATAATAAN 60  
GCCATTTCTT ACCTGCACAA A 81

SEQ ID NO:4879

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05814

SEQUENCE DESCRIPTION:

50 GATCCANAGA GGACCCCCGN CCCAGAGAC TTGGTTTTGG CTCCAGCCTT CCCCTGGCCC 60

55



CGTGACACTC AGGAGTTAAT AAATGCCTTG GAGGAAAACA AA

102

SEQ ID NO:4880

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05815

SEQUENCE DESCRIPTION:

GATCAAAAGG TCTCAGATGA TGATAAAGAA AAGGGAGAGG GAGCTCTTCC AACTGGGAAA 60  
TCCAAA 66

SEQ ID NO:4881

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05816

SEQUENCE DESCRIPTION:

GATCTCTAGA GTCCATTAAA AGCAAGCTAG ATTGAGAGCT CTTGGAGGGC AGGGACTGGG 60  
CCTAGCTCAT GGTTCACAGC TCTTGAGGGT GACTGCACAG TGGACTCAGT CAGTCATGGC 120  
TGAGTTGTGT TGGCTTNATT ATCTCTAGAA TGAGTTCTC CATTCAAATG CAAATCAGCC 180  
TGGNNGGNTC ACCTGTAGTA AAGGGGGTTT CTACCTNGNG GATGGAAANA GNNNTCTTAG 240  
GNACCTTCCT TGGGCTCCA GNACTTATTT TNGATATCCC NTTATGN 287

SEQ ID NO:4882

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05817

SEQUENCE DESCRIPTION:

GATCATACCA TTGCACTCCA GCCTGAGTGA CCTGACTGAG ACTGTCTCAA AAAGNGTAAA 60  
ANATAAAAAT TAAA 74

SEQ ID NO:4883

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05818

SEQUENCE DESCRIPTION:

GATCTNACTC CAGCAGAGTC TGTNCCAATN TGGGGTGAGC AGGGCCCCTG CCATGGAGCA 60  
GCAGGAATTT NAGGGATGGA GCAGGTAAAT GAATGGGAAA CATAAA 106

SEQ ID NO:4884

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS05819

SEQUENCE DESCRIPTION:

5 GATCTTAGTG GTGAAAGTAT GTGTAACCAT GTGATGGTTA AAACANGACT TACAATNCCT 60  
AAATGTGTAA CTGAGAATAA AACGTACTCT NTTAAA 96

SEQ ID NO:4885

SEQUENCE LENGTH:63

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05820

SEQUENCE DESCRIPTION:

15 GATCCNAAGN CTCCGGGCAG CCGTTATCCC GTGGTTTAAT AAAGCTNCCG CGCGCTCACC 60  
AAA 63

SEQ ID NO:4886

SEQUENCE LENGTH:61

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05821

SEQUENCE DESCRIPTION:

25 GATCCTGCTG TGTGTCCTGT TCCATGTTCC GGTTCATCC AAATACACTT TCTGGAACAA 60  
A 61

SEQ ID NO:4887

SEQUENCE LENGTH:274

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05823

SEQUENCE DESCRIPTION:

35 GATCTCCTTG TCAGGAGCAC CTAAGAACTG GCATGACTCT ACACCCTNTC TCCTTCTNCA 60  
ATGACCTCGT GTCAAGATGG CAGACCTGCA GAGATGAATT TGCCTNGATA CCTGAGTCAC 120  
CAGNGNGGAG GAAACTCCCA TTNGACATGC ATCACACTCC ACATATGAAA CCCTNCTTTT 180  
GCTGCACTGT CACTGGGGGN TAGGGGTAT TACTCACTGC AACTTAGCCT AGCATTAAGT 240  
40 TGNTTTGACT NATNCANGTT TCAGTAAANG TCGN 274

SEQ ID NO:4888

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS05824

SEQUENCE DESCRIPTION:

50 GATCTGTGTT GGTTCCTTAG ATTGCTAGCT TTTCTCCAG GGGACCACAG CAGGTGAAGC 60  
TCAAGAGCGC ATGGCTCTGC TAATAGTAAA TTGTTTTCAG GGCCTTGTCC AGCTGAGAGC 120  
TTTCCATGTCCA CCAGATTCTG AGAGGTGTCA GCAGCACTTT TTTTNTNATT TGTNGTTNGG 180  
TTTCCNCCCG GTTATCGGAC CATGGGCTNA GCTCAGGCAC TTGCTGTAGG AGACTNGNNA 240

55

TTNCTGTAAA GGANNGGTNA TTTANCCN

268

SEQ ID NO:4889

5

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05825

10

SEQUENCE DESCRIPTION:

GATCAAACTT GGTCTGGGTA TTGATGAAGA TGACCCTACT GCTGATGATA CCAGTGCTGC 60

TGTAAGTAA GAAATGCCAC CCCTTGAAGG AGATGACGAC ACATCACGCA TGGAAGAAGT 120

AGACTAATCT CTGGCTGAGG GATGACTTAC CTGTTTCAGTA CTCTACAATT CCTCTGATAA 180

15

TATATTTTCA AGGNTGTTTT TCTTTATTTT TGTNAATATT AAAAAGTCTG TATGGCATGA 240

CAACTACTTT AAGGGGAAGA TAAGATTTTC TGTCTACTAA AGTGATGCTG TGGTACCTTA 300

GGCACTNAAAG CAGNGCTAGT ATN 323

SEQ ID NO:4890

20

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05826

25

SEQUENCE DESCRIPTION:

GATCTAAGAG TATGGCTAAA CATCTATATA TGCAATCTAT TAAAAGAACT TAATTCGGCT 60

ATTAAA 66

SEQ ID NO:4891

30

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05827

35

SEQUENCE DESCRIPTION:

GATCTCTGGA GCTCAAGAGG TTGAGGCTGC AGTGAGCCGA TGTGCCAGTA CACTGCAGCN 60

TNGGTGACAG AGCAAGACCC TGTCTCAAA 89

SEQ ID NO:4892

40

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05829

45

SEQUENCE DESCRIPTION:

GATCGCCACT TACCGCAAGC TGCTGGAGGG CGAGGAATGC AGACTCAGTG GAGAAGGAGT 60

TGGACCAGTC AACATCTCTN TTGTCACAAG CAGTGTTCCT TCTGGATATG GCAGTGGCAG 120

TGGCTATGGC GGTGGCCTCG GTGGAGGTCT TGGCGNCGGC CTCGGTGGAG GNCTTGCCGG 180

50

AGGTAGCAGT GGAAGCTACT ACTCCAGCAG CAGTGGGGGT NTCGGCCTAG TNNNNNGGGC 240

TCAGTGTGGG GTGCTCTTGG CTTCAAGTGA AGCAGTAGCC NGAGGGCTGG GGGTGGNCTT 300

NTGGCANTGG CGGNTNTAGC AGNTCCAGCG TCAAATTTN CTCN 344

55

SEQ ID NO:4893

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05830

SEQUENCE DESCRIPTION:

GATCAGGNAG CCTCCTGATG CCAGAACACC TNAGGCAGAG CCCTACTCAG CTGTACCTGT 60  
 CTGCCTGGAC TGTCCCTGT CCCC GCATCT CCCCTGGGAC CANCTGGAGG GCCACATGCA 120  
 CACACAGCCT AGCTGCCCC AGGGAGCTCT GCTGCCCTTG NTGGCCCTGC CCTTCCCACA 180  
 GGTGAGCAGG GCTCCTGTCC ACCAGNACAC TNAGTTCTNT TCCCTGCAGT GTTTTCATTT 240  
 TATNGGGGNC AAACATTTTG CCTGTTTTCT GGTTCAAAC ATGATAGTTG ATATGAGACT 300  
 GAAANCCCTG GGTGTGGAG GGGAAATTGG GNTNAGAGGG GN 342

SEQ ID NO:4894

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05831

SEQUENCE DESCRIPTION:

GATCCTGGAC TTNCCCTCA GCAAAGATGC CTCNTGGTG GTGACCACGT CAGGAGACCA 60  
 CAAAGCGAAA NTNTTNTTT TCCAAAGGCC TGACCGTTAA TGGCTGCAGC CCCTGCCTGT 120  
 TTGNTGGTG TTGAGGGN 138

SEQ ID NO:4895

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05832

SEQUENCE DESCRIPTION:

GATCCACCCG CCTCAGCCTC CCAAAGTGCT GGGATTACAG GTGGGAGCCA CAACACCCGG 60  
 CCATGAATTA ACTCCGTAA AAAATAAACG TATACATTCT GTGAGCAA 109

SEQ ID NO:4896

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05833

SEQUENCE DESCRIPTION:

GATCGGTTTC GCCATCATGA CGCAGTGTCT CCCAGTGGCC CTGTTCTCCC TGGTGGGCTT 60  
 CACCCAGATG ACCATNTGGG CCAAGGGCAA GCACCGCAGC TACCTGAAGG AGTTCCGGGA 120  
 CTACCGCCC CTGCGCATGC CCATNATNCC CTTCTGCTC TGAGCGCTCA CCCCTGCTGA 180  
 GGCTCAGCCC CTNAACCCGG TGGCATTCTG GGGGAGGAGT GGGGCCACA GNTCTCCAGC 240  
 ACCCGGAATA AAGCCCGNCT GCCCAGTCG GAAA 274

# EP 0 679 716 A1

SEQ ID NO:4897

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05834

SEQUENCE DESCRIPTION:

GATCTTGCTG GATGTGAAGA CGCGGCTGGA GCAGGAGATT GCCACCTACC GCCGCCTGCT 60  
GGAGGGCGAG GATGCCACC TTTCCTCCCA GCAAGCATCT GGCCAATCCT ATTCTTCCCG 120  
CGAGGTCTTC ACCTCCTCCT CGTCCTCTTC GAGCCGTCAG ACCCGGCCCA TCCTCAAGGA 180  
GCAGAGCTCA TCCAGCTTNA GCCAGGGCCA GAGCTCCTAG AACTGAGCTG CCTCTACCAN 240  
AGCCTNCTGC CCACCAGCTG GCCTCACCTC CTGAAGGNCC GGGTCAGGAC CCTGCTCTNC 300  
TGGNGNAGTT TCCCAGGTAT NTTCNNTGGT TCCTGTTGGT GAN 343

SEQ ID NO:4898

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05835

SEQUENCE DESCRIPTION:

GATCAGNAGC CCCAACACA GGCAAGTCCA CCCATAATA ACCCTGCCAG TGCCAGGGTG 60  
GGCTGGGGAC TCTGGCACAG TGATGCCGGG CGCCAGGACA GCAGCACTCC CGCTGCACAC 120  
AGACGGCCTA GGGGTGGCGC TCAGACCCCA CCNTACGCTC ATCTCTGGAN GGGGCAGCCC 180  
TGAGTGGTCA CTGGTCAGGG CAGTGGCCAA GCCTGCTGTG TCCTTCCTNC ACAAGGTCCC 240  
CCCACCGTTC AGTGTACGCG GGTGACGTGT GTTCTTTTGA GTCCTTGTAT GANTAAAAGN 300  
CTGGAACCTN ANAAAAAGTG NGNNGNGGTN TNTGNTAN 338

SEQ ID NO:4899

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05836

SEQUENCE DESCRIPTION:

GATCAGCCCC TGACTTTNTT AAAAGATATC AGAAGTGTCT TGGAGCCAAC TAGAGGCAGG 60  
GTCATCCTTG CCCTTNTCCT CCCCTTTCAT CCCTATGTGG AAAACGTAGG TGGCAAGTGG 120  
GAGAAACCAT CAGAAATTTT GGAAATCAAA GGACAGAACT GGGGAAGANCA AGTGAATAGT 180  
CTGCCTGANG TTTTCAGAAA ANCTGGTTTT NTTATCGAAG CTTTCACCAG ACTACCATAC 240  
CTGTNTGAAG GCGACATGTN TAANGNCTAC TNCGTTCTGG NTGACGCTNT CTTTGTCTCTC 300  
AANCCAGTAT AAACACGTGG NGGTCGAAGT CTTCAGAGTC CGTACCNTNC TGGATN 356

SEQ ID NO:4900

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05837

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCCCCCAG AAAAGAAAGC TACAGAAGAA ACTGGGGCTC CTCCAGGGTG GCAGCAACAA 60  
TAAATAGACA CGCACGGCAG CCACAGCTTG GGTGTGTGTT CATCCTTGAA A 111

5 SEQ ID NO:4901  
SEQUENCE LENGTH:293  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS05838

SEQUENCE DESCRIPTION:  
GATCTTAATG GGTTTCGATGG TAGGGAATAC GGAAAGGATA CACTGCTAAT ATTGTGTCTA 60  
ACAATAAAGC AAACAACCTCG ATGCTGTAAG AAGACAAGCT GTTTGAGCTT TCAAACACAC 120  
AGGGGCACAG CACAATTCAG AAATACCCAG GAGGATTCTT GCAGGCTTAA CAGTTGGCAT 180  
15 CGTACTGAAA TGAAACGTGT ATTAACANGA AANTGTCAA CTTTTGGGGA AACAAATTTT 240  
CTGTTACTTC CCACCCNACT AAAAGGGAAG ATAAACCAT CATCACCAGN NNN 293

20 SEQ ID NO:4902  
SEQUENCE LENGTH:99  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05839

SEQUENCE DESCRIPTION:  
25 GATCTACATA AGGAAAGGAA GAATATTAAA GAAGAAATAA ATGAAGACGA GATAAAATCT 60  
TTTTTCTTAA TTATCAAATA AAAGTTTGTT AAAAGTAAA 99

30 SEQ ID NO:4903  
SEQUENCE LENGTH:290  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05840

SEQUENCE DESCRIPTION:  
35 GATCAGGCAG TTCCTGGACT GTTCCACCAC TCAGAGTGAC CTGTCCCTGT GTGAGGGCTT 60  
CAGCGAGGCC CTGAAGCAGT GCAAGTACTA CCATGGTCTG AGCTCCCTGC CCTGAAGAGG 120  
TCGGTGCAGA CTCGGGGGCC AGTCCTGCAC NCACNTCTAC CCCTCGCCGA CAGCCAGACC 180  
ACAACACCAG ATTGTACCCA GATAGCTGGG ATTGGAAGTN AGGAGGTTTC TCACCCACAC 240  
40 GATAACCCAA GACACAAATG TGCAATTAAA AGTTTATTTT AGACCACAAA 290

45 SEQ ID NO:4904  
SEQUENCE LENGTH:68  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05841

SEQUENCE DESCRIPTION:  
GATCTGCCCCG CCTGGCCTC CCAAAGTGCT GNGATTNCAG GCATGAGGCG CTGCATCAGT 60  
50 TCTGCAAA 68

SEQ ID NO:4905

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05842

SEQUENCE DESCRIPTION:

GATCTGCAAG CNGGAGCCCT CCTACCCGCA GCTTNAGCAC AGNATCATCC AGCCCTGGGG 60  
AGGCGCACCC TTAAGCAATA CAGACTGGGC TGAGGCTGAC AGGCAGAAGA CTAACAGAGC 120  
GCANTCTGCA CACGCAGGTT CTGGGGCGAC CTCTGGCCCT GGNCATCTCT GNACTAACTN 180  
ATCTGAATTA TGGAAGGTGG CAGTNTTGGT CANTAGTTTT NNN 223

SEQ ID NO:4906

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05843

SEQUENCE DESCRIPTION:

GATCCGTCCG CTTCGGCCTC CCAAAGTGCT GGGATTACAG TCGTGAGCAC CGCGCCCGGN 60  
CTGNGGTCAA TTTTCTATGT CAAGTGAGTG ACATTATTTT TACAAGTATT TTCTTCTTTT 120  
TAAAATTATA CCAGCAAATA CAGTTAATGC AGAAACCTAA GTAATTGAG TGAGCTATT 180  
CACAACTCTAT GTGAAGNNNN CAAAATAGAA TGACCAGTTT TATTATAAAT TAAGGGGCTT 240  
AATTTTCTAA AAAAGNANAN AANTGAGCCN TATCTCTGTG TTTTATAATT ATN 293

SEQ ID NO:4907

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05844

SEQUENCE DESCRIPTION:

GATCACTTGA GGCCAAGTAT TTA AAACAG CCTGGGAAAT ACAGTGAGAC CTTNTNTCTA 60  
CCAAA 65

SEQ ID NO:4908

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05845

SEQUENCE DESCRIPTION:

GATCCTGAAG GCCTTCGAGT ATTTTACTAT TTGGTACAAG ACTTGAAATG TTNGTNTTC 60  
AGTCTTATTG GATTACACTT CAAGATTAAN CCAATTTAAA TTGTATGTNT TCAGGCTGTT 120  
TGTATATTTN ATTAAGGGAT GGGAGGGGTT ATTTGTCATT TACAGTATTG GGGTTTTNAT 180  
GAATGTGAAG CAAACAANAN ANATTGTNT GTAAACTGTT TTNTN 225

SEQ ID NO:4909

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05846

SEQUENCE DESCRIPTION:

GATCAGGTTG GGGGGCAGCC CCCAGTCCCT TTCTGTCCCA GCTCAGTTTT CCAAAAGACA 60  
CTGACATGTA ATTCTTCTCT ATTGTAAGGT TTCCATTTAG TTTGCTTCG ATGATTAAAT 120  
CTAAGTCATT TGAAG 135

SEQ ID NO:4910

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05847

SEQUENCE DESCRIPTION:

GATCCAGTAT TTGATGAAAC TCATGAAAGT GGGTGGAGCC CATCTNGCCC CTCCTCTTTT 60  
CTAGGACGCA CTATATGTGA CTGTGACTTT CAAGGACATT TGTTGCCAT TTGCTGATTT 120  
TTTTGGGAAG TNAATTNCTA ACTNCTTTCA CTGATAAATG NAGAAAAGTA TTGCACCNGT 180  
GAAATGCACC AAATGAATNG NGTTTTGTAA TTAAAAAAN NTNTN 225

SEQ ID NO:4911

SEQUENCE LENGTH:281

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05848

SEQUENCE DESCRIPTION:

GATCCCTTAA GGTCTGGCC CAGGNCTGCC CAAAGAGAAG CCCAGGATGG TCGGCTGCCT 60  
GGGGGCATTG TCACCACGTN GCCATGACGG CTGGTCCNA CAGGNCCAGC TGGGAGGACT 120  
GGTTGTGCTG CTGGAGAAGG GCTGGAGAAG GCAATGGCAT GCTGCCGCTT TGCCAGTCCC 180  
TAGAAGTCGC GGTGCAGGTG ATGTGTNGNG AGCCGTNCCT NCANTGGGCA GGCCNNGGAG 240  
TNTACTTGTG TGCAGCTGAC CCAAGGGCAG CCACATNTNN N 281

SEQ ID NO:4912

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05849

SEQUENCE DESCRIPTION:

GATCAAAACC CAGCAGAGTG CAAGCAGCAG TGAAGCAGGA TGTATGTGGC CTTGAGGATA 60  
ACCTGCACTG GTCTACCTTC TGCTTCCCTG GAAAGGATGG ANTTTACATC ATTTGGGCAA 120  
GGCCTATTTT CAAGGTTTNT TTGGTNTGNT TGGNTNGCTT GTTTTGGNT TNTGGCAGN 179

SEQ ID NO:4913

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



CLONE:HUMGS05850

SEQUENCE DESCRIPTION:

5 GATCGAGGGC TGGGNACCCC GGTGTNAGCA GGATGGGGCC CTGCCCTCCC GTGGNAGTTG 60  
TGGACTCGAG CCCAGGGGCT GCCCGTAACA GCGGTGTCCC AGGTCCCTGC CATCCNATTT 120  
TACCTGGAAT GTCTTCTCTG GAGTTTGGA TTTGCTTGAGG AACCTGCGT GTGCTTGGAG 180  
AGGCCAGAGG GCTTGCTGAG AACCCCATGG ACAGTGGAGA GCGGGATTCTG AACCAAGGGC 240  
TGGACTCCCA CACCTNTGGC CTGCGTCGCC CAGTTCTTTG TGGCTCTGAA GAATTGGNCG 300  
10 CTGTGGAAAA GTN 313

SEQ ID NO:4914

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS05851

SEQUENCE DESCRIPTION:

20 GATCTTATGT GTTACAAAAT TGGAGAAAGT ATTTAATAAA ACCTGTTAAT TTTTATACTG 60  
ACAATAAAAA TGTTTCTACA GATATTAATG TTAACAAGAC AAAATAAATG TCACGCAACT 120  
TAAA 124

SEQ ID NO:4915

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS05852

SEQUENCE DESCRIPTION:

30 GATCCCCTGA ATGCCTTTGG AGGCCAGTAG AGCACACAGG GTATCCACAT GTTACCCTGC 60  
AGCTACATTG TTGAGTTAGT GATGATATTG TATATGCTCA TGGTCTNAAC TGGATTACAA 120  
AAAGCAAATA CTAGAACAGC TAGCTCATCT TTNACCCAAT GTACTTAGTA TTTTCNTGCA 180  
CTGGTTTAAT CATGNTTAAT ACTACAAANC AAAANTAANT ATTCACAGT GGTGNTTGG 240  
35 TTTTGTGTTT AANCCACAGT TNGANTTAGT TAGCCTTGCT GGGGCCATAA TATGCTTCAG 300  
GGTGTGTAAN TGN 313

SEQ ID NO:4916

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS05854

SEQUENCE DESCRIPTION:

45 GATCTGGGGA CTACCAGAGA CTCTGGGAAA TGGACAAGGT GGGGGGCCCC ACTCTTTCTC 60  
TCCTGCAGTC CCGTAGCTGG GGCTCCTTC CTTCTCAGGG TCTCCCCAGC CCAGTCCCCT 120  
TGCTCCCATC CCACTCGGTG CTGTTGGGTA GGGGCCCTGC CAGGAACTGA CCAGCTNAGC 180  
GAGGAGCCAT AATGTGCATA TGTGCACAAG CAGGGTTTGG GGAGGGGGNT GTGAGGGGNT 240  
50 GTGCCCAGGT GTGCCCCCT ATCTCCTGGG GAGGGTGAGG NAGGGCAGGG ACAGTNTCCA 300  
GGGGTNAATT TN 312

55

SEQ ID NO:4917

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05856

SEQUENCE DESCRIPTION:

GATCTAAATA TTCTGGTTTG GATTAGGCAA TTAAAATTTT TTTGGCAACA GGAAA 55

SEQ ID NO:4918

SEQUENCE LENGTH:370

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05857

SEQUENCE DESCRIPTION:

GATCCAAGGA NCGTTTGGNT TTTCTAGCT ACATCTGGTA CCTTGGCTGG CATTATGGGA 60  
ATNAGTTCT ACCACTCTGG AAAATTCATG CCTGCAGGT TAATTGCAGG TGCCAGTTG 120  
CTGATGGTCG CCAAAGTTGG AGTTAGTATG TTCAACAGAC CCCATTAGCA GAAGTCATGT 180  
TCCAGCTTAG ACTGATGAAG AATTAAAAAT CTGCATCTTC CACTATTTTC AATATATTAN 240  
GAGAAATAAG TGCAGCATTT TTNCATCTGN CATTTTACCT AAAAAAAG ACACCAAANC 300  
TTGGCAGAGA GGTGGGAAAA TCAGTCATGT TTTACCAANC CTANCNGAGG TTGGCGTGTT 360  
TTGTTACCTN 370

SEQ ID NO:4919

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05858

SEQUENCE DESCRIPTION:

GATCTTGAAA GGAAGTATGC TGTCTCTAT CAGCCTCTAT TTGATAAGCG ATTTGAAATT 60  
ATTAATGCAA TTTATGAACC TACGGAAGAA GAATGTGAAT GGAAACCAGA TGAAGAAGAT 120  
GAGATTCGG AGGAATTGAA AGAAAAGGCC AAGATTGAAG ATGAGAAA 168

SEQ ID NO:4920

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05859

SEQUENCE DESCRIPTION:

GATCATGGGA GGGAGCTGAG GGGTTAATAT ATATACATAC ATACACATAT ATATATTTNN 60  
GTAAATAAAC AGGAACTGAT TTNCTGCCTC CATCCCACCC ATGAGGGCTG CAGGNACTAC 120  
AAGAGAAA 128

SEQ ID NO:4921

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear  
 CLONE:HUMGS05860  
 SEQUENCE DESCRIPTION:  
 5 GATCGGGTCC CCAGAGCCAC CATCTCCTGA GCCTCCCACC CCGCTGCCTG GGCCCTGTGG 60  
 TTGCTGGGCC TCCCACCTCA AGGAGGGGAA GGTGTACAG CCCGAACCCG TGGAGCAATG 120  
 CCCTGTNTGG NCTCCAAAAC CAAAATAAAA CTGGTGTAC TTTAAA 166

10 SEQ ID NO:4922  
 SEQUENCE LENGTH:97  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05862  
 15 SEQUENCE DESCRIPTION:  
 GATCTTTAAA CTGCTTTATA CACTGTCACG TGGCTTCATC AGNTGTGTGC ATTTCAGGAT 60  
 GGTTTTTAAA GNAACCTCAG AAAGNTATTT CCTTAAA 97

20 SEQ ID NO:4923  
 SEQUENCE LENGTH:211  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05863  
 25 SEQUENCE DESCRIPTION:  
 GATCACAGAA AAATTAAAAA TCCAAGTGCT CTCTAGATTT GTTGATAAAC ATTTTATGCT 60  
 TGCATTTAAA CTTGAAATGT ATGAGCAGAA TGAGACAATC AGTTAAATCA GAAATGAGAA 120  
 GTATTATAAT GTAAAGGCCT TGTTTTGCTG TAGCAATANN ATGACCAAGT GCAATGACTT 180  
 30 GATTTAATAA AATCATATNT TAAAAGTTAA A 211

35 SEQ ID NO:4924  
 SEQUENCE LENGTH:338  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05864  
 SEQUENCE DESCRIPTION:  
 40 GATCAACGCC TCACTGAAAC ATGGCTGTGT TTGCAGCCTG CTCTAGTGGG ACAGCCCAGA 60  
 GCCTGGCTGC CCATCATNTG GCCCCACCCA ATCAAGGGAA GAAGGAGGAA TGCTGGACTG 120  
 GAGGCCCTG GAGCCAGATG GCAAGAGGGT GACAGCTTGC TTTCTGTGT GTACTCTGTC 180  
 CAGTTCCTTT AGAAAAATG GATGCCCAGA GGACTCCCAA CCCTTGCTT GGGGTCAANG 240  
 AAACAGCCAG CAAGGNGTTA GGGGNCTAG GGCACCTGGG CTTGTTTGTT CCCATTGAA 300  
 45 NGCGGNCTT NTGGGCCCTG GGCCCTTNG GTTTGCTN 338

50 SEQ ID NO:4925  
 SEQUENCE LENGTH:259  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05865

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCTGTCT TCTTTCATGT TTACTACGAG GCATGACATT CATGGCAAAA CAGGGATGCC 60  
 GTTCCAAGA GCAGCTATAA AACAATCTGT TTCCTAAAG ACAGCCACTC TGAGAAGGNG 120  
 ATGANGGAAC ACGGCAGGGT TCATCANTTC ATAGACTGTT TCCAAAAATA ATTTTAAAC 180  
 TTTCCACTA GGCATCTGTG TCTTTAACCA CTGCACANTG GCNTTGCCTG TTTAATANAA 240  
 GGTNNTCANN ACGTGGAAG 259

SEQ ID NO:4926  
 SEQUENCE LENGTH:195  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05866

SEQUENCE DESCRIPTION:  
 GATCCACCCA CCTCGGCTC CCAAAGTTTT GGGATTACAG GCACGAGCCA CAGTGCCAGC 60  
 TGAAAACGTT TCCTAAACAG AAGTGCGCAG AGCATGATGG AGCCCAGCCT GGGCTTGACA 120  
 TTTGGAGAGA ACTACAGAGA AGTATCCAGA CTGTTGTTAC TAATAAATAA ATACATAAGC 180  
 TCCGCTGNAC GGAAA 195

SEQ ID NO:4927  
 SEQUENCE LENGTH:56  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05867  
 SEQUENCE DESCRIPTION:  
 GATCCAACAA TAAATATTA ATTTATAAAA AAGAAATTTT AAAAAGTAAC AAGAAA 56

SEQ ID NO:4928  
 SEQUENCE LENGTH:82  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05868  
 SEQUENCE DESCRIPTION:  
 GATCATCCTC CAAGCAGTCC TGTTCATTCA TGTCTGCCTC AAATTGCTGG TGAATACATA 60  
 AAATAGTTAC TTGCTAATCA AA 82

SEQ ID NO:4929  
 SEQUENCE LENGTH:286  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05869  
 SEQUENCE DESCRIPTION:  
 GATCCACCCG CCTCAGCCTC CCAAAGTGCT GGGATTACAG GCAAAAGCCA ACACACCCGG 60  
 CCTGGATATG AATTTATAAT ACCCTACAGT GCAGCACAAG AAGATGCACT CAAAGCACTG 120  
 ATGTGAGGAA GTACTTGCCC CGTAGCAGCT ATTCACCTCTA CCAGTGTAAG CAAACTCTAA 180  
 GGCTAGGGCG GGGCAGCACA GGCACANGNN TATACTAGCC AGGGGTTTAA TATAANTACA 240

EP 0 679 716 A1

ACCAGCATAG NAAGNCCCAA ANCTNTACAG NNNCCAANAC CNGGNN

286

SEQ ID NO:4930

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05870

SEQUENCE DESCRIPTION:

GATCTGTGCC CCATGCCTGT CCAGCCTGGG CAGCCAGGCT GCCAAGGCCA GAGTGGCCTG 60  
GCCAGGGGCT CTTCAGGCCT CCCTCTCTCT TCTGCTCCAC CCTTGGCCTG TTTCATCCCC 120  
AGGGGTCCCA GCCACCCCGG GCTCTCTGCT GTACATATTT GAGACTAGTT TTTATTCCTT 180  
GTGAAGATGA TATACTATTN TGNTNAAGCG TGTCTGTANT TANTGTGTGA GGANCTGCTG 240  
GGNTTCANTT CGNGTGNACG GTGGGAGAGN TTGGGTGCCC GNGAGAATNG ACGGGCTNAT 300  
GGNTTCCTTT N 311

SEQ ID NO:4931

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05871

SEQUENCE DESCRIPTION:

GATCAAAAAA CTACCTATCT GGTACTATGC TTTNATCTG GATGATGAAA TAATCTGTAC 60  
AACAAACCCT GGTGACATGC AATTTACCTA TATAGCAAGC CTACACATGT GCCCCTGAAC 120  
CTAAAAAAA AGTTAAAAGA AAAACGTTTG GNTTATTTTC CCTCTTNGA ACAANGNCAT 180  
TGGTTTGCCC AAGGNTACA AATAANCCAA CGGGAAAAAN GANAGGTTCC AGTTTTGTNT 240  
GANAATTCTG ATTAAGCCTC TGGGCCCTAC AGCCTGGGGA ACCTGGNGAN TCCTACACCC 300  
GGGAN 305

SEQ ID NO:4932

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05872

SEQUENCE DESCRIPTION:

GATCCAGAGA CACACAAGAG CACCAAAGCA GCTCATCCCA CTGATGACAC CACGACGCTC 60  
TCTGAGAGAC CATCCCAAG CACAGACGTC CAGACAGACC CCCAGACCCT CAAGCCATCT 120  
GGTTTTCATG AGGATGACCC CTTCTTNTAT GATGANCACA CCCTNCGNAA ACGGGGTCTG 180  
TTGGTCGNAG NTGTGCTNTT CATCACAGGG ATNATNATTN CTNACCAGTT GGN 233

SEQ ID NO:4933

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05874

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCTACTAA AACACTAAGT TTCATACTAA ACCGTTTCAT GTATCTTTAT CATATTCTGT 60  
 AAAGTTTACA CTTTGATGTA CCTGTATTTT ATTGAAATAC TGTCCAGCTT CAAATGGAAC 120  
 AATATTGTAT GTAGAAATTC CAATTACTGG TTTGTCAGTN GGATTCTTAG CTCTGTAAAA 180  
 CGCCAGTGCA GTCTCTCCTG GCACCACCTG TTTTAAAGAG TATATATATN ATCAGTNCTT 240  
 TGNNTCTCAC AAAGNGCCTC NNTTCCCTG CTAAGN 276

10 SEQ ID NO:4934  
 SEQUENCE LENGTH:89  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05875  
 SEQUENCE DESCRIPTION:  
 15 GATCTGGTGG GCTGGGTCCC CCTCTCGACC NCAGACGCCC CTAAGTCGCC CCTTCTCATT 60  
 TTATACAATA AACATTCTCC ACCTACAAA 89

20 SEQ ID NO:4935  
 SEQUENCE LENGTH:313  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05876  
 SEQUENCE DESCRIPTION:  
 25 GATCAGGAGT TCTAGGCTGT AGTGTGCTAT GAGCACATCT ATGAATAGGC ACTGCGTTCC 60  
 AGCCTGGGCA ACATAGTGAG GCCCATCTC TTTAAAGGGC ACACGTGTAT AGGACAGCTC 120  
 CATTATAATC TTATGGGACC ACTGTAATAT GTGTAATCCA TTGTTGACTG GAACATCCTT 180  
 ATGCAGCACA TGAAGTGTA CATAACTTAA AATTTATCAT TTAAACCATT TTTAAGTGTA 240  
 30 CAATTCGGTG GTATAAAGTA CATTTACATT ATTTGTGAAC TATCACCTCT ATCCATCTCC 300  
 CTAACCTTTT CNN 313

35 SEQ ID NO:4936  
 SEQUENCE LENGTH:224  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05877  
 SEQUENCE DESCRIPTION:  
 40 GATCCGGGT CAGAGTGACG TTTTCTCTCA CAAGCAGAAG GTAACAAATT TCATGCTCTC 60  
 CCTAAATTCT GTCTGATTTT GCCTNGTGGT GATAGATTGT CANGAACACA ATGTCCTCTG 120  
 GAGAAATCTA TTGACAGAAA TTGGTGCAGT GTTANCAACG CTAATGTAAA ACACAGANTT 180  
 TACAGAAAAAN TAGAGAAAAT AAACACATTT GTNNGCCTCA GAAA 224

45 SEQ ID NO:4937  
 SEQUENCE LENGTH:314  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 50 CLONE:HUMGS05879  
 SEQUENCE DESCRIPTION:

55

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GATCCTCTCT CCCAGGGAAT CCGACACAGG AGGAACCCCT TCTNTGGTTG ANCTGGGCCA 60  
 GGCCTAAGAG TAGCAGGAAC TCTAAGACCA CAGAGTTTTT TATAAATGTA TAAATGTATC 120  
 AAGCCAAATN TGCAGATGCT AACTGGACAT TCTGGGGAAC TGGGCACCAG GNGTGCCTTC 180  
 ATACACTGTA CCCAGCTCT NTTCTAAAAG AGAAGTNGGT GGGCACACTT GAACTGTTTG 240  
 GTGGNCCNAA CCACAGGANG CTGCAATTNT NTGGNTTAGG GTGATACTTT TGGCCCTNCN 300  
 TGTGGCCCCT NTTN 314

SEQ ID NO:4938  
 SEQUENCE LENGTH:143  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05880

SEQUENCE DESCRIPTION:  
 GATCTGAAAG TATAAACTG CTAGAAGAAA ACATGGATAT TTGATTGGAC AATGATATTT 60  
 GGATATGACA CCAAAAGCCT AGGCAACTAA TGCAAAAATA GACAGGGAGA GTACATCAAT 120  
 CTTAAAAACC TTATGATGGC AAA 143

SEQ ID NO:4939  
 SEQUENCE LENGTH:389  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05882

SEQUENCE DESCRIPTION:  
 GATCTGAAAT ACCATCTCTA CCAGAGACTC TGGGAAAAAT AATGGATTCC AAGTGTTAAA 60  
 CGGAATTAAG TTTGGCCTAA AACTGCCTCT GTACATAGTG ACTTATAACC TCACTTAATG 120  
 TATAAGCAAA CTGGGACCTG ACTTGAGAGT ACATTCTGT AACAAGCAGC AGAGTCTCAC 180  
 CAATCACATG CTGAAGGCTC CCAAACATG NCTATGTGAG GTGGAGGCTG ACCTGCAGTC 240  
 AGTCTGGCCA TGTACATGNG TCTTCCCTT NCTGTGGCTA TAAATAAATA CAGCCTGNAC 300  
 ACANCGGACA GGNNGACCGT TCTGNACCAN GNTTGGGTCC TGNGNGNTAC CNAGGTNGAN 360  
 GNAACTTTTT TTNGGCTCAN TTAACTGN 389

SEQ ID NO:4940  
 SEQUENCE LENGTH:131  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05885

SEQUENCE DESCRIPTION:  
 GATCTCTCCG CCTTAGTTAA GAGCATGTGT CGGGAAATTC CTCAGAGTGC TCAGAGTCCC 60  
 TGTATNTTTA TACCTTTTAA CAATGTTAAC TGTTCAGAAC TGNTTTTGT AACAAAACCT 120  
 NNTGTTTTAA A 131

SEQ ID NO:4941  
 SEQUENCE LENGTH:115  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS05886

SEQUENCE DESCRIPTION:

GATCATGGCG CAGTTGGNCA GGAGATGTTT TCCCCATCT GCTGTAGCGA ATATGTGAAG 60  
TGGGAGGTGG CAACNGAGCT GCCNTTCCAC CACTATTNCC ACAAGCCGTG TGTNN 115

SEQ ID NO:4942

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05887

SEQUENCE DESCRIPTION:

GATCCTCCCG CCTTNGTCTG CCAAAGCACT NGGGTTACAG ATGTGAGCCA CTNCACCCAG 60  
CCTAATCTTN ATAAATCTCC ATCCCCATTA CTCTGGTTCA CCCNN 105

SEQ ID NO:4943

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05888

SEQUENCE DESCRIPTION:

GATCACGGAC GTGCAGCTCG CCATCTNCGN CAACATGCTG GGC GTGTCGC TCTTCTNGCT 60  
TGTNGTTCTC TATCACTACG TGGCCGTCAA CAATCCCAAG AAGCAGGANT GAAAGTGGCG 120  
CTTTCTCCGC CCCAGGGTTC CAGGACATAG TCTGAGGCAA GATGGAGGGT ATGAGGGGCC 180  
TTCACACTNC ACTTCATCCC TTCTACCCAT CACAACATAC AAAGCAACTA CACCTGGGAT 240  
TTTNCCAAGC AGCTTTNATT TCCTCAGNGT CTTCTTAAT CCTATGGGNA CANGGAAGCT 300  
GCCACTNGNN TAGGGNCCAG TATAGGGGGC TTNGCTTTTT TAACTGCNTN 350

SEQ ID NO:4944

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05889

SEQUENCE DESCRIPTION:

GATCCAGCGG CAGTGACAGA ATCCAAAGAG GGAACAGAGG CATCAGCATC GAAGGGGCTG 60  
GAGAAGAAAG AGAAATGATG CAGCTGGTGC CCGAGCCTCT CAGGGCCAGA CCAGACAGAT 120  
GGGGGCTGGG CCCACACAGG CGTGACCCGG GTAGAGNGCA CAGGTAGGCC AAGGGGNAGC 180  
TCCCAGGACA GGGCAAGGGG GCAGCANGGA TACCTGCNAG CCAGGGNCTC TNTGGCCTNT 240  
NTTTCCTAN TCCNTTTTTT TGGCCCTTCT TTTTNTNTG CCGTACANCN TGCAGGCAAA 300  
AGNN 304

SEQ ID NO:4945

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05890



## SEQUENCE DESCRIPTION:

GATCAAAACA AAACAAAAA GTTGTCTCTG AAAAAAAAC AAAACAAAA AGTTGTCTCT 60  
GAAA 64

5  
SEQ ID NO:4946

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

10  
TOPOLOGY:linear

CLONE:HUMGS05892

## SEQUENCE DESCRIPTION:

GATCAACCTT TGTNTGCGAG GGTCTAAGTA GGGTCGAACA CAGAAGTGGG AAGNAGAGGG 60  
GTGGGCCAGG GGCTAATGGT GTCAGTGTGT AAAGTTTTG ACATACTAGC TCTATAAATA 120  
TATGAATATG GACAAA 136

20  
SEQ ID NO:4947

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05893

## SEQUENCE DESCRIPTION:

GATCCTCTGC TACCAAACAA TGATGTGGAT TCTTTTGCAC AGAAATATTT AAGGTGGGAT 60  
GGTAAAAAAT GTCACAAAAG ACTCCTCACC AATACTTNAT GTTGATATCA CTTAATATTA 120  
ACCAGACTTT GCTGTATTGC AATAAACAG AGAACTGTTA AA 162

30  
SEQ ID NO:4948

SEQUENCE LENGTH:405

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05894

## SEQUENCE DESCRIPTION:

35  
GATCATCGCC TCCCTGGTTT ATAGTAGACA GACCTTTTCT GTTTTTCATC CGACATAATC 60  
CTACAGGTGC TGTGTTATTC ATGGGGCAGA TAAACAAACC CTGAAGAGTA TACAAAAGAA 120  
ACCATGCAAA GCAACGACTA CTTTGCTACG AAGAAAGACT CCTTCCTGC ATCTTTCATA 180  
GTTCTGTAA ATATTTTGT ACATCGCTT TTTTCAAAA CTAGTTCTTA GGAACAGACT 240  
40  
CGATGCAAGT GTTCTGTTC TGGGAGGTAT TNGAGGGAAA AANCAAGCAG GATGGCTGGA 300  
ACACTGTACT GAGGAATGAA TAGAAAGGCT TCCAGATGTC TAAAAAGATT CTTTAAACT 360  
ACTGNAACTG TTACCTAGGT TAACCANCCC TGTTTGAGGT ATTN 405

45  
SEQ ID NO:4949

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05895

## SEQUENCE DESCRIPTION:

50  
GATCTGCTCG GAATCCTCCT GCTAAAGAAG GNTCTGGGCG TGAGCTCAGC CGCCCCGCAC 60

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CCCAAATCCA GTACAGGAGG CTGCTGGTAC AAATACTGCA GTAATGACAC CAATAATGGG 120  
 GCAGACACAA CAGCGTGGCT TAGATTGTGC CCACCNAGGG AAGGTGCTGA ATGGGACCCT 180  
 GTTGATGGCC CCATCTGGAT GTAAATCCTG AGCTCAAATC TCTGTTACTC CATTACTGTG 240  
 ATTTCTGGCT GGGTCACCAG AAATATCGNT GATNCAGACA CAGATTATTG TTCCTGCTGT 300  
 ATTTGCTGGT TTNCCTGGTT GAATTGGTTN 330

SEQ ID NO:4950  
 SEQUENCE LENGTH:308  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05896

SEQUENCE DESCRIPTION:  
 GATCCAGAAT TTATTAGTTT AAAATGCAGG TGAACTTTTT TTTGCGTTTG GTTTACTTGT 60  
 CTGTCAAATG TTTCTTAAAT CATGAAACTG AATAAGGAGA AGAGTATTTT TAACACTTAA 120  
 ATTTCTTGGC AAATTTTAAA ACATTTTNA GTCTGTAATA CACTCCACTT GANGCACTTA 180  
 AGTNTTCCTT AAATGACTTT CCTTAGGTAA TGATACTGGT GTGTTTTCCN AAGGCCCTTT 240  
 TAAAAAAGTN TNNNTAANTG ACTATCTGTT GAAANGGTGT CCTGTNCCTT NCTNCTAGNA 300  
 ATNTGGGN 308

SEQ ID NO:4951  
 SEQUENCE LENGTH:97  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05897

SEQUENCE DESCRIPTION:  
 GATCGGAAGC AGAAGATGGC CTTCTTAAAG AGTTTAGAAG AATTTATGGC AAATGTTGGT 60  
 GGTCTCCTTT GTGTAAAATA AACAACAGAA CTTTAA 97

SEQ ID NO:4952  
 SEQUENCE LENGTH:229  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05898

SEQUENCE DESCRIPTION:  
 GATCTGATAT TAAAACATCC AGTAGTACGA GTCTGTTTAT TGAATTTTAT GGTCCCTTTC 60  
 TTTGATGGTG CTTGCAGGTT TTCTAGGTAG AAATTATTTT ATTATTATAA TAAAACAATG 120  
 TTTGATTCAA AATTTGAACA AAATTGTTTT AAATAAATTG TCTGTATACC AGTACAAGTT 180  
 TATTGTTTCA GTATACTCGT ACTAATAAAA TAACAGTGCC AATTGCAAA 229

SEQ ID NO:4953  
 SEQUENCE LENGTH:144  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05899  
 SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCCAGAGC CCCTCCCCAT CTCCTCTCT CTAAAAACAA CCCTACCCCC CATTGCCACC 60  
TTCACCTCTG TGTCTCCAGC TGATTAGCCT CAGACTCTTC TTNTATTGTT TTTCTTTTGT 120  
AAATAAAAAG CACCAGGTTC CAAA 144

SEQ ID NO:4954  
SEQUENCE LENGTH:105  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05900

SEQUENCE DESCRIPTION:  
GATCCGTGCC CTGTAAAATG GATATNATGT TTTACTGATG TCTNTAATAC ATTTGTAAAC 60  
TTCCAATAAA ATTTGAATAA AAGAAATNTT GCCATTCTTC TCAAA 105

SEQ ID NO:4955  
SEQUENCE LENGTH:325  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05902

SEQUENCE DESCRIPTION:  
GATCTGGCAG CCCTGGAGAG GGAATATGAG GAAGTGGCGC AAAGTTTCTG AGGCATGTAT 60  
GATGGGTGCA AATGAATGTC AAGTTAAAAT GGCATGTTTT CTTTTCAAGC CGNTATATGC 120  
CTAGTGGGTA GTTCCCCTGA TGAGCAGAAA AATTGAACTC AAATCAGGCA AGACTCTAGG 180  
NTCCACACTA AATTAAGTGG GTCAGTANCG NCANTGANCA CATTATTTC TGGTCTACTG 240  
GGTACANGTC AGCTCTGCTT ACCTGNGGAG CNTTTTGGAA GCTTAAGAGT NCTTTTGAAC 300  
CTGGCTTGAG GTCAACTTGT TAGGN 325

SEQ ID NO:4956  
SEQUENCE LENGTH:321  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05903

SEQUENCE DESCRIPTION:  
GATCTGTACA GACAGGACAG AATGAACTC CTGCGGCTCT TTGGCCTGAA AGTTGGGAAT 60  
GGTTGGGGGA GAGAAGGGCA GCAGCTTATT GGTGGTCTTT TCACCATTGG CAGAAACAGT 120  
GAGAGCTGTG TGGTGCAGAA ATCCAGAAAT GAGGTGTAGG GAATTTTGCC TNCCTTCCTG 180  
CAGACCTGAG CTGGCTTTGG AATGAGGTTA AAGTGTCAGG GACGTTGCCT GAGCCCAAAT 240  
GTTGTAGTGT GGTCTGGGCA GGCAGACCTT TTAGGNTTTT NCTGCTTTAG TTCCTGAGGN 300  
ANNTNGGNCA CTCTTTNTNT N 321

SEQ ID NO:4957  
SEQUENCE LENGTH:313  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS05907  
SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCCAGGGG CTGATTGGCA GCGTGGAGGA GCAGCTGGCC CAGCTTCGCT GCTGAGATGG 60  
 AGCAGCAGAA CCAGGAATAC AAAATCCTNC TGGATGTGAA GACGCGGCTG GAGCAGGAGA 120  
 TTGCCACCTA CCGCCGCCTN CTGGAGGGAG AGGATNCCCA CCTGACTCAG TACAAGAAAG 180  
 AACCGGTGAC CACCCGTCAG GTGCGTACCA TTGTGGAAGA GGTCCAGGAT GGNAAGGTCA 240  
 TCTNCTNCCG NGNGCAGGTT CACCAGACCA CCNGTTTGAG GNCTCANCTA CCCC GGNTCG 300  
 GNCANCCATN TNN 313

SEQ ID NO:4958

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05908

SEQUENCE DESCRIPTION:

GATCATTAAAT GTCATTGCAA TNGTTATTTT TAAAAATAAA TTTATAAAAA TAAA 54

SEQ ID NO:4959

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05912

SEQUENCE DESCRIPTION:

GATCTACAAG AGCAAGCCAA CAGAGTAAAG TGGAAGGAAG TTTATTCAGA AAATAAAGGA 60  
 GTATCACAGC TCTTTTAGAA TTTGTCTAGC AGGCTTTCCA GTTTTACCA GAAAACCCCT 120  
 ATAAATTAATA AATTTTTTAC TTAAATTTAA GAATTAAAAA AATACAAAAA AGAAAAAATG 180  
 AAAATAAAGG AATAAGAAGT TACCTAAA 208

SEQ ID NO:4960

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05913

SEQUENCE DESCRIPTION:

GATCCAAGTT ATAGATGGAA TTGAAGCCCT TGNGCTGTA GATGTGCGTG CAGTCTGNCA 60  
 GCCTTAAGCC CACCTNGGCA CTTT TAGATA AA 92

SEQ ID NO:4961

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05914

SEQUENCE DESCRIPTION:

GATCAACAGT AACTGGATGT TTTNAGGNG CTCAATTGGA ATAAAAATAT TNNAATCTAT 60  
 TTGGAGACCA AAGGCAAAAT CGGTTTTCTT ACCTTTGGAA TTATTCGTAC CTTTATGGT 120  
 AAATTT CAGC TTTGACANGT ATTATGAGGA ACGTACCAA AACC GGTTTG TAACAAATCT 180  
 NTAGAGNAGG TCTGAATCTN TCGNNCTTGC CTTTTCAGGT GCCATTCTA CTGGCCTAAT 240

ACAGNGCCAT TTGGCTTGTG AAGNNCCATN

270

SEQ ID NO:4962

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05916

SEQUENCE DESCRIPTION:

GATCTATGCC CNTNTTAATC TCCATCCATA TAGGAGTCAC GTTCTTTAAG ACAGATGGTG 60  
 GTAGTTATTT TTGTGGCATG GTTAGATTG ACTGGTTTGT CAGAAGATTA CAGTTATGTA 120  
 CTGCATAATG NCATATACAA TAGTGGTCCC ATAAANNNNN TAATGGAGCA GAAAACTAT 180  
 TGCCTCATGA TGTTTATGCC GGTTTANTGT CATAGNCTAG TGCATNACTC ACGTGN 236

SEQ ID NO:4963

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05917

SEQUENCE DESCRIPTION:

GATCGAGTAA GGAATGACCT NTAGATTGTG CGACTTTTGT TTTGTTTTN TTAAATTTTT 60  
 ATAAACCAAG AATGATTCT CCNGCTCCN TCTCCTCACC ATCTCCAG ACGGAGTTCA 120  
 AAGGCCACTT CTCAAGCAGC TTTTGGCACC TTCAGCCTCA GAGTGGAATC TTTTAAAGAC 180  
 AGGACCCCTA TGTCCAGGNA AGGGGAAAAG GAACNTTGCC ANTGATAGTG ACCACAGCAN 240  
 NNGCAANTAA TAGTAATNTT NATAN 265

SEQ ID NO:4964

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05918

SEQUENCE DESCRIPTION:

GATCACATTT ATACAGTTAT AAAAATAAAG GTTTGATTTT GGTCGTTCTT CAAA 54

SEQ ID NO:4965

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05919

SEQUENCE DESCRIPTION:

GATCTCTATG GCTGTAAAT ATTTCTTTAT AGCGTTATTA AAGTGTGTCT TAATAAAATT 60  
 AAA 63

SEQ ID NO:4966

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05920

SEQUENCE DESCRIPTION:

5 GATCCACAAA AGAAGTGAAA GTAGCCTTAA CTGATGACAT TCCACCATTG TNATTTGTTC 60  
 CTGCCCCACG CTAATGATA CCATATATTC TTCCCCCGCC CTTGAGAATG TACTTTGTAC 120  
 ACCTATCCCA AACCTATAAG AACTAATGAT AATCCNACCA CCCTTTGCTG ACTCTCTTTT 180  
 TGGACTCAGC CCGNCTGCAC CCAGGTGAAA TAAACAGCCC TGTTGCTCAC AAA 233

10

SEQ ID NO:4967

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS05921

SEQUENCE DESCRIPTION:

20 GATCTCTGCG TTTTATACT GAGTGTGCCT AGGTTGCCCC TTATTTTNA TTTTCCCTGT 60  
 TGC GTT GCTA TAGATGAAGG GTGAGGACAA TCGTGTATAT GTACTAGAAC TTTTATTATA 120  
 AAGAACTTT TCCCAA 137

25

SEQ ID NO:4968

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear

CLONE:HUMGS05923

SEQUENCE DESCRIPTION:

30 GATCTGTAAA CCCTTACCCC TTGCTGTTCA GAGAGCTACT CTTTGTAGTG TTCTTGCATG 60  
 CATATATAAT AAATATTTTT TCTATTGAAA 90

35

SEQ ID NO:4969

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

40

TOPOLOGY:linear

CLONE:HUMGS05925

SEQUENCE DESCRIPTION:

40 GATCTAAATC AATGCAATAA AGTAAGAAAA ATAAATAAAA GTATTGAAAA GATTGAAAAG 60  
 AAAGAATTGA AGCTGTCTTT ATTCACAGAT AATGACTGTG TATGTTAATA ATCCTAGANA 120  
 TCTACAAAAN TCTGCCAAAN CTAATTAGTG AGTTTGGTAA TGTTGCAGGA TATAAGCTCA 180  
 ATAGAAGTAG TCTTTNGTAT TTCTGTGTAT TAGCAGTGAG CATTGGGAAA ATGANATAAN 240  
 ANTACAGTTT CATTTCAA 259

45

SEQ ID NO:4970

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50

CLONE:HUMGS05926

SEQUENCE DESCRIPTION:

55

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GATCTGTGCC CTTGGTCCCA GGTCAGGCC ACCCCCTGCA CCTCCACCTG CCCAGCCCC 60  
 TGCCTCTNCC CCAAGTGGGG CCAGCTGCCC TCACTTCTGG GGTGGATGAT GTGACCTTCC 120  
 TTGGGGGACT GCGGAAGGGA CGAGGGTTCC CTGGAGTCTT ACGGTCCAAC ATCAGGACCA 180  
 AGTCCCATGG ACATGCTGAC AGGGTCCCCA NGGAGNCCCC GTCAGTAGGG ATGTTTGCCT 240  
 GGNTGTTTAC GTNGGGGTGT NCAGTGNACG TGNAGGAGCA CGTGGGCGGC TTCTGNGGGG 300  
 GNCAATGGTT TGGGGNANGG GAAGGTGTGC CAGCAAACCT NGGNNGGATN 350

SEQ ID NO:4971  
 SEQUENCE LENGTH:202  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05927

SEQUENCE DESCRIPTION:  
 GATCCACGGG CTGCAGAATG GATATTGTAT TAGCAGGCAT GAAAACAACA TTCATCTCCT 60  
 TGTGCTCTC TGTCTGAGTT CTTGGGTGAC CAAATGCCTT GTCAATGAGT GTAGTATTTT 120  
 GAAAGGAATC TTTTTTTTTT TTTTCNCAGC AGTAGGNCNC AANGGTGGGC TTCAATTATT 180  
 CAGTAAACTA TGTAANCAGA AA 202

SEQ ID NO:4972  
 SEQUENCE LENGTH:127  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05928

SEQUENCE DESCRIPTION:  
 GATCCAGCT ACTCAGGAGG CTGAGGCAGA AAAATCACTT GAACCCAGGA GGTGGAGGTT 60  
 GCAGTGAGCA GAGACCACAC AACTGCACTC CAGTCTGGGC AACAAAGTGA GACTCTGTNT 120  
 TACTAAA 127

SEQ ID NO:4973  
 SEQUENCE LENGTH:249  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05932

SEQUENCE DESCRIPTION:  
 GATCCTATCA ATTAGACAGT AAATAAGTGC ATCTTTTTTG AGACAAATGC AGTAGGCAAA 60  
 TGTTGACATT CACCAGGGCA CAGTCAATCC CTGACAATTT CAGAAATTTT GTTGCCAATA 120  
 CTGATTATG TGGGCAGATT CTGGNAGTCT GCTGCTCCTT CNCTCATGGA TNACCTNCNN 180  
 NNNCCTACAG TTGCACCTAT TCTACACAAG AGTGGCATTC ANTNGTATCC AGGAAAGCTA 240  
 GANCAGGTN 249

SEQ ID NO:4974  
 SEQUENCE LENGTH:189  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS05933

## SEQUENCE DESCRIPTION:

GATCCGAGTC GTCCGGAAAT CCATTGCCCC TTTTCTCACA GTTATTAACC AGACTCAGAA 60  
 AGAAAACCTC AGGAAATTCT ACAAGGGCAA GAAGTACAAG CCCCTNGACC TCGGGCCTAA 120  
 GAGACACGTG CCATGCGGCN NCGCTNAACA AAGACGGGNG AACTTAAGGC CAGGAGAGCA 180  
 NNGNAGGAN 189

SEQ ID NO:4975

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05934

## SEQUENCE DESCRIPTION:

GATCATCATC TTTCAGGTGG TCTTCCTGGG CCTCCTGGCT GGCCTGGTGG TCCTATTCTA 60  
 CGNATATCCT GTCCNCTGTG AGTGGTATGA GTTCCTCACC TGCATCCCCT TCACTGACAA 120  
 GTTCTGTGAG AAGTACGAAC TAGATGCTCA GCTCCACTGA GCTNGCTGCG GGGTTNCAGC 180  
 GNNGGGTGTG CTCCAGCAGG GCCAGAGNCA GNCAAGANCT ACNCTGNNGN 230

SEQ ID NO:4976

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05937

## SEQUENCE DESCRIPTION:

GATCATTAAT TATATGTAAA ATAATATACA TTCAGTTATT AAGAAATAAA CTGCTTTCTT 60  
 AATAAA 66

SEQ ID NO:4977

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05938

## SEQUENCE DESCRIPTION:

GATCTATGTC TTTCAGCTAT GTGCTTTTAA AACTTTGTAA TTTAGACATT GATATTGTCA 60  
 TCAGATTGCT TATCAGCATT GCCATAAATA TAATTATTAA TGAAA 105

SEQ ID NO:4978

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05939

## SEQUENCE DESCRIPTION:

GATCTGCCCA CCTCGGCCAC CCAGAGTGCT GGGATTACAG NCGTGAGCAC CGTGCCTGAC 60  
 CAAAATAAAT AAATTTTAAA ATAGAAGTAA CTCAACTTCT GAGCTATGGA-ATAGTTCTCT-120  
 GTACCTCCAG TACCTAATAA AGAACCCAAA TACTGCAATA AA 162



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SEQ ID NO:4979

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05940

SEQUENCE DESCRIPTION:

GATCGAGGAC TGGTACAGGA ACCACCAGGA GGAAGACCTG ACTGAATTCC TCTGCGCCAA 60  
 CCACGTGCTG AAGNGAAAAN ACACCAGTTN CCTGGCAGAG CAGTGGTCCG GCAAGAAGGG 120  
 AGACACAGNT GCCCTGGGNG GGANGAAGTC CAAGAAGAAG AGCATCANNG CCAAGGCAGC 180  
 AGNGGTCAN 189

SEQ ID NO:4980

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05941

SEQUENCE DESCRIPTION:

GATCTNTTTA AAAAATGTAT AAATTNCTTG AGTAATTCCT GGATTAAAGA ATATGCACTT 60  
 TTTAAA 66

SEQ ID NO:4981

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05942

SEQUENCE DESCRIPTION:

GATCGCTGGC ATCAAGAGTG GAGAGGACCG NACAGCCGNG AAGGCAGCCT TTCANGAACC 60  
 TATGCTGGTG AGTGTAGGAG ATNGCTTANG AAGAGCTCAG ACCCTCTATC AAN 113

SEQ ID NO:4982

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05943

SEQUENCE DESCRIPTION:

GATCATAGTT ATTATACAAT GTAGTGAGTC CTGCATGGGT NCTCGATGTG TAATGAAACC 60  
 TGAAATAATA AGATAATAAG AAAAGCAATA ATTTTCTAAA GCTGTGCTGT CGGTGATACA 120  
 GAGATGATAC TCAAATTATA ATAAACTCT TCATTTTGTG AATTATAGAA GCTACTNNNN 180  
 NTAAAGCCAT ATTTTTTTAG GGAAACTAAG GAGTGACATA GAACTGATGA ATGAGCAAAA 240  
 GTAAGTTTTG CTGGATTTTT GTAGAACTCT GGACGTTGAG GATTCATTAT GCTGTGGTTA 300  
 ACTTTAAATA TTTTN 316

SEQ ID NO:4983

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05946

SEQUENCE DESCRIPTION:

5 GATCAGCCCA CTTCACTCTC CCAAAGTGCT NGGATTACAG ACATGAGCCA CCTACCTGNC 60  
CGGAGTTATT TCTAAACACA ACTAATATCA GAATCGCCTA TTTCATAAAA ATTGGATTCA 120  
TCAAATNAAT CTTTGGCCAA CAACCATTG AGAATGATNN NNANCATCAT ACATAGGAAT 180  
GCTACGTTTT CTAGGATTTG ACATTTACAG CANTCGAGAN TTACCCTATT TTGTAAATNG 240  
10 AAATAACCAT TACTAAAATC ATGCAAGCTT CAGCTNCTCG GGTCCTATA GNGTCACCTA 300  
AATCGTATGT GNATGGATAC ATAAGGNTTA TGNATCAN 338

SEQ ID NO:4984

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05947

SEQUENCE DESCRIPTION:

20 GATCCGCCCG CCTTGGCCTC CCAAGGTGCT GGGATTGTAG GCGTGAGCAC CCCTGGCCTC 60  
NAATNTTCAC ATTTATATAC TGAATTATAC ATTACATTAT GTACATATGA TAACTAGTTG 120  
CTTAAATATT TTAATAAATT ATATCTAATG TAAA 154

SEQ ID NO:4985

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05948

SEQUENCE DESCRIPTION:

30 GATCATGCAG AGAATATATA TTGTACTGTA GTAATTTTNT ATTTACATTT GTATGATGTG 60  
ACATAATAGA TGTGAATGTT AATCACTGNT TGAATATGTT AATAAAGTTG TTAACTATA 120  
AA 122

SEQ ID NO:4986

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05949

SEQUENCE DESCRIPTION:

40 GATCTCTATT TTAATNNTAA TTCTAGTTAG TTGTGCCTNA ACTCCAAAGA AATGNGAGTA 60  
TAGTGAGGTA TGTCTGACTC CCACTTCTTA TCATGCTCTG AACTAGTTNT TTATGTTTCT 120  
45 TTGTGTTNCC TTN 133

SEQ ID NO:4987

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05951

## SEQUENCE DESCRIPTION:

GATCGCACAC ATGCTTTNTT NNNATATGGA GTGAACACAA TTATGTACCA AATTAACTT 60  
 GGCAAACTTT CTATTGCCTG TCCCATGTGC ATCTTATTTA AAATTTCCCC CATGGAAATC 120  
 ACTCTCCTGT TGA CTATTTTC CAGAGCTCTA GGTGTTTAGG CAGCGTGTGG TGTCTGAGAG 180  
 GCCATAGCGC CATCATGGGC TGATTTTNA TTACCAGGTC CCCCAGAAGC AGGTGGGGAG 240  
 GCTCTGCTTN CTGCTGCCGG TCTNCAAGNC TTGGACCTNT GGACCCTGNT TTGTAAAGNG 300  
 TAAATTNGTA TCCTTNAGGG AAACCCAAGT GTCAACCTTG TTTNTTCAAT N 351

SEQ ID NO:4988

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05952

## SEQUENCE DESCRIPTION:

GATCGACACA TTCGNATCTN NAATGNGTGC TCTGGGGCCT GTCTGAGTGC CGTGGATGCC 60  
 CATTCCCAGG TGTGCTCCAT CCTCTGGTCT CCCCATTACA AGGAGCTCAT CTCAGGCCAT 120  
 GGCTTTGCAC AGAACCAGCT AGTTATTTGG AAGTACCCAA CCATGGCCAA GGTGGCTGAA 180  
 CTCAAAGGTC ACACATCCCG GGTCTGAGT CTGACCATNA GCCCAGATNG GGCCACAGTG 240  
 GCATCCCGNA GCANCAGATT GNGACCNTGA GGCTATGGNC GCTGTTTTGA NGTTGGTACC 300  
 NTGCGNNGGN 310

SEQ ID NO:4989

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05953

## SEQUENCE DESCRIPTION:

GATCTGAAAC AAAATCTTTC TAAAACATTG TTTTAGTTGT CAAAGCACCA ACAGGACATT 60  
 TTGGGATGTG AAATGTAATT TCTTGGAATC TGTAATTTGT ACTTAATATT TNAGGCTTGT 120  
 ATTTAATATA ATAAATAGGT GTTTGTTAAA 150

SEQ ID NO:4990

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05954

## SEQUENCE DESCRIPTION:

GATCATCCCT TCACAATCCC AGAGTGGCAG GCGGGACCAG CCCCATGGTC TGGCTCCTGT 60  
 CACCTGGGTC CGTGCCAGCA CAATCTGCCA AAGTTCTAGA GACCCTGTTC CCTTCCCCAT 120  
 NAGGTCACAT GCTTCTTCTG TGTGTATTTT TTTTGTGTTT TATGGTTTTT GGAGCAATTT 180  
 AAACCTCCAG TTGNNTATTT TCACAAAAGA AANTAAAATT GCAGTTGCAA GCCCTTTAAA 240

SEQ ID NO:4991

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05955

SEQUENCE DESCRIPTION:

5 GATCCTTTTT TGTACATTTA AGAATATTTT GATTATATTA AACAAGACTG CTGATTTTGC 60  
 TACTTTTTTT AAGGGGTCTT CANGTANGTA AAACATACAT CGTAGCTAGA AGAAAAATGT 120  
 ACCTTAAATT TGCATCTTCC CTCTCATACC CAAGCTGTAA ACAATTGAAA TATTTTGTCT 180  
 TAAATCACTT GGTTCATAC ATGCTTATTT GTTTTAAAC CTGTATCATC ANACTCTCTC 240  
 10 TCNAAATTTA AAATGCTGTT GAATATGATA CTTTGTAGGA GAGAGTGTGC TCAGAACTTA 300  
 GACGGGGTTT GGTAGGCCAA NGN 323

SEQ ID NO:4992

SEQUENCE LENGTH:110

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05956

SEQUENCE DESCRIPTION:

20 GATCTTAACC ATCACAAGTT TTTACCCTCT TCCTTCATGC CTGACCTCAA CCCCCTCTC 60  
 CTCATCCTAT TCCTAAATTA GGCTAATAAA GTGAAATTGG TATACTTAAA 110

SEQ ID NO:4993

SEQUENCE LENGTH:228

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05957

SEQUENCE DESCRIPTION:

30 GATCGCTTGA GCCCAAGAGT TTGGGACCAA TCTGAGCAAT ATAGCAAGAC CCCATCTCTA 60  
 CAAAGAATAA AGAAAAATTA GACTAGCTTG GTGGCATGTG CCTGTGGTCC CAGCTACTCA 120  
 AGAGGCTGAG GTAGGAGGAT TGCTTGAGCC TGGGAGGTGG AGGCATCAGT GAGCCATGAC 180  
 CGTACCACTT CATTCCAGCC TAGGTAACAG AATAAGACCC TGTCTAAA 228

35 SEQ ID NO:4994

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS05959

SEQUENCE DESCRIPTION:

GATCAAGCTA CACATCAGTT TTACAATATA AATACTTGTA CTACCTTAAT GATAAGNACT 60  
 CCTTAAAGTT CCATTGCTA ATNATTAATA CACTGTTTGG GCTGGCCAGT TTTTCATGCA 120  
 45 TGCAGCTTGA CGATTGAGCA CAGTCAGGCC TTTGTATTAA AAATGAAANA TGAAANAACA 180  
 AA 182

SEQ ID NO:4995

SEQUENCE LENGTH:300

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

CLONE:HUMGS05960

SEQUENCE DESCRIPTION:

GATCAACTGG TTTGTGTTTT GCTGCTGCAT TTATCCCAAG TNAACAGGT TTAATCTCCA 60  
GANGAAAACC AAAATACCAT GGGATTTATG CTGNATTGAC ATCTTGCCCT AAACGNACAA 120  
CATCATAGTA ATTTGTCATG GGCAACATGA CCAGNGAGAA GATTTTGTG ATGATTTTAA 180  
ATACACTGNC ACGCTACTGT TGGTTAAATT TAAACANGTT TTACCTGCAG NAATTCTCTC 240  
ACAAATAACC NGCAATAACT TGAAATGCAT NCCCTTTTGA AACTTCCTT TNCTCATGGN 300

SEQ ID NO:4996

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05961

SEQUENCE DESCRIPTION:

GATCCTGCTC CTTTCTGGGC TCTGACTCTC CTGGAAATCT CTCCAAGGCC AGAGCTATGC 60  
TTTAGGTCTC AATTTTGAA TTTCAAACAC CAGCAAAAAA TTGGAAATCG AGATAGGTTG 120  
CTGACTTTNA TTTTGTCAA TAAAGATATT AAAAAAGGCA AA 162

SEQ ID NO:4997

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05962

SEQUENCE DESCRIPTION:

GATCTCAACA ATATTCTTCC AAAATGGCAT ACATCTTTTG TACAAAGAAC TTGAAATGTA 60  
AATACTGTGT TTGTGCTGTA AGAGTTGTGT ATTTCAAAAA CTNAAATCTC ATAAAAAGTT 120  
AAATTTTTGT CTGAAA 136

SEQ ID NO:4998

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05963

SEQUENCE DESCRIPTION:

GATCTGACCT CAGAATATGC TTTCAGTGTT ATTTCTGACT AGTCCTTTTT AAA 53

SEQ ID NO:4999

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05964

SEQUENCE DESCRIPTION:

GATCTGCATA AAGTNTTACA AACAAAATCC TCTTNATGAG CAACACATTT TTCAGCTGCC 60  
AGTCAGACCA ACTGCTGTAA AGAACTTATA TCAAAGTGAG AAGCCACAGA AATGGAGAGT 120  
GGAAATATAT AGTGGTCAAA AGANGATTAA GACAGTTTGG CAACTGAGTG ACAGCTCACC 180

CATAGACCAT CTGANTTTNC ACAAACCTGA TTTTCGGAA TTATCACTAN ACGGTAGCCT 240  
 NGAAGAAAGG NTATNCTTTN CTANCATGGT TACCTGCAGC CAGGTGCATT TGCAAGTGAN 300  
 GTGTGCTGGT TGANGTCCTC TTNTAAGGGN ATTN 334

SEQ ID NO:5000

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05966

SEQUENCE DESCRIPTION:

GATCTTCCAC TAGATGTCAC CAAAAGGACT GAGAACTAGA GAAAAGGGCT GCGATTTCTG 60  
 CTCTCCTTGT AAGATTGCAC AAAAGANTAA ATTGCATTTA TCGCTGTTG CATGAAA 117

SEQ ID NO:5001

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05967

SEQUENCE DESCRIPTION:

GATCCCCCTT CNAGGTAGTG AAAATNAAAT NCGCCGGAGT GTGGCTGCCT TCACCGCGGA 60  
 CCCTCTGTCT CTCCTGCGCA ACGTCTGAGC ACAGGAGCCC ATCCTTGGCT CTAGGNTTCC 120  
 NCCGCTGGAA GCCTTCTGTT CANACACCCC TTATGNTCCA AGGCCTGATG TGAGCCAGCG 180  
 GGGGGTGCAT GGGAACTGN ACCNACAAC CCACATCCTN CATCCTGACT GCAGCANTGG 240  
 GGTCCCCGG CAGGGNTGGG TGAGGNAGGA AGGGGGTCAA GCCTGGNGTN 290

SEQ ID NO:5002

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05968

SEQUENCE DESCRIPTION:

GATCACCGTG AATCCGGCTT CCTCTGAGCA TTCGATGGCC TTAGCACCTC ATCAAGCCAG 60  
 CACATCCTGC CTGCTGTTGC AGCCTGGCTG GGTATTATTCT TCAGTTACCC TAATCCCATG 120  
 ATGCTTGAA CCTTGATTAC CGTTTTACAT CAGCTCTTGT ACTTTNAGT ATATTTTCAT 180  
 AATGAGTTAT ATTGTCATTT AGACTTTGAA CAGCTCTGGG AAATAGAAGA CTAGGGTTGT 240  
 TTCTTAAAGT TTAGCTCATG TTATAATAAA AAGTTGNAAT GAAA 284

SEQ ID NO:5003

SEQUENCE LENGTH:346

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05969

SEQUENCE DESCRIPTION:

GATCGTCCCT GGTCACCCGA CTTTGAATT TGCACCATCA TGTTCAGTG AAGATGCTGT 60  
 AAATAGGTTT AGATTTTACT GTCTATGGAT TTGGGGTGTT ACAGTAGCCT TATTCACCTT 120

TTTAATAAAA ATACACATGA NGACAAGAAA GAAATGGCTT TTCTTACCCA GATTGTGTAC 180  
 ATAGNGCAAT GTTGGTTTTT TATAAAGTCT AAGCAAGATG GTTTTGTATA AANTCTGAAT 240  
 TTTGCAATGT ATTTAGCTAC AGCTTGTTTA NCGGCAGTGT CATTNCCCTT TGCACTGNAA 300  
 NGAGGAAAAA NNNNGNATTA AAAGGGTTGC CAANTTGGCA AAAGGN 346

SEQ ID NO:5004

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05970

SEQUENCE DESCRIPTION:

GATCTGCTCG CCTCGGCCTC CCAAAGGATG GGATTACAGG CACCAGCCAC TGNGCCTGGC 60  
 TGGCCTCTGN TTTTAATAA AACNTGACTA GAGTGACTCC ATCTTAAAGT GAGTAGCTAG 120  
 GCACTTACAA GGTTCATGCT TATGGCCTGA AAATAACCAC ATCCCAGGCT GACCACCAAT 180  
 TATAATTACA GANTATTTAT GGCCATACAG NNCATGNTCC ACCAAGCCTG CAGAATGTCC 240  
 AAATNTCCTA AGAATGCAGC CNCCATTACT TANATATANC ATAAATGAGC ANGCTTAGGT 300  
 TGCAGGNTTA ATGGTCGTGG ATANCAGCAT TNGNCCN 337

SEQ ID NO:5005

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05974

SEQUENCE DESCRIPTION:

GATCAGGGTT ACATAGGTTT GGTAAAATNA GTGCTGGAAT TNACTTTCT CCCAGTAGTC 60  
 TTAGGTCATG CTCAGTGAAC TTAAACTTTA TCCAGATATG GTTTTCCTTC AGCCTTTCTA 120  
 TTCCCTTTCT AGCCAGTGAA AGACCCGCTG CCCTTTGACC TCAGCCCCCTC CAAGCCCCCA 180  
 AGTTTAAAAC GCCACCCNCT GCCACCAGAA A 211

SEQ ID NO:5006

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05975

SEQUENCE DESCRIPTION:

GATCCTCCTG CCTTGGCCTC CCAGGGTGCT GGNATTGTAG GTGTAAGCCA CCAGGCCAG 60  
 GCTAACCTT TATAAGAAAT AAAGTCTCCT CTCAAAATTT AAA 103

SEQ ID NO:5007

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05976

SEQUENCE DESCRIPTION:

GATCCGTCTG GGCACGCTGG AGCAGGAGGC CACAGCAGAC GTGGAGTGGC GCTGGCACCC 60

EP 0 679 716 A1

TTACACCAAT ACCGCACGCA AGAGAGTCTT CCTGAGCACC GAGTGAGCAC ACTCACCCT 120  
CAGTCAGGAC ATGGACTTGG AACTCAGGAT TGGGCTGTCA TAGACAGACC CACCAGTAGG 180  
AACTGTCACA GAATGGCCTG CTGAACTGGG ATGTGGAAGT GTGGCGGGTG GAGAGGTCTG 240  
AATAAACCGT CTGTGTCATG GCAAA 265

SEQ ID NO:5008

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05978

SEQUENCE DESCRIPTION:

GATCATCAGC AATNCCTTCT GCACCANCAA CTGCTTAGCA CCCCTGGCCA AGGTCATCCA 60  
TGACAACTTT GGTATCGTGG AAGGACTCAT GACCACAGTC CATGCCATCA CTNCCACCCA 120  
GAAGACTGTG GATNGCCCCT CCGGGAAACT GTGGCGTGAT GGCCGCGGGG CTCTCCAGAA 180  
CATCATNCCT GCCTCTACTG GCGCTGCCAA GGCTGTGGGC AAGGTCATCC CTGAGCTGAA 240  
CGGGAAGCTC ACTGGCATGG NCTTTCGTGT NCCCACTGGC AANGTGNTCA GTGGTGGTNC 300  
NGANCGTN 308

SEQ ID NO:5009

SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05980

SEQUENCE DESCRIPTION:

GATCCGATTT GTGGAGGATG AGAAAGATGA AGAAGACAAT NAGACGAGAA CACTTCTAAG 60  
GCGAGCCACT CCACACCCAG GGGAGTTAAA GCACATGAAA AAGACAGTGG AGAATTTACG 120  
GAATGACATG AATGCTGCTA AAGGACTGGA CTCAAACAAA AACGAGGTCA ATCATGCCAT 180  
TGACCGAGTG ACCACTTCTG TGTAAGTTT CACCTCCAAG TTTTACCTCC TGTGTCTTCC 240  
TCTGTGTGCG AGACGTTCTT GTCTGCTTNC CGGGAGCCTC ACGTGCTCCT TGTCTTAACC 300  
AGCCCCCGNG NGCCATCTTT CCCGTGGAGT GTTGTN 336

SEQ ID NO:5010

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05981

SEQUENCE DESCRIPTION:

GATCGCTTTT NTGACTGTTC ATCTGTCCTT GACAGTGGCT GTCATATTGA CTACTTTNTT 60  
GATTTGTTGG TATTGGGGAC ATTTTAAAGG CTGAGTTATT TTTGAATGTC ATGTTTATGT 120  
CATAGACGTA GTTTTCGCAT CCTTGAATTA AACTGCCTTA ACTCCTTTNG TGGTATAAGC 180  
AAAACCTCCAT GGNCNNNGTC CTGGTATCCT TTTCTGTGT GGTGCCCCTG TGTCTCTTGG 240  
CCTAGGGTTA AGTNTGCAAG ATAATACTC GTGAGTATTC AGAATGTNGT NCCTAATAAA 300  
TGCATTGTN GTCTGTCTTC TTTTNN 327

SEQ ID NO:5011



SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05982

SEQUENCE DESCRIPTION:

GATCAAGTTT TAAATCCTCC TCCTTCCCTT TTNCTGGAG TTTGAGGGC CAGAGTTTTN 60  
 NTTTTNTT TTGTTTTGT TTTCTGCTT GCTACTGTT TGTGGTGTG AAAAGTGGT 120  
 TAAACCTGAG ACTAACTAA ACACTTCCTT GACCTTCTNG TTGCCTGTNC ATTTTGTGC 180  
 CAAGGAAGTA GCTGCCCCAG TGTATGTCTT GCCTTCTCCG CGTCATTGTT GGAAGAGGAG 240  
 AGATGCATCG AGCAGTCCCA GCTGCTTTTC ATTTATAACG GCTTCTTTCC AGGACCTGAC 300  
 AGAAGTCAGG GAAGAGTCCC TGGGNN 326

SEQ ID NO:5012

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05983

SEQUENCE DESCRIPTION:

GATCATTGA CTGGGCTGGA GAACATCCTT TTACATGGCC NTCCCATGGA TGTGCTGTAC 60  
 ATCTGCTTAA AAGAAAATAA TTACTTTNAT GAGCGTCTT AAAAGGACTC TTGGTGCAAC 120  
 AGACTNAATT GGAAGTCAGC TTTTCTAACT GTCAGTGCAC CAAGCTCTGC TGGAGGAGTG 180  
 ACCAGACTCA CGATTGGTA TAGTGGGGCT CTCAAGCATC TTCAATTTGA ATGTACATGC 240  
 TGCTGAGGAG CCGGTGAAGT CATCAGTTCC GCACATCCCT TCTACCCTNC AACTGCATGG 300  
 GAAGCCAAAG TNCTGGTTTT GAAGAN 326

SEQ ID NO:5013

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05984

SEQUENCE DESCRIPTION:

GATCTGGGG CTAGCAGTGA GTACCCGCAT GGTATCAGCC TGCCTCTCCC GCCCACGCCC 60  
 TGCTGTCTCC AGGCCTATAG ACGTTTCTNT CCAAGGCCCT ATCCCCAAT GTTGTCAGCA 120  
 GATGCCTGGA CAGCACAGCC ACCCATCTCC CATTACATG GCCCACCTCC TGCTTCCCAG 180  
 AGGACTGGCC CTACGTGCTC TCTCTCGTCC TACCTATCAA TGCCAGCAT GGCAGAACCT 240  
 GCAGCCCTTG GCCACTGNAG ATGGAAACCT NTCAGTGTCT TGGNATGACC CTACCNAGGT 300  
 GGTGGGTCTC CAACANAGCC ACTTGTN 327

SEQ ID NO:5014

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05987

SEQUENCE DESCRIPTION:

GATCTCAAAA AAGAAGGAAT TTCTCCTTG TTTCTGCAG TTAATGTAAG AATACTTAA 60

EP 0 679 716 A1

ATCTCTAAGC TTCTGAAGTG TTAGAGGTAG AGATGGTCTA GTAAAGATGT AGTAGTAATG 120  
 TTTTATCCAT TTAGCATGTG TTTATNTNTC CATATGTNCT CAAAGGTGAC TTATTGGTTC 180  
 ACCTCAGTGA TATTACAGCT AAANNNTCA TTCATTAGCA AAAGGNAAAG TGGTCTCAAC 240  
 CTAACATCAG ANGTTGTTCT NATTATGNTN TNATATTGCG TTGGANTATT GGN 293

SEQ ID NO:5015

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05988

SEQUENCE DESCRIPTION:

GATCTATACA GGTATGTCTG ACGGGACGCA GCACCGTGGG CACGCACCAA ATAGAGTTTT 60  
 TAAAAGAGAA A 71

SEQ ID NO:5016

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05989

SEQUENCE DESCRIPTION:

GATCCTNTTC TTTCAGCAGG TGAAAAATAA AACGCAGTTC AAATTTTCATG GTTTTAATTT 60  
 TCANCTCAGA AGCACTCAAA AATGCAAAAT GTGATAATGG GCACTTGTTT AAAAGANTTA 120  
 GTGTATCCAG CCTTCACTCC AGCTGGTTAA AAATGTTGCA CTTNTCAGCA ACCCTACCAC 180  
 TTTTATCTGC TGAAAGGNCA NATGTGCTTG GTTTTACNAT TATGTAATCA CAACTTACTT 240  
 TCTGCTTGTN GTNGCTTAAA ATTATGTATT TGGTCTTTGG GCTGCAANTT GGTTTTATGC 300  
 TGGATTTGAT GNTNACTGGC NGNNAGTTTG ACCTTTGCTG NTATGGGGAA ANTN 354

SEQ ID NO:5017

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05991

SEQUENCE DESCRIPTION:

GATCGGAAGA GGGAGGAGAG GCAGTCTCTT NACAAAATAA AGTATTTTAA TTCATTTNTA 60  
 TTTATTAAAT NAAAAACAA TCCCATGGTG TCCCTNTTGT TTGGTGGAAC CTAATGACTG 120  
 TNGAAATAAA GTCCTGTNTT TNCCCTAAA 149

SEQ ID NO:5018

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05992

SEQUENCE DESCRIPTION:

GATCCAAAA CCTCCACCAT AGAGACTGAT AAATTGTAGC TATTGAAGCT GTACTNCTTT 60  
 GTACATAGGT GCTTTGGGAG ACTCACTCTG ATTATTGTAA ATTNCTCAC TAGCTACCCA 120

ACATTAAATT CAAATAACAG AGAATTTCTA TTGTACAGCC TTGCAACTTT NCTTTAAGTT 180  
TAANCCTTNC TNNAATAA AATTTTAAGT GGCAAAATN ATTATTAGAN GAGAAAANGT 240  
GTGCTCATTT TTNANTATN 259

SEQ ID NO:5019

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05993

SEQUENCE DESCRIPTION:

GATCACCTGA GGGGAAAGGN TTGTNTCTCT CCTTCTGTT GGGNGAGGGG GATGGGGGAC 60  
TTTTNTTGGT GGCTCCACCATATATCCC TCCTTNACCA TAGTACTCCC ACCCACTTCC 120  
ATCACCCATC CAATAAAATG CAGCCAGGTT TAGCCTTTGG CTTTGGTCAC AAA 173

SEQ ID NO:5020

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05994

SEQUENCE DESCRIPTION:

GATCTACCCT CTAGTTTACT TGCTCGGGAG AAGAACTGA CTCGTTTTAT TTAGTGCCTA 60  
TTTAGCGAGC CCAGAGTAAC GTACATTGT NCTGTTTTCA ATTTGTGCT ATCGCAAATC 120  
ACAAAAAAC TGTTATCAAT TCACATTCAT CATCAGCACG AGACCCATTT CCTTGTGCTC 180  
CTGCCAGCTC AGGNTATNAT GTTTCTTTT TCATGTTTGC CAGTCTGTTA GGTAAGANGT 240  
CATATGCGGT TGTTTAAATT TGCAAA 266

SEQ ID NO:5021

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05996

SEQUENCE DESCRIPTION:

GATCAAGGTG ATTCTGAAAG TTTTAATTTT TAATGTTGTA ATGTTATGTT ATTGTTAATT 60  
GTACTTTATT ATGTATTCAA TAGAAAATCA TGATTTATTA ATAAAAGCTT AATTTCTCAA 120  
A 121

SEQ ID NO:5022

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05997

SEQUENCE DESCRIPTION:

GATCTAGTTG TATTTCTCAT ACTAGCAATG AACAATTGGC AGTTGAAGTA AAAGCAAA 58

SEQ ID NO:5023

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05998

SEQUENCE DESCRIPTION:

GATCGTAATA TCTCGAACAT TACATAGACA CTAAAAACCT TTAGTTGTAT TTCATCAAAA 60  
 ATCTGTTTCAT GGGCCACGTT GGTTTCAAAA CATACTATGC TTTNCTTCG TGTTATTTCC 120  
 TATATNCATT TTNGTGTGTA TGTGTATGTC ACAAATATTG ATATGCCTGG TTGTTTATTT 180  
 TGGTNTGCTA TTATGCCTTT TTCAAAATAT AAAANTAAAC TNGTAANTNC TAACNAAA 238

SEQ ID NO:5024

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS05999

SEQUENCE DESCRIPTION:

GATCGAGACC AGCCTGACCA ACATGGTGAA CCCTGTCTCT ACTAAAATAC AAAAATTAGC 60  
 TGGGCGTGTT GGCACACACC TGTAATCCCA GCTACTCAGG AGGCTGAGGC AGGAGAATTA 120  
 CTTTAACCTG CGGGGGGAGC CTAGATTGCG CTA CTGCACT CCAGCCTAGG CAACAGAGGG 180  
 AGACTCTGTC TCATTAAT 198

SEQ ID NO:5025

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06000

SEQUENCE DESCRIPTION:

GATCTTGTGT CAAGTTAACA GGAAGACTGC CCACAGATGA CACTGCATTT GTATCCCTGT 60  
 GGATGTAGAG TATTGGGAAG GCATTTNTTT AGTTTCATGC CTCCAAACCA TGCATTGTCT 120  
 GTNATGTATC TGCCAGCCT TCTCAGAACT CAATGTTGTA CATTTTCCC TCTAGGACCT 180  
 GAATTGGTCT TGGAGGCAGC TTTTAGAAAT CCTCTATGTA GTTCCTGTCC ACATGCACTA 240  
 TATATNGGTT TCTCCNNGNN CCTCTCATGA ATCTGCTCGT TTCTCTACNT CTTGGCTACG 300  
 N 301

SEQ ID NO:5026

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06001

SEQUENCE DESCRIPTION:

GATCCTGGTA ACTGTTCCAG GATTGCTCCA GGTTGAGAT GGTATTGCTA AATTTAAAAT 60  
 TAAACAAGAG ACCCAACAAC AGCTTTTAAA GTGTCTTCTA TNGCATTGTA TTTNNNTNAA 120  
 CTTGCCCAA TGATAGAAAA GTCTTTTGCT GAAATNATTT TNATGATTTT GGTTTATCGT 180  
 TTATAAANG GAAAAGANAT ATACAACTT TGACTTTGGT GACTTTGTGA AGGTTTCTTT 240  
 AAGATGTGCA TTCCTTTCTG CTTGCNCTCT AGTAAAGGNT TTA CTACCGG GAAAAAAAAG 300

N

301

SEQ ID NO:5027

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06004

SEQUENCE DESCRIPTION:

GATCANGAAA AAGACAAAAT CTNTCAAAGC CTTCAAAACC AGGAAAAGAT AAGGAGCCCA 60  
 GGAAAAGNAA AAGGTAAAGT TCGAAGAANT TTAACCATTT TTNACTAGCG ACAGCAN 117

SEQ ID NO:5028

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06005

SEQUENCE DESCRIPTION:

GATCAGGAAT GGTGTGGATT GAGAACTTGT TACTTGAAGA AAAAGAATTT TGATATTGGA 60  
 ATAGCCTGCT AAGCGGTACA TGTGGGTATT TTGGNGTTAC TTAAAAANNA TTTTNGGGAT 120  
 AAGAGAATTT CAGCAAAGAT GTTNTAAATA TATATAGTAA GTATAATGNA TANTANGTAC 180  
 AATGGAAAAAN ACAATTATAT TGTAATAATTA TANCTGGGCA AGCATGGNTG N 231

SEQ ID NO:5029

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06008

SEQUENCE DESCRIPTION:

GATCATGGAA CAGAATCACC CTCTCCTGCA TGTTTTTNTT TCTGTCTCCT GCTTINCTGT 60  
 TCTTTTCCA CTTTCTCTAT GTGTGAGTTG ACTTGGCTGC CTGTAGCTTC ATCGTCAAAG 120  
 CTGGTCCACG TGGGNTCAAC TTGGTGCTCT CACTCTCCTC CAGCATTGTT TTTGGCATCA 180  
 AAGCTAGAAT TAAA 194

SEQ ID NO:5030

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06010

SEQUENCE DESCRIPTION:

GATCNTTTTT AAGAGCGTTT CCATACTATG NTTACATTTT CATATTTNTA TGAATAATTT 60  
 TGCATTCAAT AAACAACCAG ACTCAGAAA 89

SEQ ID NO:5031

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06011

SEQUENCE DESCRIPTION:

5 GATCTTGGAG AGTTTCTCCT TGTGATTTTA GTTCATAAGT ATGTCACCTT TCATTTTATA 60  
GNGTTCATCA TTGAGTAATG GATTAAGTGA AAATCCAGGA GTATCCATCT NCAGTTATGT 120  
NCTGAGGTGA TAATNCATCC AACATATTTN TNAGCATAAA TATNANGCTT CAGN 174

10 SEQ ID NO:5032

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06013

15 SEQUENCE DESCRIPTION:

20 GATCTAAAGC AGCCCTTTTT ACAGTCTAGT TAGGAGAGAG AAAATAATTG CAAATATCCA 60  
CTTAGAGGCA AAGAACAATT TTNATTATC AAAAAGGTTT CTGCACATTG TTGTGGCAAT 120  
ATTGTATCTG TTTAGAAAAT GGGCTTTTCC AAAAGCAAAC AAAGATAGGT TCCTCAGGTG 180  
ACCAAAACTG AAAATCAATA TTTCCATGTT TCATTAATCA NGGCATAAAA TACAATTAAN 240  
GCAAAATATT TTACATTAAA 260

SEQ ID NO:5033

25 SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06014

SEQUENCE DESCRIPTION:

30 GATCTCTGGA GGTCTGAGGCT GCAAGTGAGT CATGTTCTGT TCACTACACT NCAGCCTGGG 60  
CGATAGAGTG AGAACCTGTC TCAAA 85

SEQ ID NO:5034

35 SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06015

SEQUENCE DESCRIPTION:

40 GATCCAGAAC ATGACAACAG AGAGCTGCGT CCACAGGGAA CAAAGCCCTG ACCTNTCTCT 60  
CCACATTACC CTTACAAAAA CAGGCCCTCC CCATGAGAGA GCTACACGGC AGGGGCAGAC 120  
ACTGTGAGTA TAAGCTACTT TCCTCCCTGG AGTGCTCTAT GTGGGCAGAA CATGCTCTCC 180  
TTGCCTCTCC TGGAAGGTGT CTTCTCTATG GCCTGGCTAG AGCTGNAAAA AAGGGACACA 240  
45 CCCNACTTCG GTAAAAGAAA NTAGGGAAAG GCCATATACA NNGNCAGACT TTGTAGTTTA 300  
TTTTGTATTT TTTTNTAAAT NNTTTNCACT TTTACATTTA ANGGNAGATT GN 352

SEQ ID NO:5035

50 SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06016

SEQUENCE DESCRIPTION:

GATCTTAATG GCAAGAAGGC CACAGAGGTA CTTTNCCTTN TTNAGCTCAG GAAAATATGT 60  
 CAGGCTCAAA CCACTTCTCA GGCAGTTTAA TGGACACTAA GTCCATTGTT ACATGAAAGT 120  
 NATAGATAGC AACAAGTTTT GGAGAAGAGA GAGGGNGATA AAAGGGGGAT ACAANNGATG 180  
 TACAGAAATN NTTTCCTGGC TGGNCN 206

SEQ ID NO:5036

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06017

SEQUENCE DESCRIPTION:

GATCTGGCCA TGTATATGGT AGCTGTGTTT TAATTTGAGA ATCTTGAGGG TAGAGCCACA 60  
 AATTTCAATT CTNACATTTT CATTGCAAA GTGACTAGAG AAAAAGAAAT CAGCTTAAAT 120  
 GAGGTATTAA GTAATGTTA GAGTCGTAGG TATTAAGTAG AATATAAATC CTTAGAAATT 180  
 GTCTTTTATAC CTTCAAAAAT TATNCTATGC ATTTNTCATA GANCTGTGAT TACAANGNNG 240  
 TCTGACTACC ATGTCTTTAA ACATATGGCA TCTCTCATCT TTCCTTCCCT TATGGGGGCT 300  
 ACATTTNGTN CCATTTTCCA GNAGTAGNCT TTAACCTNCC GGTGCCNNNC N 351

SEQ ID NO:5037

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06018

SEQUENCE DESCRIPTION:

GATCCTGAGA CTATNTGCAT GCTNCTNTCT AAATGATAAT TAANAGGAAA TTTCATGGAT 60  
 TAACCCATGG GTTTAATGCA GCAAGGAAAC TTACAATGTC CCTNTATATA TAACATGCAN 120  
 CTTGTTTTGG N 131

SEQ ID NO:5038

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06020

SEQUENCE DESCRIPTION:

GATCCTNCAG GAGATTGAGC GTCTCCGCCT GGAACACGAG CAGGCCTCCC AGCCCACCCN 60  
 TGAGAAGGCA CAGCAGAACC CCACGCTGCT GGCAGAGCTG CGGCTGCTGA GGCAAAGGAA 120  
 GNATGAACTG GAGCAGAGGA TGTCGGCCCT GCAGNAGAGC AGGCGGGAGC TGATGNGTCC 180  
 ANNTGGAAGA GCTGATGAAG TTGNCCNN 208

SEQ ID NO:5039

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS06021

SEQUENCE DESCRIPTION:

GATCTGAGTG ACAGGGTCAA GTTCTCTTTG AAAACAGGAG CTTTTCAGGT GGTAACCTCCC 60  
 CAACCTGACA TTGGTACTGT GCAATAAAGA CACCCCCTAC CCTCACCCAC GGCTGGCTGC 120  
 TTCAGCCTTG GGCATCTTCA TAAATGGAAA 150

SEQ ID NO:5040

SEQUENCE LENGTH:365

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06022

SEQUENCE DESCRIPTION:

GATCTGCTGG GTTTTAAGGA GTGATTNCT TTCTNCCCCT TGAAGGGGAA AAAGCTATTT 60  
 CAATTGGTAC ATTTAAAGTC CCCCAACTAT GGGGAGGTAC CAATTCTGGA CANNNTGCCA 120  
 CTACAACAAC ACTAAACCTG AACTTTTCAA CTCCGTTGGT GGTGGGAGGC AGCGGGCAGA 180  
 AATTTACTGT TGGCCACTGN CAGGTCTATT TNATATTTCA AAGGAATATT GGGTGCTGCA 240  
 TATAGGNACT GAAGGGGTCA ATGNATTAAA CCTGTGATTA GGTGNTTTC CTGTCATTTT 300  
 TGAGAGACTA AAATNGTGGG GGGGCAGATG TNCANAATAC CTGGTACANG TTTTAAAAA 360  
 NTGGN 365

SEQ ID NO:5041

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06023

SEQUENCE DESCRIPTION:

GATCTTNACC TTATTCAGTC AACTCCCTTT AAACCCCTGG CACTGAAAAC ACCACCTCGT 60  
 GTACTTACGC TGAGTGAAAG ACCACTAGAT TTTNTGGATT TAGAAAGACC TCNNNCAACC 120  
 CCTCAAAATG AAGAAATCCG AGCANNN 147

SEQ ID NO:5042

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06024

SEQUENCE DESCRIPTION:

GATCCGTCCT CATTTTATTG GTGATGATGA ATGGGAATAA AATNAGGGGG CTGTCTACTA 60  
 GAGCCTGGAA TAAATATGCT GCTTTGTGGA TTTTAAA 98

SEQ ID NO:5043

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06025

SEQUENCE DESCRIPTION:



GATCTGTATG TNAATATCGC CAAGCAGGAT ATCATGTTGT CCCTGGCAAA CCTGGTGAGA 60  
 CTCAACCAAG CCCTTTTCC CCAAGCAAG AGGAAATGG AATCTNTGTA TCAGTGTGGT 120  
 TTTGATGACA CTGTAAAGTT TNTACTTAAA GAAAATTGGT TTGAATAAAA TGCATAAAAG 180  
 TTTATANTGC ATTNATTGT NNANNTGN 208

SEQ ID NO:5044

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06026

SEQUENCE DESCRIPTION:

GATCTTTGCC CACCTCTTCC TCAGAGCCCC CACTGAGGGG CCGTAGCCCT ATCTAGGGCT 60  
 GTGGAAGGAG CAGACTGGT CCTAACTCTC TCCCTCCTCC TGCCACACA CATCAAAAGA 120  
 ATCTCCCTA CACCCTTCTC TGCCTTTATT TTTGATTG TGCAACTGT AACTAGGTGT 180  
 TTATGGAGTA AAGGAGAATG GAAAAAGAA A 211

SEQ ID NO:5045

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06027

SEQUENCE DESCRIPTION:

GATCTTGTTT ACAGCAGTGC TTTGTGAAC AATTATTTAT TTGCTGAAAG NGCTCTTCTG 60  
 AACTGTGTCC TTTAATTTT TGCTTAGAAT AGAATGGAAC AAGTTTAAAT TTCAAGGAAA 120  
 TATGAAGGCA CTTCTNTTT TTCTAAGAAG GAAGTTGCTA GATGATTCTT TCATCACACT 180  
 TACTTAAAGT ACTGNGAAGA GTATCTGTAA ATAAAAGGGT TCCAACCTTT TAAANAAGNN 240  
 GGAANAACT TTTTGGTGCT CCAGTGTAGG GCTATCTGT NNANAAANTG TCAACAAGGG 300  
 GGAAANGTAA GNCTGTCNAG CTNGGGGATT GGTCATTGN NTTAN 345

SEQ ID NO:5046

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06028

SEQUENCE DESCRIPTION:

GATCTTATAA ATTTCTGGG CAAGAGTGTA TGCATACAAA GTTTTCACTN TTGTGAAATG 60  
 TAATTTNCT GTTTTGCAA NGGGATGAGG TGATTGGAAT TGCTTTNACC ATGCTGCCTT 120  
 TATTCTCAA CTGGCAAAC TAGCATGTTA GGTGTATTAA CCTCATCAGT CTTGAAGAAC 180  
 ATGTGGCTCA TGAGTATAAC ACTTCTGTAG NGNNCCCCN NACANAAGTG AAGAATTAAC 240  
 TTCTCCTNCA GAACAAGTGC ANTTCAGAAG GCAAGCTCTG CATTCTACCT TGNTTGAN 298

SEQ ID NO:5047

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS06030

SEQUENCE DESCRIPTION:

GATCGGGGAG CCACAGGGTG TCCAGACCCA GCGGGAGCCG AGGATTCAGG AGAATCTCCC 60  
 CAGTCAGCTT CAGAGGTGCC CACAGTNTGA GCTCTAGTGT CTNCCAGGTA GGGGGNCAAA 120  
 GCGGNAANCT GNCCGGGCCT NGGGGGTGCA AGN 153

SEQ ID NO:5048

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06031

SEQUENCE DESCRIPTION:

GATCAACATT CGCAATGCCC GGAAACACTT TAAGAAGCTG GAGAGAGTGG ATGGCCCCAA 60  
 GCACAGTCTC CTTATGCGTT GAATATTGCC AAATNCTCTT NCTGAAAATC CTGAATTGCC 120  
 TTTTNGTTT GCATCCTTTA TTTTNAATAT TCATAATGTC GTGTGCTTAA AAGTGGGCTT 180  
 TGAAGTGTGT GCTGCTTACT CCTNTCATCT TTCTCCCCGC TTCCCAGTC TTAAACATT 240  
 GGACGNTATT TACTCAGCTA CCCAGTAGAG CTTGAAGCTG ACCTTTCTGA GAAAGTTGGG 300  
 TATGGTGGTA ACACTTAAAG TAGGTGGTTC CGTGTGGTGT TCTTCANTNN N 351

SEQ ID NO:5049

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06032

SEQUENCE DESCRIPTION:

GATCAACAAA TTGCTCAACC TGCAAAATCT TTGATTAGAC TTAGCCAGCC CATCTGGCCT 60  
 GCTTTGGGTT TAAAAAATAA AAAAAANNTT TTTTAACCNC ANAANTGGAA AAAGGGGAAG 120  
 GGNN 124

SEQ ID NO:5050

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06034

SEQUENCE DESCRIPTION:

GATCATGACT ACTGGGTTGT CATTTCATG GACAGTGCTA TGAAATAAGT ATTTTGTAAA 60  
 NCAACGGAAA TAGTTTATAT CGATATTTCT GATTCAAATT TANCCATCCA ATTGTTTAAT 120  
 TAACCTTACT GATTTTTTAC CTATATCACT TTNCTCTNAC ACTGNAANTA TTAGTTCTAN 180  
 TAGCATTATG NCANTTACCT ATGTTGCTTT ATGAANGN 218

SEQ ID NO:5051

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06035

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCAATGCT GGCTTCCACG CCTGANTTCT ACCAAGTATG CCACACCAAA AAGGATTATN 60  
 AAGAAATTGG ACCTAGCATT TNCGTGACA ATCCAGTGTT TGGAGTCATG TCGTAAAATT 120  
 GNCNCCNN 128

SEQ ID NO:5052

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06036

## SEQUENCE DESCRIPTION:

GATCTCATTC AGATTCCAAA GAGAATCATT TACAAGTTAA TTTCTGTCTC CTTGGTCCAT 60  
 TCCTTCTCTC TAATAATCAT TTAAGTTCC TCAAAGAATT GTCTACATTA CCCATCTCCT 120  
 CTTTTGCCCTC TGAGAAAGAG TATATAAGCT TCTGTACCCC ACTGGGGGGT TGGGGTAATA 180  
 TTCTGTGGTC CTCAGCCCTG TACCTTAATA AATTTGTATG CCTTNTCTCT TAAA 234

SEQ ID NO:5053

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06038

## SEQUENCE DESCRIPTION:

GATCTGCAAG GCATAGGCAA GCCTCTTAGA GAATCAGAAA AGTGATTGG AAGGAAC TTC 60  
 AGCTGTTACT ACTTTGTTTA AGCAAATCAA ATGCTGTTCT TTAATGTTAC TGGACGTTTC 120  
 AAATTAAACA CAAGAAAACC TGAAA 145

SEQ ID NO:5054

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06039

## SEQUENCE DESCRIPTION:

GATCAACTGA AGACCCCAA AGGCCCTAC TTGATGGTTT TGAGGGGCAA CATTGACTCA 60  
 TTTGCCCCNT CCCTCTCGGA ATGTTGGACA AAGGGAATAA AATTGGGGAT ATGTCTACTT 120  
 CAAA 124

SEQ ID NO:5055

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06040

## SEQUENCE DESCRIPTION:

GATCTAAAC ANCTTCAGAC TACCTANGAA ATANTTNNAC CAAATAAGAA ACAGCACTGT 60  
 GGAATAAAAT ATACCATTGT GAACATATCT GATGCTGCAA TGAAATGTAA AGTTCCTN 118

SEQ ID NO:5056

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06041

SEQUENCE DESCRIPTION:

GATCTCCTAC TCCATCCAGT CCTGAGGAGC CTTAGGATGC AGCATNCCTT CAGGAGACAC 60  
TGCTGGACCT CAGCATTCCC TTGATATCAG TCCCCTTCAC TGCAGAGCCT TGCCTTTCCC 120  
CTCTGCCTGT TTCCTTTTCC TCTCCCAACC CTCTGGTTGG TGATTCAACT TGGGCTCCAA 180  
GACTTGGGTA AGCTCTGGGC CTTACAGAA TGATGGCACC TNNNNNAACC CTCATGGGTG 240  
GTGTCTGAGA GCGTGAAGG GCCTGGAGCC ACTCTGCTAG AAGAGACCAA TAAAGGGCAG 300  
GTGTGGAAC GGCAAA 316

SEQ ID NO:5057

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06042

SEQUENCE DESCRIPTION:

GATCTATTC TTNCACTTG TATACTTG NAATAAATNC CTCATCCCTT AGACTAAGAG 60  
AGTGGGTGTC TGTGAAAATN GTNTTCTCCT TCATAATACC TAAATN 106

SEQ ID NO:5058

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06043

SEQUENCE DESCRIPTION:

GATCGAATT AAAAGAACAA TGGAACCCTG ACTACGTTTC AACAAAAATA AAACNGTTT 60  
TTTTCCCTCC TAAA 74

SEQ ID NO:5059

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06044

SEQUENCE DESCRIPTION:

GATCTCTGGC GCTGGCAGAA GCAGAATCCT TCAGGCTTTG GCANGCAAGC NTGAGGACCC 60  
TCCCCTACCA AGGACCAGGA AAAGCAGCAG CTGCCTGCTC TCCAGCCTNT GGCAGGAACT 120  
CAGGGCCCTG GAGCTGCTGG GGCCAAGCCA AGGCCTNCCC TACCTCAAAC CCCAGCTGGG 180  
CCCGNTTAGC CCACCAGGCA TGAGGCCAAG GGCTCCACTG ACCAGGAGGC CGAGGTCTCT 240  
AACTCTTATN TTCCACAGGG TCCAAGAGTT CATCAGGACC NNNAAGAGTG AGTTNAGGGG 300  
GGGCAAGGNT TCTNGNAACA AAAGN 325

SEQ ID NO:5060

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06045

SEQUENCE DESCRIPTION:

GATCTGCCTN TAAAGCCAGT TTAAGAAGCA CTNATGANAA CACCTGGACT GTGTATAGNG 60  
ATTGCACATT CCTTATCCTT CAGCTNCAGG ACAGGTGGAG CAAATGN 107

SEQ ID NO:5061

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06046

SEQUENCE DESCRIPTION:

GATCTCAGAG CATTCAATT AGGGATGCTC AAACGCAACT TTTTCTACTT CCCCATTTCA 60  
GGTGTGAGAT GTAACCCACC TTNACCATAA ATTGGCTTTN NATAGTGCTA AA 112

SEQ ID NO:5062

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06047

SEQUENCE DESCRIPTION:

GATCACAACA TACAAATTCA ATTCAGTGCA TGCTTTAGGT GTTAAGCATG AGATTGTACA 60  
TGTTTACTGT TAGGTCCTTG CATCTGTGGT GCTAGGTGAG TATGAGAAGA TGCAAGGAC 120  
TGGACGTATT TTGTTGCCTA AAAAAAAAAAG GNTGTTTGTN GGCGTTTAA ATATGCTTAT 180  
TTNGTGTGTC NCNNNCTACC TTTTACACAC TGTGCTTTG TGGGTTTGTT TNGNATGTGC 240  
GTGTGTTATA CAGTNGTTAA ATTTCCNTGC AGAAAAATAA ATGTCCNGAA TTCTCAAA 298

SEQ ID NO:5063

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06048

SEQUENCE DESCRIPTION:

GATCTCCCAG TGAGCCATCA CGATGCCCGN TTTCAAATAA ATNTTAATAT TGTCACCAGA 60  
AA 62

SEQ ID NO:5064

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06049

SEQUENCE DESCRIPTION:

GATCTNCTGC CATGATGCCT ATTTGGTGTN TTTCTAATTA AAATGAAATC ACAA 55

# EP 0 679 716 A1

SEQ ID NO:5065  
SEQUENCE LENGTH:51  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06050  
SEQUENCE DESCRIPTION:  
GATCGCATCA TTGCACTCTA ACCTGGGCAA CAAGAGCAAA ACTCCATCAA A 51

SEQ ID NO:5066  
SEQUENCE LENGTH:210  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06051  
SEQUENCE DESCRIPTION:  
GATCTGCTGA AAGGNAAGCA AGAACTATAA GGAGGNTGTG TAGTTGCAAA AATGGCTCCA 60  
TCGGTAACTC AAGCTTCAGA ATGTTATGAC ATACAGAAAA TCAAAGATGC TGTGTCTTAG 120  
CATTGAGTAA TATGGGTGGT GCTGTCTGGT CAGATTCAGT NAACTGTTCA GAACAAAATT 180  
NCCTCTGAAA TNCNGTTGAG AAAGNCTGTN 210

SEQ ID NO:5067  
SEQUENCE LENGTH:211  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06052  
SEQUENCE DESCRIPTION:  
GATCAAGTCA GCATTGCGG TCGGGATTG GGCAGGGAAC TTTGGGGTGC AAATATCTGG 60  
TGAAACCACC AGAGAATTTN TTTGTCAAAG TGACATGTAT AATTTTAGTT GAGACGTGTT 120  
TGTGTATATA TGTGTATTTG CCTTTNTTA GTAGCACGGT TATTTGCTAA AATAATTGTC 180  
AAAAAATTGC TCTGTCGGTC GGTCTTTGAT N 211

SEQ ID NO:5068  
SEQUENCE LENGTH:230  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06053  
SEQUENCE DESCRIPTION:  
GATCTAGAAT CTTGTCCTCA GGCTTCTAGG GGNTTATCTG AGTCTTTTAT CTAAGACAAA 60  
TGCAACAGTT TTCTTTTCAA ATGCTCAGAA AAATAGTGAT GATGATGATG ATGATGATGT 120  
TCATTTGTAT ACATTTACAT GCAACCACAG CATTGTTTTT ATTATAATAC CTTAGCAATA 180  
ACTAATGAGA ACATGTTAGG TGATGTTAAA TAAATAATT TTTTCCCAAA 230

SEQ ID NO:5069  
SEQUENCE LENGTH:108  
SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS06054

SEQUENCE DESCRIPTION:

GATCGCACGG ATGCAGCAGG AAGACCAGGA GGGGCCGCCT ACGTAGCCCC AGCTCCAGCC 60  
ATCCACCCCN CAGCCCTTN CTNCAACGTC ACCANTAAAT TTNTTTTN 108

SEQ ID NO:5070

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06055

SEQUENCE DESCRIPTION:

GATCACTGTT AATGATTTGC CTGTGGGACG CTCCGTGGAT GAGGCTCTGC GGCTGGTCCA 60  
NNNNTTCCAG TACACAGACG AGCATGGGGA AGTTTGTCCC GCTGGCTGGA AGCTGGCAGT 120  
GACACGATTA AGCCCAACGT GGATGACAGC AAGGAATATT TNTCCAAACA CAATTAGGCT 180  
GGCTAACGGA TAGTGAGCTT GTGCCCCTGC CTAGGTGCCT GTNCTGGGTG TCCACCTGTG 240  
CCCCACCTG GNTGCCCTAT GCTGACCCAG GAAAGGCCAG ACCTGCCCCCT CCAAACCTCA 300  
CAGTATGGGA CCCTGGAGGG CTAGGCCAAG GNCTTTTTN 339

SEQ ID NO:5071

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06056

SEQUENCE DESCRIPTION:

GATCACAACC TCANCNAAGA CCACGANGAA GCCCNCAACA GCCACGCCCA CGACTGCCCG 60  
GACGAGGCCG ACCACAGACG TAAGTGCAGG TAAAAATNGA GN 102

SEQ ID NO:5072

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06057

SEQUENCE DESCRIPTION:

GATCGCCTTA ATACCAGAAA TGATTAGAAG TGCTGATTTA GATTCAACAA ATACCATATG 60  
TCCTTATCAT TTTTGTAAAG AAGAAATTGG TTAAGTCCTA ACTTCAATG TGTACCCAAA 120  
TACTTGTATT TTATGCTTTT NATAAAATGT AATTTTCAGC ATTANTACAC ATCCGATTAT 180  
GCCTTATTTA TATATGGNGG ANTAAAGGTT ACCATGTTTA TACCTGTAA A 231

SEQ ID NO:5073

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06059

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTTGGTT TCATGTGTTT TTGAAAGTGT TATTGTTTAA AAAATGAAAA AAGCATATNT 60  
GCTAAAGAGC TGTCAGGTTT TCATTACTGA CTCTGTANAA TACACTGNTC TTTGTGTACT 120  
GTGTGTTATT TTGCCCAGCT NGCTGCATTA GCCTTCAAAN GTATTTGGGA AACCTNAAGG 180  
ATGAACCTAC AGTTTCTNGC AAAGGTACCA TTNCCTTTCC TGGGGGTANT TTNGGTCCCN 240  
GTNAACTGGN 250

SEQ ID NO:5074

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06060

SEQUENCE DESCRIPTION:

GATCCTCGCG GGCCTCGGAG AATTCCCCCA CTGCCATGCC CTCCCCCAG TACCAGTGCA 60  
CTAAGGCGCA CTTGGCCGAA CTTATGGTCC AGGCAGGCC AGGCCTCCGT GATGGCCGTG 120  
GTGTTGCTCA GCATGCACAC CGNCCGCTGC ACTTTGGCCA GGTCTCCAC AGGGACCACC 180  
GTGGGGGGCT GGTAGTTAAT NCCCACCTGT CAGAGATGGG CAGCATAGAA TGAAGTTTAT 240  
ATTGGGCTCA GAAATGGGGA GCTCATTAAA AATCAGAGCT TGTGGNACCA GTTNCAAA 298

SEQ ID NO:5075

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06061

SEQUENCE DESCRIPTION:

GATCACTGTG TCAATGGAT GGGAAATNTT ATNTTAATAT AAACAGTAAA ATAGCATTGT 60  
TTTCACTTGC AGCTTTNAAA 80

SEQ ID NO:5076

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06062

SEQUENCE DESCRIPTION:

GATCTGTATG TNCAATATGG TAGCTACTAG CTACATACAT CTATGAGCCA GACACTTAAG 60  
CACTTGANGT TTGGCTACTG CACATTGACA CATGGTGTTA GTAAAANCAT ACACTGGATA 120  
CACTGGATTT TTGGNCTTAG TATGGAAAAA TATATTANGT ACCTCANTTT AAAAATACTT 180  
ATTACATGTT AATATTTTGG TTGTANNNNN 210

SEQ ID NO:5077

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06064

SEQUENCE DESCRIPTION:

GATCATGTTG TATTTNATTT TACTTATTTT TTTTACATTT CCCAAGGCTC TGTCATCCAC 60



CTTTTCATTA AATCATTCTA CCAATCTCAA A

91

SEQ ID NO:5078

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06065

SEQUENCE DESCRIPTION:

GATCAATGTA AATCCTCACC TGCCCTTTGA AGAGCCAATA AGGGCATCTT TGTCTTTAAA 60  
TACAGCAAAT GTTATTCAGA TTTTGTACTT GTCTATCTGT TTACCTCAGT GTAGATGATA 120  
TGAGGATGGN ATAACATATGT AAATTGTTTT TGAAAATAAT TTGTTTCCCC ACAACTTTTG 180  
AAGGTTTTAT TTGTNGTTGT TATTACTAGT TCAGTCCCAA ACTNACCCTG TCCTTTTCAG 240  
AGAGCTAATG GCCATGCTTT NCTTCAAAGG AAAGAATAAT TNATTTGGAA TGANAGTGGG 300  
GATTACTTTG CATAANN 317

SEQ ID NO:5079

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06066

SEQUENCE DESCRIPTION:

GATCTTTATT CTAACCTTTT TTTGTAAAN ATATCTATTG ATTTCCATAT GCAATAAACC 60  
TTTTTTTCAG AGAAA 75

SEQ ID NO:5080

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06067

SEQUENCE DESCRIPTION:

GATCGCACCA CTGCACTCCA GTCTGGCGAC AGAGTGAGAC TACATCTCAA AAAAAAANGC 60  
CGCAATTTTN CATTGNTTC ANCAGANCTC TGCCATTCTA AACATTTCTA AACTTTTACT 120  
CTCAATTNCT GTACTTAAN 139

SEQ ID NO:5081

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06068

SEQUENCE DESCRIPTION:

GATCTCATTT TCAGTTTAAG TAACTNCTGT TACTTAAGTG ATTGCACTTT TCTCAAATTG 60  
AAGTTTAATG GAATAATAGT TCTCAGGATA GTATTTTGTA AATAAAGATG GNCTTGAATA 120  
TGAAA 125

SEQ ID NO:5082

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06069

SEQUENCE DESCRIPTION:

GATCCTACCA TGGCAAGAAG AGCTTCGAGA CTTTCTCTCA CCGCCGCTCT TGCCTGGTGA 60  
GGCCTCTAAT GAATGATGAA GGCCTGAAGG TCAGATACCC CCCGAGCCCG GCCAAGATGA 120  
CCCAGCACTG AGGAGGGGTT GCTCCGCCTG GCCTGGCCAT ACTGTGTCCC ATCGGAGTGC 180  
GGACCACNT NACTGGCTCT CCTGGCCCTG GGAGAATCGC TCCTGCAGCC CCAGCCCAGN 240  
CNCANTNCTA TGNTGACCTG CTGACCTGTG CACACCCNAC TTN 284

SEQ ID NO:5083

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06070

SEQUENCE DESCRIPTION:

GATCTAACCA TGACCTGTTT CACGTCATTC ACATTCAAAA TGAATGAAGG GATGANCATT 60  
TTCTCTGGTC ATTTTTTATT ATTTATACCC TTTTGCAAAT NCTAGTAGAG AATGAAGTGG 120  
AGGAATAAGT TATAAATGAA CAGTGGCTTA TGA CTCCAAG AGTTAATCGT GTTATTTTGG 180  
TAGCTGTCTG TGTAGGTGTG CATGTNGTTG CGAGTTTGTA TTGNGNTTTA CAAGCAAAAN 240  
TTATATNATG NTTCAACTTT CTGGAAATGC TTNTAATTTN 280

SEQ ID NO:5084

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06071

SEQUENCE DESCRIPTION:

GATCATAATA TGAATNTCCC ACTTATTAAT AGCCTTTTAA TAAATATATA ATTAATTTCA 60  
AA 62

SEQ ID NO:5085

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06072

SEQUENCE DESCRIPTION:

GATCTATAAT CACCA GTGCA CTCCACCCTG GGTGACAGAA TAAGACCCTG GCTGAAA 57

SEQ ID NO:5086

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06074

## SEQUENCE DESCRIPTION:

GATCTCAGGA TTNAAGCACA GTGCCTGGCA TACAGCAGGT GCTCAATAAA TACTTATCAA 60  
ATTGGAAA 68

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SEQ ID NO:5087

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06075

## SEQUENCE DESCRIPTION:

GATCAAGGTT TAGTTTAACT TCCACTGTGA AAATAAAGCT TACATAGTTT TCTTCCTTTG 60  
AAAGACTGTG CTGTCCTTTA ACATAGGTTT TTAANGACTA GGATATTGAA TGTGAAACAT 120  
CCGTTTTTCAT TGTTCACTTC TAAACCAAAA ATTATGTGTT GCCAAAACCA AACCCAGGTT 180  
CATGAGTATG GTGTCTATTA TAGTGAACAT GTACTTNGAG CTTATTGGTT TTATTCTGTT 240  
ATTAGATNTT TCAGGGTGTA AACANGNNN 269

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SEQ ID NO:5088

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06076

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## SEQUENCE DESCRIPTION:

GATCGGCAGG GCAGGAATCT GAGCGCTGGC CCCGTGGTGA GGCCATGTTC TCATAATCAG 60  
GCTCCAGCCA GAAAAATAAG AAACACCGCA ACAGGCTTCA GTATCAGGGC TGAAACTGCT 120  
GGATGANTAA ACTATTTATT AAAAACGGAA A 151

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SEQ ID NO:5089

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06077

## SEQUENCE DESCRIPTION:

GATCTTGGCT TAATTTAATG TATTAATCTG TTTGTGCAA CATAGTACCA CCATTTAAAA 60  
ATGTTAGGGA GATGAGTTGC AGTTTTTATA ATAGATTTT TTTAAAGTTT GGTATTGTAA 120  
ANCATTACA CCTCTGTCCC TCAAANTTGN TAATTACGGT TAAAGTGCAG TCATTTGTGG 180  
NTAGAATCTT GTTTNGTTGC TNCCATTATT GGGGTCCNCC NAAGGAATTG AGGAGAGGNC 240  
CGAATAGAGC CCAATTCNTA TAANGAN 267

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SEQ ID NO:5090

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06078

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## SEQUENCE DESCRIPTION:

GATCTCAGGG AAAAATTTTA ATCACTGTGT ATAATGATAC TGAACCTGA TTAATAACAG 60

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AAATTCAGGA TGTAAGCCA CAGAATGGGN TTTATTAATG TGGGATACCT CAGACTGTTT 120  
GTTTTCTTTC TGGGNAGCAA AGTGTGTTCT ATAATGAATA AATATAGAGT GGTTTTTAAA 180

5 SEQ ID NO:5091  
SEQUENCE LENGTH:121  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS06079  
SEQUENCE DESCRIPTION:  
GATCTTCCTG GNACCCTGAG GGTCGTCCTC CAGCAGGGGC TTCTTNGACC CCTGTCTGAG 60  
GGGTCGCGTC TTAGTGGGCG GGATTCTTTT CCCTTTGAAT AAAAATGGAT TCAAACCCAA 120  
A 121

15 SEQ ID NO:5092  
SEQUENCE LENGTH:378  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS06080

SEQUENCE DESCRIPTION:  
GATCTGTNTT GTTCCTGCAG CAAAAATCCT CTATGGACAT AGGAGGTGCT GTGTCCCATG 60  
CCCTCTTGCC CTGNCAGTGT CCCATGGGCC CCCTTCTGCT CCCTGCCCCC TCCCTGCTAC 120  
25 TGCTGATGCA CTGTCCTCTC CCTGCAGCCC CTGGCTTCN AGCCTTCCTC CTGACCCCTT 180  
CCAACAGCCT TGGAACCTCA GCTGCCACCA CCCTNTGGGT CGGACACTGG GACCCANTGG 240  
NCCAGTCTTG GNTGCTGNTT ACCCCTAGCC TTGATGNCTG CCCAGGGGAC CCCNAGCCCN 300  
CTTCNGTTGN CNTGCAGCTT TAACAGAGTG AACCATGTGT ATTGTACAGG CGGGGGTTGT 360  
30 TAATTGNAGA AAACNNAN 378

SEQ ID NO:5093  
SEQUENCE LENGTH:81  
SEQUENCE TYPE:nucleic acid  
35 TOPOLOGY:linear  
CLONE:HUMGS06081

SEQUENCE DESCRIPTION:  
GATCACACCA CTGCACTCCA ACCTGGACAA CAGAGCAATA TTGTGTCTCA AAAAATAATA 60  
40 AATAAATAAA TAAATAGTAA A 81

SEQ ID NO:5094  
SEQUENCE LENGTH:302  
SEQUENCE TYPE:nucleic acid  
45 TOPOLOGY:linear  
CLONE:HUMGS06083

SEQUENCE DESCRIPTION:  
GATCACCCGG AAGTTCAGGC TGAATTCTGA AGGCAAACTT GAGCAGACGG TCTCCATGGC 60  
50 AACCACGACA CAGCCAATNA CTCAGCATCT TCACGTCACC TACAAGAAGG TGACCCCGTA 120  
AACCTAGAGC TTCTGGAGCC CTCGGGAGGG CCTGGCTACT GTGCCTCAAC GGTTCCGGCTC 180

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EP 0 679 716 A1

CTCAACAGAC AGTCCCTGCG GCAGAAGTGG GTGTGGCCGT GAGCCTCTGC AGGCTCAAGA 240  
GTGTTGTCCA GATGTTTCTG TACTGGCATA GAAAAACCAA ATAAAAGGCC TTTNTTTT 300  
AA 302

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SEQ ID NO:5095  
SEQUENCE LENGTH:55  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS06084  
SEQUENCE DESCRIPTION:  
GATCTGACTT CAGTTGTGCA GATNACAGCA TGATAAATGA GTCGGGACCA TCAAA 55

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SEQ ID NO:5096  
SEQUENCE LENGTH:145  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS06085  
SEQUENCE DESCRIPTION:  
GATCAACAGA TGCTGGCAGA AATGGCTGTN TCCCTGGCCT TGAGAAGCAG ATNCAGCTCC 60  
CTGTCCCCAG AGGCCTACAG TCATATGGTA CNCCACAGN CTCGCTTGGN TCGCTACAG 120  
GAGGCGGCGT CANGGAAGCT TNCTN 145

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SEQ ID NO:5097  
SEQUENCE LENGTH:199  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS06086  
SEQUENCE DESCRIPTION:  
GATCTCATGA GAATTCACCTC ACTATTATGA GAACAGCATG GGGAAAACCN CTCCCATAAT 60  
TCAATCACTN TCCTCTCTCC ACACGTGGGG ATTACAATTT GAGACAAAAC CTGGGTGGGG 120  
ACACAGAGCC AGACTATATC AGGGGGCTTA TGTTTATCCA NTTGTNATGG CCTCACTTNT 180  
TGNAAGACT GTNCTNNCN 199

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SEQ ID NO:5098  
SEQUENCE LENGTH:249  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06087

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SEQUENCE DESCRIPTION:  
GATCACAGAC TGTAAGATTT TGAAAAGTCA CTTTTATTTT NAATTATTTN ACATATGCAA 60  
CATGAAGAAA TCGTGTAGGT GGGTTTTTTT TTNAATAAC AAAATCACTG TTAAAGAAA 120  
CAGTGGCATA GACTCCTTCA CACATCACTG TGGCACCAGC AACTACTTCT TTATATTGTN 180  
CTTCATATCC CAAATTAGAG TTTACAGGGN CAGTCTTCAT TACTTGTA ATAAANTATG 240  
ANTCTCAA 249

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EP 0 679 716 A1

SEQ ID NO:5099

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06089

SEQUENCE DESCRIPTION:

GATCTGCAGT CCTGCCTCTG CCACAGTCTC TCTGTTGTCC CCACATCTAC CCAACTTCCT 60  
GTACTGTTGC CCTTCTGATG TTAATAAAAG CAGCTGTTAC TCCCACAAA 109

SEQ ID NO:5100

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06090

SEQUENCE DESCRIPTION:

GATCACGGAC GTGCAGCTCG CCATCTTCGN CAACATGCTG GCGTGTGCG TCTTCTTGCT 60  
TGTCGTTCTC TATCACTACG TGGCCGTCAA CAATCCCAAG AAGCAGGAAT GAAAGTGGCG 120  
CTTTCTCCGN CCCAGGGTTC CAGGACATAG TCTGAGGCAA GATGGAGGGT ATGTGGGGCC 180  
TTCACACTTC ACTTCATCCC TTCTACCCAT CACANCATAC AAAGCANCTA CACCTGGATT 240  
TTTCCAAACA ACTTTATTT CCTCAGAGTC NGNNGNAATN CTATGGNNCA AGANGCTGNC 300  
ACTGAATAGG GCCNAGTATA GGGGCTTGCT TTTCTACTCT N 341

SEQ ID NO:5101

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06091

SEQUENCE DESCRIPTION:

GATCTGGTAC CGCAGTAGCG CCGCCGCCGC CGCCGNCGGA GCCTGTCGTC GTCCTGTCCC 60  
CAGCCTNCTT GTGTCCCGTG AGGTTGTCAA TAAACCTGCC CTCGGGCTGC CGGCAAA 117

SEQ ID NO:5102

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06092

SEQUENCE DESCRIPTION:

GATCCAAAAG GACTCATCTA AAACACAAGT TGGGTAGAGG AGATAGGTGA GTACTATTAT 60  
ATTATGTTCA TGGAAAATNA GTTCATGGGC TTTCTCTAA TTTTATTTT AAAAATAAAT 120  
GTAAATATTA AATAAAATTT TTAAATGAA A 151

SEQ ID NO:5103

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS06093

SEQUENCE DESCRIPTION:

5 GATCAGCTTT TAATATCTGT CAAATAAAAA TTGAAATTGA AGATGGTATA TAAGATTTC 60  
GNAATAAAC TACTCTGAAT ACTAAA 86

SEQ ID NO:5104

SEQUENCE LENGTH:210

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06094

SEQUENCE DESCRIPTION:

15 GATCTAATCC GTNTCCCACA TGTCAGGG AATCCNAGGT CTGCCCTGAG CTCCTGTGT 60  
CCTTGGNAAA GTCGGTTAAT CTCTGGGCCT CACTGTCCTC ATCGCTGAGC TTGGGGACTT 120  
GTAACANATG ATTTCTAAGT ATCTNCCAGC TTTGANTAGA GCATTTGTNT TGGGTGGCCA 180  
GGCTTAANGT TTAAAGGCAT AANGAAAANN 210

20 SEQ ID NO:5105

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS06095

SEQUENCE DESCRIPTION:

30 GATCATATTG GTCATGTCTA TTGGTGTATT ATTCAGTAT CACCAATGTT TTCAGAAATA 60  
CAGTACTAAT TCATCATTAA ACTCTTTGAA GTTAATATTT TCCTGCCTTC TAACTTATAG 120  
ACTCAACTAT GTATCTGTAG TTTTGGGAA TGGGGTGGTG TTTTNNCTT TGTGTTGGGA 180  
AGTTATTGAG AAAACCTATA TAATANAATT NAANATTATA GTTTAAAAA AANNNCANNN 240  
NN 242

35 SEQ ID NO:5106

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS06097

SEQUENCE DESCRIPTION:

45 GATCTGCCCT TGGCCTCCCA AAGTGTCGGA ANNACAGGCA TGNGCCACTG AGCCTGANCC 60  
ACTTTAGCTA TTTTAAAAA TAGGACCTAT TGTTTTGGAT TACTATCTGA GAATTCATG 120  
GATTCACCTC TGGGTATAGG AGNTAAGAAT ACGTTTAATT CATAACTTTT ATATTANCCA 180  
ATATAGTAAA AAAATAAAGC TCACACATAC ANAANCAAA 219

50 SEQ ID NO:5107

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

55 TOPOLOGY:linear

CLONE:HUMGS06098

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTATTTT TTGGGCTTTT AATATTCTGT TCCATTGACC TATNTCNCTT NTCTTTTACC 60  
AATACCGCAA CATCTTGGTT ACTGTAGCTT CACGGTAAGT CTAAAACTT GGATATTGTC 120  
AGTCCTCCAA CTATGTTCTA CTCCTTCAAT ATTGTGTTGG TTATTCTGAG TCTTGNNGGG 180  
TCTCCATATA AATNGTAGAA TTAGAAAAAA AANNGNGGGG GGGANNN 227

SEQ ID NO:5108

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06100

SEQUENCE DESCRIPTION:

GATCAGTTTG GACTCTGTAA CTCATAGGTG CATTCTTTTT TTCTTTGGTG TCTCACAAAT 60  
NACCCAATTG TTGAATAAAA CTATAAATAT GTTAATACCA GCTTTTTCCA ATAAATAAC 120  
AAATGTTACA TCAAA 135

SEQ ID NO:5109

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06101

SEQUENCE DESCRIPTION:

GATCTNATGG GTTTAAAAGN GCGGCATTTT CCTCCNCTTT CTCCCTCTCC TGCACCATGT 60  
TAAGATGTGC CTTGCTTCCC CTTTGCCTTC GACCATGATT GTAAGTTTCC TGAGGCCTCC 120  
CCTGCCATTC AGAACTGTGA GTAAATTAAA TCTCTTTNCT TTATAAA 167

SEQ ID NO:5110

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06102

SEQUENCE DESCRIPTION:

GATCTTCTGC CACCATCAGG GNCAAACGGG TGCAGGAGGA AAGTCACTGA TGCCCAGATG 60  
TTTGCNTCCT GCACAGCTAC AGGTCCTTAA NAAAAAGTNT N 101

SEQ ID NO:5111

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06103

SEQUENCE DESCRIPTION:

GATCTGTGGC TACTTTCACA CCACAACAGA GTACCATGGT TCTGACAGAG ACTAGGAGAC 60  
ACAGTCTAAA TGACTTCTGA CCTGGACCTT TACTGAAAAAT CCTGCCAATC ATTCTGTTGG 120  
CAAGANTGAT GTATTACTTT TAGCAATAAG AAACAAGTAA CCTTTGCAGA-AA 172

SEQ ID NO:5112



SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06104

SEQUENCE DESCRIPTION:

GATCTCCAAA GCTGTCCTCT GCGTCCAGG AGTGCCTCTT ATGTGAGTCC TAATAAACTC 60  
ATCTATTCAC CAAA 74

SEQ ID NO:5113

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06105

SEQUENCE DESCRIPTION:

GATCTNTTCC CACCCATAAA AAGCCCAGAG AACAAAAAGT TGGCCCAGGA AATGCAATTN 60  
GGAAGCTGAA GAAGATTATA GTATTTNTNG CAGTCAAGAT TTGAAAAGTT ACCNACTAAG 120  
AAGCTACAAT ATNN 134

SEQ ID NO:5114

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06107

SEQUENCE DESCRIPTION:

GATCTTGAAA TNAAACTAAG ATTTTCCTGG GGAAATGTTT AGATACAGTT TTGTGAACTG 60  
TAAATCAAAA TACCTTTTNC TACAGTTTAT CTTTATNTC CTGCAAATTT AGGAACATAT 120  
TTCCTCGTTT NCACATTGAA TCTTAAGTTT AAGCNCTTCA TTTGGNATTT NGGCAATATA 180  
TGNGAN 186

SEQ ID NO:5115

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06108

SEQUENCE DESCRIPTION:

GATCTTTNTG ACTAGAGTTA GTGTCCTAGG AAAACCAGAA CTCAGAACTT GCCTCCATGG 60  
TTGAGTAACA AGCTGTACAA GAACCCCTTT TATCCCTGGA AGAGGCTGTG TATGAAACCA 120  
ATGCCCAGGG TTTGAAGGGT GTTAGCATCC ATTNCAGGGG AGTGTGGATT GGCTGGCTCT 180  
CTGGTAGCAT TTTGTCCTNA CACACCCATC TACTATGTCC AACCGGTCTG TCTGCTTCCC 240  
TCACCCCTTG CCAATAAAG GNCAAGNNCT TCAAA 275

SEQ ID NO:5116

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS06109

SEQUENCE DESCRIPTION:

GATCGAGTGG TCTGTGTTCC TATTGCTGGT GGGGTGATAG GGTGGGCTAA AAACCATGCA 60  
CTCTGGGAATN TTTTGTATTT TCTCCAGTA AAGCTTTTCT TCTCCGAAA AAAAAAAGA 120  
AA 122

SEQ ID NO:5117

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06110

SEQUENCE DESCRIPTION:

GATCACAAAC TACAGCCTGC AGGCCAAATC CAGCCACAG CCTGTNTTTG TAAATAAAGC 60  
TTTGTGGAN CAAAGCCACA CCCCTTAATC TAAA 94

SEQ ID NO:5118

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06111

SEQUENCE DESCRIPTION:

GATCTGAATC CAGNTCATTT GAGGGAACCC CCAAGGTTCT CTGGTTGTGG CCTCTTGAAT 60  
AAACCTCTCA CATTTGAAA 80

SEQ ID NO:5119

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06112

SEQUENCE DESCRIPTION:

GATCTATTAT CTAGCTGCAA AGCCTGGCTT TGNTTTGNAA TTTTGTA AAA ATTTCATGGC 60  
ACCCAAGGTT TCTGNTTCTG ACCCAGCAGT GGTCTGAAG AGAGCTGATG GCAAGTNTTG 120  
TAGTCATTTT GATTTTAATT GAAGGGTGAG CATAACCTTG TGAACCAGCA CTAGCTTGTT 180  
CCAAGCTGGA ATTTATCTAA TCTATTTTGG TGTTAAAAA AGCTGTACCT ACCAAATAAA 240  
TAAATAGTTT ATAAAATGTA TTACTTAAGG TAAA 274

SEQ ID NO:5120

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06113

SEQUENCE DESCRIPTION:

GATCTTTGAA GATATCCTCA ACGTGAGGCT CTNCTGCCAT GAAGGTGAAG ATTAAGTGCT 60  
GGAACGGCGT GGCCACTTGG CTCTGGGTGG CCAACGATGA GAACTGTGGC ATCTGCAGGA 120  
TGGCATTAA CGGATGCTGC CCTGACTGCA AGGTGCCCGG CGACGACTGC CCGCTGGTGT 180

EP 0 679 716 A1

GGGGCCAGNG NNCCCACTGC TTCCACATGC ATTGCATCCT CAAGTGGCTG CACGNACANC 240  
AGGNGCAGCA GCACTGNCCC ATGGTGCCGN CAGGAATGGA AGTTCAAGGA GTGAGGCCCG 300  
ACCTNGNNTC TAGNTGGGAG GGGNATNCTG AAGACTTCTT TNCTTNATTN 350

SEQ ID NO:5121  
SEQUENCE LENGTH:360  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06114

SEQUENCE DESCRIPTION:  
GATCTTATTC AGTCTGCTGN TTTGTATAGT GTGATGACCC TAGTAAGCAC ATATTTGGTA 60  
GCCTTTGTCAT ACAAGANTGT GAAATTTGTT CTCAAGCACA AAGTAGCACA GNAGNGGGAA 120  
GATGCTGTTT CCAAAGAAGT GACTCGAAAA CTTTCTGAAG CTGATAATAG AAAGATGTCT 180  
CGGAAGGAGA AAGATGAAAG ATTCTTGTGG AAGAAGAATG AAGTNNCINN ATTATGAAGC 240  
TACANCANNT TCCATCTTCT ATAACAACAC TCNGTTCCTG GTCGTNGTCA TTGTTGCTTC 300  
CTTCTTCATA TTGAAGAAT TTCAACCCCA CAGTGAACCA CANATTTGTC CATAAGTTGN 360

SEQ ID NO:5122  
SEQUENCE LENGTH:88  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06115

SEQUENCE DESCRIPTION:  
GATCTGGTCA CACCTAAAGT CATTAAAATC ACTGAAATGT TTAGATACAC AGCCCAATAA 60  
ATTCTCTTTA TAAACACAA GCAGTAAA 88

SEQ ID NO:5123  
SEQUENCE LENGTH:177  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06116

SEQUENCE DESCRIPTION:  
GATCAGGCCA CATAAGGAAC AGGGGAATTC CAGGGGTGGG ACACAGCTNG GGGAGTCCAG 60  
ACCAGGGCAG GGAAAGGAGA CTCACAAGCC AAACAGAGCT GCTTTGGGGA AAGTTCTTAT 120  
CAGCTGGTGC TGCTTCCTGA GCCATATGCC CATTCTCAA GCTGTACCN NNNNNN 177

SEQ ID NO:5124  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06117

SEQUENCE DESCRIPTION:  
GATCTTGGAC CTCCAGCCT CCAGAACTGT GAGAAATAAA TNTGTTTTGT TTCAGCTAAA 60

SEQ ID NO:5125

EP 0 679 716 A1

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06118

SEQUENCE DESCRIPTION:

GATCTGGCTG ACTCACACGC GACTGGAGAA TAAACAAACA GCAACATAAG GAAA 54

SEQ ID NO:5126

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06119

SEQUENCE DESCRIPTION:

GATCTCCCAT GGGTCACCCA GGTCTATGC CTCCGCATGG TATGCGTGGA CCTCCTCCAC 60  
TGATGCCCCC CCATGGATAC ACTGGCCCTC CACGACCCCC ACCCTATGGC TACCAGCGGG 120  
GGCCTCTCCC TNCACCCAGA CCCACTCCCC GGCCACCACT TCCCCNTGA GGCCCACTTN 180  
GAGGCCCTCT NCCTCAGTAA ATTCACATTT TNCTTCCTNC TGTTACATTT TNCNAATATN 240  
TTTTCTATTC CTTGGACCAA TCAGAGATGC TGTAGCTTNC TTGGGGCAAA GGGTACTAAA 300  
TCNCNTTNA GCACNN 316

SEQ ID NO:5127

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06122

SEQUENCE DESCRIPTION:

GATCTGTTC CTGTCACCAT TGCTCTCGAT TCACTCAGCT GGCTGCTACT TCGCCTTCCC 60  
TGCACCACAC TCTGCCAGGT CCTGCATGCT GTGAGCCATC AGGACTCTTG TCCTGGTGAG 120  
ACCCCTCCTT CATTGTTTCC CCTCATACAT CTCCCTCTGC CAAGGAGTGT GCCCCTTTTC 180  
CTTTCTACCC TAGAATAAAC ATCTGGGTTC TCCAGTCAGA AA 222

SEQ ID NO:5128

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06123

SEQUENCE DESCRIPTION:

GATCGACTGG AACAAAGTGA CCGCTGNGTA AAACACTGCT CTTGCCACTC ACTGTTGTAT 60  
ACATTCTTA TTTACGATTT TCATTGTGTA TATATATATA TAAANATACN GTATANANAT 120  
GCAACATANN 130

SEQ ID NO:5129

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS06125

SEQUENCE DESCRIPTION:

5 GATCTTAGAG CTA AAAAGGA CTGTAAAAAT TACCCAGAAC AGCGTCCTCA GACTTAACCT 60  
TCTGCAAGTT ATGTCTGTAT ATAAGANGAT TCTAATTGCT AACTGTTTAT ACTTTNCTGN 120  
ATAAAATAGT TGTTCCTAAT TAAAANGTAG CCAAGCTAAA 160

SEQ ID NO:5130

10 SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06126

SEQUENCE DESCRIPTION:

15 GATCTTCGTT CAGGGCATCA TCTGGGACAT CAACAGCTTT NACCAGTGGG GAGTGGAGCT 60  
GGGAAAGCAG CTGGCTAAGA AAATAGAGCC TGAGCTTGAT GGCAGTGCTC AAGTNACCTC 120  
TCACGACGCT TCTACCAATG GGCTCATCAA CTTTCATCAAG CAGCAGCGCG AGGCCAGAGT 180  
CCAATAAACT CGTGCTCATC TGCAGCCTCC TCTGTNACTC CCCTTTCTNT TCTCGTCCCT 240  
20 NCTNCCCGGA GCCGGCACTG CATGTTCTTG GACAACACCC AGAGCACCCCT NTNGTTGTGG 300  
GNTTTTGNNC NNCGAGCCCT TTAGCNGGGA ANGNCCTGGT CTTCNCCAN 349

SEQ ID NO:5131

25 SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06127

SEQUENCE DESCRIPTION:

30 GATCCTCAAG GACCTGTAAT TTTTGGTAT TTAAATTA AATAACATTA TTTTATTTT 60  
GANTTTTTTT CAAACAGTAA GAATAATATA TCAGCAGCAT GTATCTGCCA ATCATATGTA 120  
ATAAATTNTT TATTTTGCCA AAACCAA 148

SEQ ID NO:5132

35 SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06128

SEQUENCE DESCRIPTION:

40 GATCTAATAC AAGANCTAGC AAAGCAAAAG TTTTGCAAG TGACAGCATA AAGACGGANC 60  
ACAACAAATC CTTCTGNAG TGAATTAGGA AACTCCANGG N 101

SEQ ID NO:5133

45 SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06129

SEQUENCE DESCRIPTION:

50 GATCCTCATT CTTTCCCCCG TACAGTGGA AACATCTTN ATGTTTCCTT CATTATACGG 60

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GATGGTTTTN CAAGAATAAG ACTTGACCAA GACCGACTGC CAGTAATAGA GCCTGTNAGT 120  
 ATTAATGAAG AAAATNAGGG ATTTGAACAT AACACACAAG TTAGAAATCA AGGAATTATA 180  
 GCTTTGAGTT ACCGTGACTG GGNGGNGATT GTGAAGACCT TTTGAGATT CAGAGCCTGT 240  
 GATTACTCCA AGTCAGAGGC AGCAGNNGNC AAGTNCTTG NTTGCTAGCT GAAAGGACTT 300  
 AAATGGNTAG TGAAGGTCCA AAACCGGGNA AGCGGCATNG TGTTGGN 347

SEQ ID NO:5134

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06130

SEQUENCE DESCRIPTION:

GATCACACTG CAGTTTCCAT GTTAGCACTG TGGATGGGTT TTNAATCAAT AAAAAGTGGG 60  
 GGTTCCTTCA AA 72

SEQ ID NO:5135

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06131

SEQUENCE DESCRIPTION:

GATCTGTAAA ATAAAACTC AGCTGGGTCC AGATATCAGG TGTTCTAAAT CTAAGAATGT 60  
 AAGAACAATC TTAATAGAAA TATGTNTTA ATAAGTGGCT AATATCTACA AATAGTACCT 120  
 TTGCTAAATG ANTTCTTTTT NATGACTATN TTGTTTTNA GNAATTGGGT GAAAANNCAA 180  
 CTGANATGAG ATTATTTATN ATN 203

SEQ ID NO:5136

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06133

SEQUENCE DESCRIPTION:

GATCTTAGAT TTNATGAAGC ACAGTATGCA GGTAGGCCTA ATGGGGGAAG ATGGTAATAT 60  
 AAAAGCAAGA AGTATTTTTT TTTTGAAT GCCTGAANGC TGTNCTGNGG NTGCCCTCCC 120  
 CTTNCCTTN 129

SEQ ID NO:5137

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06136

SEQUENCE DESCRIPTION:

GATCACCTGA GGTGGGAGT TCGAGACCAG CCTGACCAAC ATGGAGAAAC CCCATTCTA 60  
 CTAATAATAC AAAATTAGTC AGGCATGGTG GCGCATGCNT GTAATCCCAG CTACTTGGGA 120  
 GGCTGAGGCA GAAGAATCGC TTGAACTGG GAGCGGAGG TTGCGGTGAG CCGAGANCAT 180

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GCCATTGCAC TCCAGCCTGG GCAGCAAGAG TGAAGCTCCA TCTAAAAATA AATAANTAAA 240  
TAAATAANTA ANCCCTCANA NNNAAAAATN 270

5 SEQ ID NO:5138  
SEQUENCE LENGTH:51  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS06137  
SEQUENCE DESCRIPTION:  
GATCTGTAGG GGAGGGAGTT CAAATAAAGC TTTATTTTTT TCATTTTCAA A 51

15 SEQ ID NO:5139  
SEQUENCE LENGTH:190  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06138  
20 SEQUENCE DESCRIPTION:  
GATCTGGGCT CCCTGACTTT CTGAAGCTAG AAAAAGGTTG TGTCTCCCAA CCACCTTTCC 60  
ATCCCCAGCC CCTCTCATCC CTGGAGCACT CTGCCGCTCA AGAGCTGGTT TGTTAATTAT 120  
TGTTAGACTT TGCCATTGTN TTCTTTTGTA CCTGAAGCAT TTTGAAAATA AAGTTTACTT 180  
25 AAGTTATAAA 190

SEQ ID NO:5140  
SEQUENCE LENGTH:199  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS06139  
SEQUENCE DESCRIPTION:  
GATCGGGAGG ACCTGTATGC CTGACCGTTT CCCTGCCTCC TGCTTCAGCC TCCCGAGGCC 60  
35 GAAGTCTCAG CCCCTCCAGA CAGGCCGCTG ACATTCAGCA GTTTGGCCTC TTTCCCTCTG 120  
TCTGTGCTTG TGTTGTTGAC CTCCTGATGG CTTGTCATCN TGAATAAAAT ATANTAATAA 180  
ATTTNGTATA AATAGGAAA 199

40 SEQ ID NO:5141  
SEQUENCE LENGTH:312  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06141  
45 SEQUENCE DESCRIPTION:  
GATCCAACCA CCTCAGCCTC CCAAAATGCT GGGATTATAG GCGTGAGCAC TTGCACCTGG 60  
CAAAAAAATT TTTTAAAAA AAGGAGAAAAG CAGTTTAACC ACAAACAGTG AAACAGAGCT 120  
GGCAGACGCC TGAAACTCCA TGGAACCATG CAGCTGTACC CTAGGGCTCC TCCCAGGAAA 180  
AGAGAGATGT CAACGTGGCC CAAGGTGTCC TGAAGCACTG GGATTGGNTT ANCTCGAGCG 240  
50 NTGGCCTTCC CAGCCCTNCG TGCTGCAGAG CCTCTGCTCG CTAGGCTNCC TTCATNCTNA 300  
CTCTGTGTGC TN 312

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SEQ ID NO:5142

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06142

SEQUENCE DESCRIPTION:

GATCTAAGAC AGCAAAGAAG TGTGCAAGGA GGGCCCTGTT AGCTCCCACT GTCCTGGTTT 60  
 CTCCTCCTGG AGTCTAATTT CCTTGGCCCT CTGAGCCTTT TGAGTCTGGG CCCTGGTCCA 120  
 ATGCTGCTGT TGTCTGAGGA ATGGTTTGGT GAGAACAGAT GTTAGAACTT GTTTGTTGAT 180  
 TCTTGTCTGG CTAATAAATC ANCACCAACT GNCTTCTCCN ACAGGGAAA 229

SEQ ID NO:5143

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06144

SEQUENCE DESCRIPTION:

GATCTAAGAT TATTCCCATG AGAAATGTTG AATTTATGAA GAATAGATTT TAAGGCTTTG 60  
 AAAATGGTTA ATTTCTCAA AACATCAATG TCCAAACATC TACCTTTTTT CATAGGNGTA 120  
 GACACTAGCA AGCTGGNCAA ACTATCACAA AAGTATTGT CACACATAAC CTNTGGTCTG 180  
 TTGCTGATTA NTACAGTACT TTTTCTTTGT GTGATTCTNA ACATTATAGC ACAAGTATTA 240  
 TCTCAGTGGG TTATCCGGAA TAACATCTGA AAGNGGGGTT CATCTNTGGT NGNGTTTGCT 300  
 CNNTAAACTA GNGTNTCTCC TGGTCCANT GN 332

SEQ ID NO:5144

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06145

SEQUENCE DESCRIPTION:

GATCACATCA CGGAATATTC TTTGCCTTTC CACTTTCAG GAAATCTCTC GGA CTGGGCT 60  
 AGCCTCCTTG TGTGTGATGA AAGATGGGCT ATATTTCAGA ACANAGTGCT GTGTTGTCAT 120  
 GATTTGCCTG GACTCCCAGG GCGTCTCTTA CCAACTTGA TAACGATGCT GTTCATTAGC 180  
 AGCCTGTGTT AACTGATAAC CAAGAGCGGT AATGTGATAC TCATAAGCAA TTTTCTGTGT 240  
 GTAGGATAAA ATANNCCATC TTGTATNATT NCAAA 275

SEQ ID NO:5145

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06146

SEQUENCE DESCRIPTION:

GATCTCTTTT CAAGTTCACT CATTCTTTCT TCTGTAATGT TCAATCTCTC TTAAGAAAGT 60  
 CCAAATAAAT TTTTCATTTT AGAGAGTGGA AA 92



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SEQ ID NO:5146

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06148

SEQUENCE DESCRIPTION:

GATCTGGGCA TTAAGTCAGT GGCTTTGCAT AGCTTTCACA AGTCTCCTAG ACACTCCCCA 60  
 CGGGAAACTC AAGGAGGTGG TGAATTTTGA ATCAGCAATA TTGCCTGTGC TTCTCTTCTT 120  
 TATTGCACTA GGAATNCTTT GCATTCCCTA CTTGCACTGT TACTCTTAAT NTTAAAGACC 180  
 CAACTTGCCA AAATNTTGG CTGCGTACTC CACTGGTCTG TCTTTGGATA NTAGGNATTC 240  
 AATTTGGCAA AACAAAGTGT AATGTCAGAC TTTGCTGCAT NTTACACATG TGCTGATGNT 300  
 NACAATGGTG NCGAACATNA GTN 323

SEQ ID NO:5147

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06150

SEQUENCE DESCRIPTION:

GATCTTTTGA GTGGAGGTGG GTAGAGAGAG CAAGNAGGGC AGGACACTTA GCAGGCACTG 60  
 AGCAAGCAGG CCCCCACCTG CCCTTAGTGA TGTTTGGAGT CGTTTTACCC TCTTCTATTG 120  
 AATTGCCTTG GGATTTCCTT CTCCCTTTCC CTGCCCCACC TGTCCCCTAC AATTGTGCT 180  
 TCTNAGTTGA GGAGCCTTCA CCTCTGTTGC TGAGGAAATG GTAGAATGCT GCCTATCACC 240  
 TNCAGCACAA TCCCAGCGAA AAAGGGTGTG AAGNACCCAC CATGTTCTTG GAGCANTCAA 300  
 GGGTTNCTAA ATNNNNCGGC TGGGACCANT NANATAGTGA GTNNNNN 347

SEQ ID NO:5148

SEQUENCE LENGTH:388

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06151

SEQUENCE DESCRIPTION:

GATCTGCCAT ACCACTGTGA CTGCATTGAA AGATGTCCCT TTCTCTCTCT GCCAGTCGGT 60  
 CGGTGTGGGA CAAAACACAG ATATACAGCA GATAGCGGCC AAAAATTCA CAGACACCTC 120  
 TCTCATGTAC CCAGAGGACA CTTGTAAATC TGGACCAAGT ACGAATACAC AGAGTGGTCT 180  
 TTTCAACACT CCTCCCCCTA CTCCACCGGA CCTCAACCAG GACTTCAGTG GATTTCAGCT 240  
 TCTTAGTGGA TGTTGCACTC AAACGGGGCT GCAGAGATGG AGGCTTNAGG GNANANCTTT 300  
 ACAGNTTAAC CCNATTTTCA AGCANAAACA GTTCTCANGA AGTGTCATGA TTGNCCGGGG 360  
 TAGAAGGGAA AGAGATTGAA TTTGCTTN 388

SEQ ID NO:5149

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06152

SEQUENCE DESCRIPTION:

5 GATCTATAAT GGGATACATT GTCATCCTCT AGCAACTCCT ATATAGAAAAG TTTTAACTGA 60  
 ATATGTTACA TATANGAATT AAATTCTTCT CAAATAATTC TTAACCTCAG TNATGAGCCT 120  
 AAATTTACTC TGCTTGGCTC TCTACACATG GCATTTTCAGG GTATAAGATG TAGCATTNA 180  
 ATGTGTAAGA TATATGTACN NNNCATATGT GTTGCTATCN TCATCATTAA CATCCTTCTT 240  
 TNCTATTGCT TGGCTGTAAT TTTTGTAAG ATAAATTATA TTGTNTNNNT GTATGTGTGT 300  
 10 TTGTAGTN 308

SEQ ID NO:5150

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS06153

SEQUENCE DESCRIPTION:

20 GATCTGTCCT GTGAGGCATT TAGGGGCTTT CAGGAATTTA GTAAAAGGTG GAGTATGCCT 60  
 TTCCAGTATC TTCCATCTTC CTTTGTATAC TTGTCCTTCC TCCCATTTCC TCCCTTTGGC 120  
 CCGAGGTAGG AGGATGGAGG GAGGCTGCTA CTCTACCACT TCCTGTGTGC CTCTACTGTG 180  
 GCCTCAACCC TGGCAATTAT AGCTACTCCC ATCCCTTACC TGGGCATGTG TGAGCCCTTC 240  
 TCACTGGATT TTATACCCTT GTGTCTGTGT ACATAAATAT ATATACATAT ATATATACAT 300  
 25 AAAANCTTTG TACAAA 316

SEQ ID NO:5151

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS06154

SEQUENCE DESCRIPTION:

35 GATCAGGCAG GAGAAAACT TTAGATGGGA GTCTTGTCTAT CAAAAATAAA TACAGTTGCA 60  
 TGGAAA 66

SEQ ID NO:5152

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS06155

SEQUENCE DESCRIPTION:

45 GATCAGGACA AGAGCGANGC ACCAGGGGAG CTCTCTCCCA AAGGCCTTGT CGCCCCAGAC 60  
 CTAACCTGCT CCCCTCAAC CTGCCTGAGG AAGAACTCT CAGGATTGCA CGGATATTTT 120  
 CTTCTCAGTA CTCCAGAAA GACTGACGCA GCCTGAGGGG CTGGGGTTGA AGGAGACACC 180  
 TGCCANCNN NCGTCAGNTT TGTCCAGCTT GCAGGAGGCA CCAGGTCTGG CTCCTTCAGG 240  
 GCTGTCACAG TCCTGAAACC ACCACTTGCC TAGGTCACGG ATGCCTNAAAG AGACCCGGTN 300  
 50 AGGCTAGATN N 311

SEQ ID NO:5153

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SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06156

SEQUENCE DESCRIPTION:

GATCTAGGGC TGGCCCCTAG TGAGTGGGCT CGAGGGAGGG TTNCCTGGGA ACCCCAGGAA 60  
TTGACCCTGA GTTTTAAATT CGAAAATAAA GTGGGGCTGG GACACACGAA A 111

SEQ ID NO:5154

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06157

SEQUENCE DESCRIPTION:

GATCTCCTNN TCCAGTGCTG CACACTCCTG TTTTGGAACT TTAATAGCG TTGCAACGAA 60  
ATCCTATATC CAGTTTCCTG TAATTTANTT GAAGAAAAAT ACATCCAAAT AAAGACTTTA 120  
TTATTAACAG ACCAGATAGC ATCAGAAATC ATGTGACTGT TNTGCTTATC AGANTATGTC 180  
TNAACTNTTT AGGGCAAAGT TAACACTGAA AGTTCTAGCT TAAGTGTTGA NCCTNTNGTG 240  
GGAAAAANAA TTCCACTTGT GAAACNTCAG GCTN 274

SEQ ID NO:5155

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06158

SEQUENCE DESCRIPTION:

GATCACTCTG GTGCGGGTGT TTGGTTTTGT TTTAAAATAG CTTTGCAGTG AAAGCTTTCA 60  
TGACCATACA AATNATCTTT TTTCTTCCTA TTTCTTGTA GAGGTTTTTT TCCTCCTTGT 120  
CTTAAGGTCA TAAAAATATT GTTATGTGGG ACAA 155

SEQ ID NO:5156

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06159

SEQUENCE DESCRIPTION:

GATCTGTGGC TTTGCTCCAC CATCCCTAAC CAACCTCTCA TCACAGCTTT NTGTGTGGGC 60  
TGAGTGCTGG CCTTAACCCT AGGCGTGGA GAGAAAATGT GAGGTTGTTT AGATACTCAT 120  
CAGGACCTCA CAGGAGCTGA GACTTATCAG CCAGAAATNG TTCTTCGGAC AGTCGTACAC 180  
ATCTTACAGA AAACCCTCCT TNGTAGAGTT GGNTTGTGGT ATGTGTTTGA TGCTATAAAG 240  
CTCATTTTTA ATGGTGTA CCGTNTTCTA GGGNCGATTT CGTTTTGGAA GNGGGTAANG 300  
NTGCNTTAAC CAGGTAACTN ATCCTTGGGN TTTAAGGTGN AAAAAATNTT CTNGNCAAAG 360  
GGAANCCNN 369

SEQ ID NO:5157

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06160

SEQUENCE DESCRIPTION:

GATCAAAATC AAAAGAACCG TG TAGATATA CTTNATTGTA TAAGTAGAAA ATTACTTAAT 60  
TNCATACTAG AAATGGATGG ATGCTGCAAG TTGAAATGGA CTGTCCATTG ACGGTCCTAA 120  
TGTGGTAGCA GAAAAANATG GTGTCTTAAG TNCTTAGNGT TTGATGTCAT TAACAGTTTC 180  
GTAAACTCT ACAGTG TAGN AAGTTTTTTC AATACTAAAC TGTGCGTTGT NCATAGTTCT 240  
AATGCATTGT NTTNGCCNCC CGGTACTTTC TNTNAANGN 279

SEQ ID NO:5158

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06161

SEQUENCE DESCRIPTION:

GATCTCAAGT GAGATAGCAG AGCAAGATGC CAAAAGACCA TAAATAGAGT AAGGTTTCTA 60  
TAGATGTNAG ACAGATTTGA GAGAGCATTT ACTCTGTCTC CCTGTGGATG AAAGTCTGTC 120  
TGAAATGGTT CCAATTTTNA GGAATCTGCT TACCCNCTTC ATTATTTGAC AGCTTTCCTT 180  
GGTGACCCAA ACCTTG TAGC CTAAGCCATT TGTCTTTTTC TCAGTGGAGG GAGTGTATGG 240  
ACCTGGCCCC ATGGCTTTGC ATGTTAGAGA CCTGGCNGAC TAAAGTCNCN GGGTGTGTTGT 300  
TTGCTCACAT TTGCTGAGTG ACAGNTATGG TGNCCNN 337

SEQ ID NO:5159

SEQUENCE LENGTH:378

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06163

SEQUENCE DESCRIPTION:

GATCTACAAC CCCTTGGAGC AGTGCTGTNA CAATNACGCC ATCGTGTCCC TNAGCGAGAC 60  
CCGCCAATGT GGTCCCCCCT GCACCTTCTG GCCCTGCTTT NAGCTCTGCT GTCTTNATTC 120  
CTTTNGCCTC ACAAACGATT TTATTGTGAA GCTGAAGGTT CAGGGTGTGA ATTCCCAGTG 180  
CCACTCATCT CCCATCTCCA GTAAATGTGA AAGCAGAAGA CGTTTTCCCT GAGAAGACAT 240  
AGAAAGAAAA TCAACTTTTC ACTAAGGCAT CTNAGAAACA TAGGCTAAGG TAATATGTGT 300  
ACCAGTAGAG AAGCCTGAGG AATTTACAAA ATGNTGCAGC TCCAAGCCAT TTGTATGGCC 360  
CATGTGGGAG ACTGNTGN 378

SEQ ID NO:5160

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06164

SEQUENCE DESCRIPTION:

GATCAGCCCC ACCCTGGCCT AGACCAGCAG ACAGAGCCAG GAGAGGCTCA GCTGCATTCC 60

GCAGCCCCCA CCCCCAAGGT TCTCCAACAT CACAGCCCAG CCCACCCACT GGGTAATAAA 120  
AGTGGTTTGT GGAAA 135

5 SEQ ID NO:5161  
SEQUENCE LENGTH:350  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS06165  
SEQUENCE DESCRIPTION:  
GATCTCGTAA GATTAAATGT AGCATTCTAT ACTCCCTACA TGCACAGTAN GATTTGTTTA 60  
ATGAATGGAA GGAAAGACTA AATACAATGT CAAATGTNAC TATTAATTGG ACAAGAAAAT 120  
CCAAGTAGCA AATGACCATT ATGTGTAAGA CTTACTCTAA AAAGACCNTT TTAAATAGCT 180  
15 CATATATTAA TNTNGTTTAA AACCTGCTAT TTTCCAAAAC TGCAAAACTA GGGCTATAAA 240  
AATCTAAGTT AAAAAATCAG CTNATCCTCA TTGGTATAGT GGTNTGGNNA AAAAAATCCA 300  
GTTTAAACC NGNNTNNATT GANAGGNTGT CTCCATGCCT NCCATTGGGN 350

20 SEQ ID NO:5162  
SEQUENCE LENGTH:57  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06166  
25 SEQUENCE DESCRIPTION:  
GATCACTTTT ATGTAAAAAT TATAATTTAA TTAATAAAAA ATTTCTTAAG AAGTAAA 57

30 SEQ ID NO:5163  
SEQUENCE LENGTH:203  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06167  
35 SEQUENCE DESCRIPTION:  
GATCAGGCCT TGGCCTCTNA GCCCTGCCTG CTCTGGGCCA TGCAGAGGAA GGACAGAGNG 60  
TGGGCGCAGG GCACCAACTC AGGGACATCC CCTCTCCTGG GCGACGTCAG TGGACCTTCC 120  
TGCACCCCCA GCCTGGAATG TAAATNAGCT GTGTGGTGCC CGCGTNGCTG GAAGGAAATA 180  
40 GACCCTTTTN TAGCTCCCTG AAA 203

45 SEQ ID NO:5164  
SEQUENCE LENGTH:274  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06168  
SEQUENCE DESCRIPTION:  
GATCCTCTGT GATACAAAAA TCCATGGATG CTAAAGTCCC TTTTAAAAA TGGCATAGTA 60  
50 TTTGCATATA ACCCAAACAC ACCCTCCTGT GTATTTTAAA TCATCTGTAG ATTACTTATA 120  
ATACATAATG TAATGTAAAT GCTATAAAN TAGTTATTAG ACTGTATTTA GGGAATAATG 180  
ACAAGANGAA AAAGTCTGTA CATGTTCACT ACAGAGGCAA CCTTTGTAGG TCTAAATANN 240

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TTTTTAATAC AGNANTNNGG ATGTNAGNNN NGGN

274

SEQ ID NO:5165

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06169

SEQUENCE DESCRIPTION:

GATCTCTTTT TATTTAAATG TGAATTTCAA CTTTGACAA TCAAAGAAAA GACTTTTGTT 60  
GAAATAGCTT TACTGTTTCT CAAGTGTTTT GGAGAAAAAA ATCAACCCTG CAATCACTTT 120  
TTGGAATTGT CTTGATTTTT CGGCAGTTCA AGCTATATCG AATATAGTTC TGTGTAGAGA 180  
ATGTCACGTG AGTTTTGAGT GTATACATGT GTGGGTGCTG ATAATNGTGT ATGTCCTTTG 240  
GGGGTGGAAG NGGATAACAA TTCAAGCTGA GAAANGTATT CTCAAAGATG CATTTTTATA 300  
ANTNTNATTA ANCAATNTTG TNANAGNNNG ANGNGTGGGN NTN 343

SEQ ID NO:5166

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06170

SEQUENCE DESCRIPTION:

GATCATACGA GGCATGTAAT ACCAAGAATT GTTACTTTAC AATGTTCCCT TAAGCAAAAT 60  
TGAATTTCTT TTGAACTTTT AGTNATGCAC AGACTNATAA TAAACCCTCT AAANCCTGCC 120  
CAAA 124

SEQ ID NO:5167

SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06171

SEQUENCE DESCRIPTION:

GATCTTGGAC CCAGTCTGGC CCGTGCCCAG CATGGGGCTG CTTCTCCTCC ACAGCTCCTT 60  
CCCAGAGGGC TGGGGCCTCA GCCTCCCTGC CACGTCCACT CTGGGCTGGC CTGGAACATA 120  
CTACTATGTT GACAGTAACA ATAAAGCTCC TCAGGGACCA CCGTACAGGC CCGCAGCCCC 180  
ACTGNCTGCT GTTGGAAGAA AGCTGTGGAA AGAAAGCAGG GGGNCCCTGC CCCAGGCCAA 240  
GGCCCTGCCC TTGCCACACA CGGTACACAN ATGCAGCCTC TCTNTCTCTN TGTGTCCACT 300  
TGTGAAAATA ANCTGCAGGN CTGGNTNGGA CAACAAAGGN AGNNGNACAG TGTCTNGGNN 360  
GGCANNN 367

SEQ ID NO:5168

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06172

SEQUENCE DESCRIPTION:

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GATCAGTTCA GTATATTGCA CTAATTATTT TAGGTATTTT CATTATATGA AAGCTACCAT 60  
 GTGTCAGAGA TGATTTAATC TATTTAAGTG TTGGACTGCT AGGAGAACTT GTACATTTAT 120  
 GATAATGCAG AATTAGGAAA ACGGTTCCACC AGTGTTTAGT TTTATATTGA GGTGCTCAGG 180  
 TTGGTATAAA GTGGTATAAA AAGCAAA 207

SEQ ID NO:5169

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06173

SEQUENCE DESCRIPTION:

GATCATGCCC TTTGTAGTAN CACAAATGGN GCTGGAGACC ATTATATTAA GCAAACCTAAC 60  
 ACAGTNCAG ANAACCAAAT ACAGTATGTT CTCACCTATA AATGGGAACCT AAAGNN 116

SEQ ID NO:5170

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06174

SEQUENCE DESCRIPTION:

GATCTGCTAG GGATTGTCAA AATAATCTCC TTGAGGCATC TTTATTTTAA AAATGAGATT 60  
 AAAGTATGTG ATTTGCTTGT TATGTGGCTA AA 92

SEQ ID NO:5171

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06175

SEQUENCE DESCRIPTION:

GATCANCAGA AAAGGCAAAT TTCACTCGNC TAAACACTTT CAATTTTCAG TTNTAATTTT 60  
 ATNTTCTATA TACCCAGTCA TAAAGTATAA GCATCAGTTG TCATTAAAAG TTTTCAGAAA 120

SEQ ID NO:5172

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06176

SEQUENCE DESCRIPTION:

GATCTGTAAT GAAAAGAATC TGNTACTGCA AGTAAACCT ACTCCCCAAA AATGTGTGGC 60  
 TTTGGGTCTG CATTAAACGC TGTAGTCCNN GTTCATGCCA AA 102

SEQ ID NO:5173

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06177

SEQUENCE DESCRIPTION:

5 GATCACTTNT NGTCTGATTC CAGCCTGCTT GCAACCCTGG GNTCCTCTTG TTCCCTGCTG 60  
NCCTGCCCTT TGGGAAGGGG CAGTGATGGC TTTGAGGGGA AGGAGGAGAC CCTCTTTCTC 120  
CCATGCTGCA CTTACTCCTT TTGCTAATAA AAGNGTNTNT AGATTGTCAA A 171

SEQ ID NO:5174

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06179

SEQUENCE DESCRIPTION:

15 GATCTAAACT GTATTGNCCA ATTTAAATAA AAAATNNAAT ATAGATTCAG AAAGGTTTCAT 60  
ATTTTTCTAA TGACTTCATT CTATATTATN TTGTTAGGTT GCATAAAGAA GCAAGGAATT 120  
GTACTTGTAT TAAAAGATGA AGAAAGCTAT TAGGTATATT TGTACATGNC TGCANNTGTG 180  
TCTATNNN 188

SEQ ID NO:5175

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06180

SEQUENCE DESCRIPTION:

25 GATCTTGAGA GGTGGAGGTT GCAGTGAGCC AAGATTGTGC CACTGNCTTC CAGCCTGGGA 60  
GACAGCAAA 69

SEQ ID NO:5176

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06181

SEQUENCE DESCRIPTION:

35 GATCTGTAA TATGTAACAT ATTAATGGGT AACTTGCTGT GTAAAATTAT AAGCCATATT 60  
TTAAAAGGTT TAAAAAATAC TTATTGTGCT CCATTTGTGA TATAATTNCT AACATTTCTG 120  
CTCTGTGANN NNNN 134

SEQ ID NO:5177

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06182

SEQUENCE DESCRIPTION:

50 GATCTTNGAG ATTGTTCCAC ATCAGTACAT AAAGTACATA AAGATTGTCA CCCCACAAA --59--

SEQ ID NO:5178



SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06183

SEQUENCE DESCRIPTION:

GATCTGTCTA CTTNNCTTAT CCTGATTCAA ATGGAATGCC AGTATGGAAC TCCTAGGATT 60  
TGTCACGAAT GGGGAAGCCAA GTGCCATCTT CAAAATTTCA GGTCTTAAAC NTGGAGAAGG 120  
AAGCCAACAT CCTTTTGGAG CCATGAATNT TGTCCGAACT CCANNNTGTT GCTCAGANTG 180  
GANTTTCAGT GGN 193

SEQ ID NO:5179

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06184

SEQUENCE DESCRIPTION:

GATCATTATT TGGNAATATG TCCTATGGAA AGAATAAAAG CATGTNCTTC ACAGCTAGCA 60  
TGTTACACAGA TTTGAAAGAA GTTTCATTAA AAGCACCATT GCTTTCAAA 109

SEQ ID NO:5180

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06185

SEQUENCE DESCRIPTION:

GATCTTAATT TAAATAGGTG CTTTAATTTT ACAGCTTTCA AAAGTAGTTA CTGTAAATTT 60  
TACTCCTGTT AATGCTGGAT TGGTTTAAAG GATTATAAG GGCTGTGTTT NCTCTNTACA 120  
AGGCAAGATG CCATACAGNG TTCANTAATA GAAGGTCTNG ATACAACCGA CATTTTAAAT 180  
ATTCTNTATA CATGNGGACT GCGTCTTTT CACTGACCCT ATGANTTCAC TGTGGAGTAG 240  
GGTGAACTGG NCTGCANATT AGTTTATTG TTGCCATAAT CACATTNNG AAAAGAN 297

SEQ ID NO:5181

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06186

SEQUENCE DESCRIPTION:

GATCTNATTG CTTATAAACT TTGGTGACGG TAGTGTGTAA GGCCGTATTT NNAGCATCTN 60  
ACAGGTGTTT ACAAAAAAGT GGTTGTCGCA CTGGGAAGTG GAGTGATGGC CTCGTCTCCA 120  
GTGCTCCTCT GGGCTCTTGA GTTGCTGCTT GANTTGCCGT GTAGACATTT NCTTGGAGAG 180  
TCCACTTGTN ATTTGACGGA GGTAGGTTTC AACCAGAGT TAATGTCAAG CATGCTAATT 240  
TANCTAGTCA CTCACAGATG ACTTTCCTTT AATAAAAGTC CCTTTTCCT AAAANAAAAA 300  
A 301

SEQ ID NO:5182

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06187

SEQUENCE DESCRIPTION:

GATCTTTGGG CAAGTCACTT AACCTCTCTT TNCCTCAATT TCCTCATCTT GAAATGAGGA 60  
 TAATAATACC TGCTGTACCT ACCTCACAGG GCTGTTGTGA GGATTAAATG AGNTGGCATG 120  
 TGAAAGCACT TTGAAAATTG TAAAGCGCTA TGTAATGTA AGGTATTATA GAANCATCTT 180  
 TAACATATAG TTTCATACCA TTCATTTTTT ACCAAAGAAA GGGAAAGTNT GCTNGTANGC 240  
 TGGTTGAAAA AGTTANNCTT GGTATAANNT TGNGTTTGGT TGANGNANAA GGN 293

SEQ ID NO:5183

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06188

SEQUENCE DESCRIPTION:

GATCACAAAA GTATATAAAA AGTCTACTAG AGCAACATTT TCCCATATTT TTNGGTTCTC 60  
 AAAGCAACTT ATGTATGNTT TAGAGANGNC AAAAGAGGAA GCCTAGGGGG AAAAGAAAGA 120  
 NAATTAGAAT TTGCAAATNC TAGAAAANN 149

SEQ ID NO:5184

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06189

SEQUENCE DESCRIPTION:

GATCGAAAAG AAATTTNTTT ATACTTGATG CCTTAAGATN CCCAAAGCTG CCCAAAGCTC 60  
 TGAAAGACTT TAAGATAGGC AGTAATGCTT ACTACAATAC TACTGANTTT TTNTAGAGTT 120  
 AACATTTGAT AATAAAACTT GCCTGTTTAA TCTCAAA 157

SEQ ID NO:5185

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06190

SEQUENCE DESCRIPTION:

GATCTTGCTT GGAAGGTGTT TTAAGTTTNN TAATAAACAA GATGATGTCT GAAAAATNTGA 60  
 AA 62

SEQ ID NO:5186

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06191

## SEQUENCE DESCRIPTION:

GATCTAGAGC AGCATGGAGC TGTTGGTAGA ATATTAGTTT TTAACCATAC ATTGTCCCAA 60  
AAGTGTCTNT GCATTGTGCA AAANGTAAAC TTAGGAACAT TTNGGTATTA AAAGGATTAT 120  
TTTAATTGNN AAAAGCCNGA NGCGN 145

SEQ ID NO:5187

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06192

## SEQUENCE DESCRIPTION:

GATCAACAGC TCCGCCTACC GCAAAGCATT TGANAGCAGA CTAGCCANCA GTNGTGCTCT 60  
GAGAGTGAAC GNGCACCTCC AGGTNGAGGG CCACAGCAAC GTN 103

SEQ ID NO:5188

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06195

## SEQUENCE DESCRIPTION:

GATCTGATAG AGGGGGAGGC AGAAGCAGAT ACTAGAAACA AACAAACTT TGGACCAAAA 60  
TCCCAGTTCA AAGAAACAAA AAAAAGAGTG GAAACTATTC TATCATAACT ACCCAAGGAC 120  
TACTAAAAGG ANAAATTGTG TTACCTTTTT TAAATTCCTT GTTAAGTCCC TTCCGTAATT 180  
TTNATGTTCT TGTGAGGANA AAAGTAAANC ATGTTTANTT TTAANNAAGG NGANAGNGGG 240  
NGTNTAGN 248

SEQ ID NO:5189

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06196

## SEQUENCE DESCRIPTION:

GATCTCTTAT ACAGACGCAC CAAAGCCCTC ATTGACTATG AGAACTCAAA CAAAGCTCTG 60  
GATAAGGCCG GGTAAAGAG CAAAGACGTC AAGTTGGCTG AGGCACACCA GCAGGAGTGC 120  
TGCCAGAAAT TTGAACAACT TTCCGAATCT GCAAAAGAAG AACTGATAAA TTTCAAACGG 180  
AAGAGAGTGG CAGCATTTAG AAAGAATCTA ATTGAAATGT CTGAACTGGA AATAAACAT 240  
GCCAGGNACA ATGCTCCCT TTTGCAGNGC TGGTNTTGAC TTGTTCAAGA GTAAGTGGTT 300  
ATGCCTTCAC TCNGTAGGAA NNGGAGTTGA ATTGTTGTAA GGAAGCCNAN GTGN 354

SEQ ID NO:5190

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06197

## SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTCTATT TTAAACTAG CTTTTTAAGC AGCTGTATGA AATAAATNCT GAGTGAGCCC 60  
CAGCCCGCCC CTGCAA 77

5

SEQ ID NO:5191  
SEQUENCE LENGTH:257  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS06198

SEQUENCE DESCRIPTION:

15

GATCTAGCTT CANAGGAAGT CTACACCCCA TTCCCTTCTG CTTACAATGT ACCCATGATA 60  
TGTGTTTAGC ACAGTAATAC TGTAACAGGA CATCACATGG AAAAATCAA GCAGCTGGCT 120  
CACTGTATTT AACTGAAAAG AATGCCTACA GATTGGATAT TTNGTAGGGG NAATTAAGGC 180  
ACTTTNNTAA CAAACTTCAT INTGTGAAAC TNGGTTGAAT ATTAACATAC AATTNNGNCG 240  
GGNNTATTAA TGCCATN 257

20

SEQ ID NO:5192  
SEQUENCE LENGTH:185  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06199

25

SEQUENCE DESCRIPTION:  
GATCCCAGGC TGCCCTGGAC TTAGACCAGT GTCTGAGGTG GTAACAGCGG CCGCACAGGG 60  
TTGGCCTAGA CCTNGGATTT GTGGGAAAAG CTGCTGGTGT GACCANCTGA GCACCCAGCC 120  
AGGAGACCTG CAGCCCTNCG NCTTCCAGAA GCAGGTCCCA AATAAAGNCA GTGCCNACCT 180  
NCAAA 185

30

SEQ ID NO:5193  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06200

35

SEQUENCE DESCRIPTION:  
GATCTGTATA TAACTTTAAT TTTAAGGACC ATAATCAACT TTGTAATATT CTNATATAAA 60

40

SEQ ID NO:5194  
SEQUENCE LENGTH:286  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06201

45

SEQUENCE DESCRIPTION:  
GATCACCTC TACGGGAGAA CCAAGGAGCT GACTTCGGAA CTAAAGGAGA ACTTCATCCG 60  
CTTCTCCAAA TCTNTGGGCC TCCCTGAAAA CCACATCGTC TTCCCTGTCC CAATCGACCA 120  
GTGTATCGAC GGCTGAGTGC ACAGGTGCCG CCAGCTGCCG NACCAGCCCG AACACCATTG 180  
AGGGAGCTGG GAGACCCTCC CCACAGTGCC ACCCATGCAG CTGCTCCCA -GGNCACCCNG 240  
NTGATGGAGC CCCACCTTGT NTGCTAAATA AACATNTGCC CTCAAA 286

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55

5 SEQ ID NO:5195  
 SEQUENCE LENGTH:138  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06202  
 SEQUENCE DESCRIPTION:  
 10 GATCTCTTGT TCTCTCCTGA GTGTCTTCT ACTNTGCTGA GNGTCTTCT GCTGTCCTTA 60  
 TCCTGTTCTC TTATCCTNAT CCCCTCCAGT CTCTGCCTAA TTTTNAGTGT TTAATAACAA 120  
 CCGNATGTCT AGTAAATN 138

15 SEQ ID NO:5196  
 SEQUENCE LENGTH:96  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06203  
 SEQUENCE DESCRIPTION:  
 20 GATCAAGAAC TTGGAACCGC AGAAAACGAA ATCCCATAGT AGCACAAAGC TTGGCTGTTC 60  
 AGTGAATAAC ATTTAAATAA TCGTAAANTA CAGAAA 96

25 SEQ ID NO:5197  
 SEQUENCE LENGTH:222  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06204  
 SEQUENCE DESCRIPTION:  
 30 GATCTTGCAG CTTTATTTGA GTATTTGTTC TTTTGTGTAG TTTCCATCTT TTTAAATATT 60  
 TAAAATATTT TCAAGATAAA GTATTATCTT CTCTGCAAAA ATTCCTGGAG TAATTTNCTC 120  
 TCATAATATT TGAGGTCAGT GGTTCCTCAGT TGTATTAGTG GGGTAACTAC ATCAAAGTAA 180  
 ATAANGTCTT ATTTTNNANA TGCAAATTTT AGACCATAGA AA 222

35 SEQ ID NO:5198  
 SEQUENCE LENGTH:53  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 40 CLONE:HUMGS06205  
 SEQUENCE DESCRIPTION:  
 GATCAAGTGA ACCATCCCTA GTCTTCCCTC AATAAATAAC TTTTAACTCC AAA 53

45 SEQ ID NO:5199  
 SEQUENCE LENGTH:239  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06206  
 50 SEQUENCE DESCRIPTION:

55

GATCANAGTG AACCTCAGT TTGTACAAAA GAGTATGGGC TCACAAGANG ATGATTCAGG 60  
AAACAAACCA TCCAGTTATT CTTGAAACTA ACATCCATCC TGAGCTAAAC NAGAGAAACT 120  
ACCATCTTGG CCAGTGNCAN GTGTTCCGGAG GGCAGCAGAG NGGACCAAGC CTGTGTCACC 180  
TGGNGACTAA GAANTTAAGT TTTGTNTTGA CATATTCAGT CCTGTGTGCT TNCAGNAAN 239

SEQ ID NO:5200

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06207

SEQUENCE DESCRIPTION:

GATCGAATAC GTGGATGNGA CGGGCCGGAA ACTCACACCC AAGGAGGCTT TCCGGCAGCT 60  
GTCGCACCGN TTCCATGGCA AGGGCTCAGG CAAGATGAAG ACAGAGCGGC NGATGAAGAN 120  
GCTGGACGAG GAGGCGCTCC TNAAGAAGAT GAGCTCCAGC GACACGCCCC TNGGCACCGT 180  
GGCCCTGCTC CAGGNGAAGC AGAANGCTCA GANNGACCCC NTACATCGTG CTN 233

SEQ ID NO:5201

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06208

SEQUENCE DESCRIPTION:

GATCAAAAAG GGGTTGATTA CAAGGGCAGG AAGGAATTGT TAGTGTGATT CTACAGTTCT 60  
GCATCTTGNT TATGGTATGA CTGTGCGTTT GTCAAACCTT AACAGGATGA ATTTTGCTGA 120  
ATGTAAAATC ATACTTCAAT AAACATGACT TTAANAANCTT AAA 163

SEQ ID NO:5202

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06209

SEQUENCE DESCRIPTION:

GATCAGTTTA TGTGTAATAT TCTAGTGCTT TAATGACTCT TTTTTCCTT GGAGGGAGGG 60  
TAACATTATT TGGACAGATG CAGAAGGAAC TGTTAGTGAG TCAAGACAAA CACATCTGAA 120  
ATAAAGGAAC TGTGTATTAA CATGTTAACA ATTCATAACT GCACTTTTTA TGACATTTTG 180  
AAAATCTATT TATAGGTACA GANCAATGGG TTTTGTTAAN CTGTATCACA TTTATNCTTG 240  
CAGAAATTTA TTNCATTGTT ATTAGTAGGA ATTTTNTTGG TTCAATAAAA TTGGCAAAAN 300  
CTGGGAAAAAN NAAANNTTN 319

SEQ ID NO:5203

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06210

SEQUENCE DESCRIPTION:

GATCTGTCTA GTTCCATTG TCTGTTCAAC CTCAGTGNTT CAAAAGTTCC TAATAAATAA 60  
 ACTCATTGA GTTGAACCTA AA 82

5 SEQ ID NO:5204  
 SEQUENCE LENGTH:145  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06211  
 10 SEQUENCE DESCRIPTION:  
 GATCAAGAAA GAAGCTATCT GGGANCANTG TAGCANTTAC GTCAGACCAG GACACTTCCT 60  
 GTTTACAGGA GACTATAAAA CCTTTGTCCT ATCATCACTT GATGTGGACG NCATTTTAGG 120  
 CCTCAGCCCG CCTGCACCCA GNNNN 145

15 SEQ ID NO:5205  
 SEQUENCE LENGTH:295  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06213  
 SEQUENCE DESCRIPTION:  
 GATCAGAAGC ACCTCTTCTT TTATAGAAGT TGATGGATGG TTCATTCCAT TCTGCTACCA 60  
 AGAAGTGCAT GCTGCTGCAG CGACACCTCA TTGCAACCTA TTATGAGAGA GTAAACACA 120  
 25 CACTCAGTGA CATTTAGGCC TGCTCTCAAG NCCCAATTTT TATTCCATCA TTAATAAAT 180  
 CCAGTAACT TNCAAATTTG GAAACCANAA ACTAAGGCAT ACCTGGCTTA GATTCTTTCA 240  
 GAATTTTCTG NTCTTTTGTA CGTAAATTNA AAAATAATTT GTGGCAGGGN TTAA 295

30 SEQ ID NO:5206  
 SEQUENCE LENGTH:87  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06215  
 SEQUENCE DESCRIPTION:  
 35 GATCTTTAAA ATNAAGTGTG CGCTTATAAT ACAAGTAATG CTTGTGTATT TCTCACTTTA 60  
 GGAAATAAAA TATTTGCCAA TTTGAAA 87

40 SEQ ID NO:5207  
 SEQUENCE LENGTH:165  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06216  
 SEQUENCE DESCRIPTION:  
 45 GATCCTCCCA TCTCAGCCTC TCGAGTAGCT NGGACCACAG TTGTGTGCCA CCACACTTGG 60  
 GCTAACTTTT TAATTTNTTT GCGGAGACGG TATTGCTATG TTGCCAAGGN TGNTTACATG 120  
 CCAGTACAAT TTATAATANA CACTCATTTT NCCTNCCGTC TGAAA 165

50 SEQ ID NO:5208

55

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06217

SEQUENCE DESCRIPTION:

GATCTTCTTC AGAAGCTTCA AGTCTCANCT GCATTAAAGC TCTCCATTGA ACCCGNTCAC 60  
 AAAAGTACAA GCTTAAAGGG GCTAAATCC ATTAATACAT NCCATNTTAT ANCCCN 116

SEQ ID NO:5209

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06218

SEQUENCE DESCRIPTION:

GATCCCGTGN ACCGAGTACA CGACCCAGGT ATGTACCAAG TAGGCACCCT TGGGCGCACC 60  
 CACTGGGGCC AAGGGTCGGG GGAGTGTGG GAGCCTCCTN CCCACCNNAC CTNCCTN 117

SEQ ID NO:5210

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06219

SEQUENCE DESCRIPTION:

GATCAGCCAC TTGCTGACCC TGGTTCTTAA GGACACATGA CATTAGTCCA ATCTTTCAAA 60  
 ATCTTGCTT AGGGCTTGTG AGGAATCAGA ACTAACCAG GACTCAGTCC TGCTTCTTTT 120  
 GCCTCGAGTG ATTTCTCTCT GTNTTCACT AAATAAGCAA ATGAAAATC TCTCCATTAA 180  
 A 181

SEQ ID NO:5211

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06220

SEQUENCE DESCRIPTION:

GATCANAACC AGTTTGTAGA TTTCTTTGTT CTTCTCCAT TCCCACTGCT TCACTTGCCT 60  
 AGTCTTGAAG NAAAAAACA AAAACAAAA AAAACCTTGT TCCTTTATAG GTTCCTGGTA 120  
 GAATCAGTAG AGATGATTTT AGCTCATTGA CATTTTTTTA AGCTATATCC CCTTGTCATT 180  
 CCATTGAGAA AGCTGACAAC TGGGATAGGG AGGGGATTCTG ATAATAGATG GGGTCAAATT 240  
 CTGTGTGAAT GTGAACCTGC CTAGTAAGCA CTTTGGTCTG TGGTTCATN CTGCGGTTAG 300  
 NGGAAATCTA TCTCCCTAT CTTNGGGTCC TTGAATACA GCNN 344

SEQ ID NO:5212

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



CLONE:HUMGS06221

SEQUENCE DESCRIPTION:

GATCACATAA CTAGGAAGTG GCAGAACTGA TTCTCCAGCC CTGGTAGCAT TTGCTCAGAG 60  
CCTACGCTTG GTCCAGAACA TCAAACTCCA AACCTGGGG ACAAACGACA TGAAATAAAT 120  
GTATTTTAAA ACATCTAAA 139

SEQ ID NO:5213

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06222

SEQUENCE DESCRIPTION:

GATCGTAAAC CATTATCCTT TAAAGGTNTA TTTGAAGATG CTGTTAAAGT ACAGAATTTT 60  
GTGTACAGGT AGATTTTNCCT GTCCCTCATT AATAGTGCCT TCTTAATTAA TACAGACTGG 120  
TGTTAGCTAT AACAAACTC CAGTANNGGG GGGTGNATCC CAAGTNCCTT GTGGCNANN 179

SEQ ID NO:5214

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06224

SEQUENCE DESCRIPTION:

GATCAAAATG TTCTGGAATT AGATGTGATG TTTGCACAAC TCTGTGAATG TACTAAGAAC 60  
CACTGAATTG TATATTTTAA AAGCATGGTA TGTGAATAAT ACCTCAATAA AGCTGTTATA 120  
AAAAATAAA 129

SEQ ID NO:5215

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06225

SEQUENCE DESCRIPTION:

GATCTTCAAG CATAGNNTTG CATATTTTAA CATCTGAAAT CAGAAAGTGT CTTNCTGGG 60  
AGTNTGGTTT TAGAAACATG AAATAGTACT GTATGTAAA ATCGATGGCA GTGTTGCCTC 120  
GATGATATNT N 131

SEQ ID NO:5216

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06226

SEQUENCE DESCRIPTION:

GATCTTTGAG CGGGACCTGA AGAAGAAGGG GCCCGAGCCG GTGCCACTGG AGTTTATCCC 60  
AGCCAGGGC CTGCTGGGAC GGCCGGGTGA ACTCTGTGCC CAGCACTTCA CGCTCAGCTG 120  
ACCCTGGCCC ACCTGTNAAT AAATCTCAGC TGACCCAGC CCACCTGTNA ATAAATNTTT 180

TTGCAGGAAA

190

SEQ ID NO:5217

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06227

SEQUENCE DESCRIPTION:

GATCCCTGGT CTTCACTG TAGCAGCCAA AAGGAACAAG CTGAAANTGG ATACCTAATG 60  
 TAAGTGGAGT CTTCTAAGTG TTTCTGGAA GAAGTCGGGT CCCAGGCTCN AGTTGCTGGT 120  
 TCTNACATGC CACCATCCAC AGTCCTTCAG CAGATTNATT CAGTGGCTAA TGCTGATATC 180  
 ATAAATGCGG CAAAGAAGTT TTTTCTGGC CAGANGTCAN TGGCAGCAAG TGGAAATTTG 240  
 GGNCATNCAC CTTTTGTG ATGAGTTGTA ATACTGNNGC GCNCATTACC AGGTGAGAGC 300  
 TGGANCGTNT TTTCAGNCCN TGN 323

SEQ ID NO:5218

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06228

SEQUENCE DESCRIPTION:

GATCAAAGTT CAAATTAATT TTAACCTAGC TAATNAACTC ATCACCAGGA CAGTTGGAGG 60  
 GGGTAGGCCG AGGTTAAATG GTCCACGTTT CAAAAATGTT AATGGCTAAT CCATAATTAA 120  
 AGAAGGTTTA ACTGTTACTG AAGTTTACAA GTTTATTGT CATGNACATG AANTACAAAC 180  
 ACGATGGCTT CGAAATGTCT TTCAATAANT GTTCTGCAT TTTAA 225

SEQ ID NO:5219

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06229

SEQUENCE DESCRIPTION:

GATCTCATTC TCACCTCAGA AACCATTAC AACCAGATT ATNATAGTAA TTTGCACCAG 60  
 ACTTTCCTTA GACTGTTAAG TAAAAATGGA CGTGACTTT TGGCCAGCAA AGCACATTAT 120  
 TTTGGTGTAG GTGGAGGTGT TCATCTCTTT CAGAAGTTTG TAGAAGAAAG AGATGTTTTT 180  
 AAGACCAGAA TACTCAAAAT AATTGATGAA GGATTGNNGA GGTTCATAAT TGNAATAACT 240  
 TTTAAGTTTC CTGGNTTANT TAACATTCAC TTNGTGTCC ANAATTGGNG ATAGACNGNN 300  
 AGGCACANGN TGTCTN 317

SEQ ID NO:5220

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06230

SEQUENCE DESCRIPTION:

GATCATATAC AGTTCCTTT TAAAAAGCA ATAAATNCTT GGAATTAGAA A 51

SEQ ID NO:5221

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06232

SEQUENCE DESCRIPTION:

GATCAAGAAAT GTTCCCAA GTTNTGAATA GAGTGTACA ATGTATCCAA GANTTGTGAA 60  
GCAATGATTC TTTACAATAC AATAAAGTTT AATTATTAC AAA 103

SEQ ID NO:5222

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06233

SEQUENCE DESCRIPTION:

GATCTCACAG ATGTNTGGAA TTTCAAAAAG CCAAACACAG AGAAGCAGAG TAGGATGGTG 60  
GTTGCCAGGG CCTGGGACGT GGGGGAAATA GGGAGATGTT TGGTGTCTGT TAGGAAGAAT 120  
GAATAAGCTC TGGAGAGCTA ATGTACAGCA TAGTGACTNN NGNTAATAGA ACCGTATTAT 180  
ATACTTGANA TTTGTGAAGA GAGTAGATGT TAANNNNN 218

SEQ ID NO:5223

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06234

SEQUENCE DESCRIPTION:

GATCTGTCAC TTAATTCTGT GTGACCTTTG AAAGGCTACT TATTCCTCT CTTAGCTTTC 60  
TCATTAAAT CAATGAACAA TGCCAAA 87

SEQ ID NO:5224

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06235

SEQUENCE DESCRIPTION:

GATCTCAGGC TGAGCAAAAT NAAACCTTGA TGTTACGGGC TAAATCAAGA GCAGCTTAAT 60  
CCTGTTTACA ATGTGAGCTT TTTGTGCGTC TGTGAAATGT TTTACAGTGT TTCTCATCAT 120  
CTGTTTCCCA GCAAGGTCTT TNNTTTTNCN ACATTGAAGT NCTGNCTATG TATCTNAATC 180  
ACAAATGGNT TCATTCACTN TN 202

SEQ ID NO:5225

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06236

SEQUENCE DESCRIPTION:

5 GATCACAAGC GTATCCATNG TGAGGTTCCG TGGATGGAAG CTNATGGATN TNCCTTCCTG 60  
ATGTTTCATCT GCCACCTTGC TATTNAATGC ATCCTGTTTA TAACTGTCTT CTAAATATTG 120  
AATAGAAATA AAGCATTGTG ACAGTAAA 148

10 SEQ ID NO:5226

SEQUENCE LENGTH:370

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06237

15 SEQUENCE DESCRIPTION:

20 GATCGAAATT GCGGGCTATG GCGCCGAAAGT TTTTCGTNAG TACTGGGATA TCCCCGATGG 60  
CACCGATTGC NACCGCAAAG CCTACAGCAC CACCACTATT GCCAGCGTCG CTGACTGACC 120  
GCCGCTGCCT ACAGAGTCAC ACTCAATCCT CCGGGCACCT TCCTTGAAGG AGTGGCTAAG 180  
GTTGGACAAT ACACGTTTAC TGCAGCTGCT GTCGGGGCCG TGTGTTGGNCT NACCACCTGN 240  
ATCAGCGTCC ATNTCCGTNA GAAGCCCGGA CGANCNCNTG AACTACTTNN CTCGGTGGCT 300  
TTCGCCGGAG GCTTNACTTT TGGGGGNANG GACGTACAAT NTACGGGGTT TGGGGCCGCC 360  
GNNTTTGGTN 370

25 SEQ ID NO:5227

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06238

30 SEQUENCE DESCRIPTION:

GATCTGTGTG AAGAATGGTA ATNACGTAGT TGNAAAGGAA AATGTACTGT TGTGTGTTTC 60  
ATTTGTGTGA TTTCGTACCA AAAAAATGTG TTTGAACTAT ATTGTATGTA ATTTGGAAGT 120  
CGTGTTAATA AAACCCTGCA GTTTCCTAAA 149

35 SEQ ID NO:5228

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06240

40 SEQUENCE DESCRIPTION:

45 GATCAGGCTT TGAAGGCTGG ATTCTATCTA CATAAGTCN TTCAATTCCA CCATGGGNCA 60  
GAGCAGCTCC ACCACGTGTG CACTTAGCCA TNGNTGGCAA CAGAAACCAA GAGACACANN 120  
TACGCAGGN 129

50 SEQ ID NO:5229

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS06241

SEQUENCE DESCRIPTION:

GATCATTTAG GAAAAATAAT TCTATTTTGA GCTTTTCATT TCTCAGCTGT CCTTNTTCT 60  
NNTTTGATTT TTGACAGCAA TGGAGAATGG GNTATATAAA GACTNCCN 108

SEQ ID NO:5230

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06243

SEQUENCE DESCRIPTION:

GATCAAGAGT TGTCATGCTA GGGAGACTAT TCTGCCTAAA ATTCTGGGGN ACTATTTTGT 60  
GTTTAAGNAT ACTATGTATA TTAAGGGT ACATATTTGA AA 102

SEQ ID NO:5231

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06244

SEQUENCE DESCRIPTION:

GATCTTAAAA GTGTTATTTT TGCTTTTATT TTTAAAAAA GGNGAGGNT TATTGGCAAA 60

SEQ ID NO:5232

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06246

SEQUENCE DESCRIPTION:

GATCTGCAGA TAGTTCTTTT TCAAAATATT GTTTAGACAA AATAAATTC TTAAATATA 60  
ATATCTCTAC TTCAAA 76

SEQ ID NO:5233

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06247

SEQUENCE DESCRIPTION:

GATCGNTCTG GTCGCAGCTT AGGAACAGCA GACGTGCACT TTGAGCGGAA GGCAGATGCC 60  
CTGAAGGCCA TGAAGCAGTA CAACGGCGTC CCTNTGGATG GCCGCCCCAT GAACATTCAG 120  
CTTGTCACGT CNNGATTGA CGCACAGCGG AGGCCTGCAC AGAGCGTAAA CAGAGGTGGC 180  
ATGACTAGAA ACCGTGGCGC TGGAGGTTT GGTGGTGGTN NNGGCACCCG GAGAGGCACC 240  
CGCGGAGGCG CCCGTGGAAG AGGCAGAGGT GCCGGCAGGA TTTCAAAGCA GCAGCTTTCG 300  
GCAGAGGAGC TTN 314

SEQ ID NO:5234

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06248

SEQUENCE DESCRIPTION:

GATCAATACC AAAAGACACT TGGAACTCTT TTTTAGACTT CAGTACGATG ATTGCAGATG 60  
ACATGTCTAA TTATGATGAA GAAGGAGCAT GGCCTGTNCT TATTGATGAC TTTTGGGAAT 120  
TTGCACGCCC TCAAATTGCT GGGNCAAAAA GTACAACAGT GTAGCACTAA AGGNNCCTTC 180  
TAGAATGTAC ATAGTCTGTA CANTAAATAC ANCAGTAAAT TGCACAGTCA GNANNNNN 238

SEQ ID NO:5235

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06249

SEQUENCE DESCRIPTION:

GATCTGCAAA CAATGAAGAA TTATGTAATA TATTGTACAA ATGTAAGCAA AGGCTCTGAA 60  
ATAAAATGCC ATAGTTTGTG AAA 83

SEQ ID NO:5236

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06250

SEQUENCE DESCRIPTION:

GATCTTAAAT ATCTTGCAGC CTAAATCAC TACAAACATT TGCATTNTTA TTATGCCAGT 60  
TATTTCCAAA ANGTAATTGN ATACATGTCA CTTATGTTTT TAAGCTANTA TTGACTGTAG 120  
GATAATCTCC TTGTTCCCT CAAAATAGTC ATGNAAGTGT ACATGAANNT NTTTTAN 178

SEQ ID NO:5237

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06251

SEQUENCE DESCRIPTION:

GATCTGAAGA GCTTTCAGC TCTNTTAAAT AGGTTGCTGN ACATGTTCTA AGGTTTGTGA 60  
GAACACGTGT GCCTGTTTAA GTGTATTGAT GTTAATANTA TTAAATATCC TAATGATNGA 120  
ATGCATTGTA TGGNTNCTN 139

SEQ ID NO:5238

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06253

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTAAGCC ACAGNGGGGA CTGGAGCCTC GTTTTCCCC TAGGCAGACC TAAATCAAGC 60  
 AGCTTACCAC AATAGTGCAT GCTGAGTAGA TTAGTTCCAA GGAAGGGAGA CTGGAATGCT 120  
 GGTGTCAAGG AAAAGCCTCC CTCATCATCT AGTCTAAGAC CATAACGGGC AGAAGCATAA 180  
 GAGGTTCCAG GGCCATAGGN GANTGAGAAG TAGGGCACAT ATAGGGAGGA AAGAAAAGTG 240  
 NAGNNGGGGG ANATCTCCGA NTTTTTTTAC TGCTTGGGAA AAGTGTAATA CATGANGGNT 300  
 GCTTNGGGCT TTGCTAACCT GCTCACCCT AACCCTNCCA AGTNTTAACC ATCCCCAGNG 360  
 GTN 363

SEQ ID NO:5239  
 SEQUENCE LENGTH:171  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06254

SEQUENCE DESCRIPTION:  
 GATCTGAGGA ACAAATGAT GTCATTTAAT CGGAATCTAA ATGTGACACA AACAACGTGC 60  
 CAGCAATACC TGCTTGTGAA ATAATGTTCT GAGCCCACAG TGTTCTGGG TATGTGAGTT 120  
 TATATCAAGT GAAAAGGCTG CTTAATTGAC ATTAAAGTTT TGGAATGTAA A 171

SEQ ID NO:5240  
 SEQUENCE LENGTH:348  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06255

SEQUENCE DESCRIPTION:  
 GATCATAAGT ATAAATGTCC TCGTTTAATC TTTCCATATT GAGGACAGCC TCTGCATATA 60  
 AAAATGTTCA TTGGGAGAAA AATTATTTTT AAAACTAAAT TTTTATAGTA GTCCTCCATT 120  
 ACTGGCAATT AAGGAGCAAC CCACAAAATG TCATTATGTG GTTCTTTGAT TAGGCATAAA 180  
 ANGTAATTGCA AACAGCTTTN CTATTCCTTT GGAATATGAN TCTTTTTAAT GTCTAANGTT 240  
 AACCTGCAAC ATATTCTAGT AGGACANGTC AATGTAAATN AGGTAATTNT NGCCTGTNTT 300  
 ATACCTNCTG TNGCCATTG GTNCAAATGN NAACCATTN TNAGNCCN 348

SEQ ID NO:5241  
 SEQUENCE LENGTH:357  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06256

SEQUENCE DESCRIPTION:  
 GATCAACAAG AGAAATAAAA AAGCCCAAGA GGAAGTGGTA GGGGAAGGAA TTTAAGAACA 60  
 GCAATAAGTA AAACCTCTAA GTAACCTCAA AAAGAAAATG GTACATTTTG CCAAAGACCA 120  
 CTTATACTTG AGAACATGGA AGAATTGGCC TGATACTNNN NGNNGGGGAA AAGAGTCTCT 180  
 CCTCTTTTCC TCAAACCCCA GTACACTCAG CCTCTNTGCC CCACCTTCTC CTGACTTTGT 240  
 CCTCACTTGC TTCTGCAGTA CATTGGAACC TGNNTTGAAA GAAAGTCTTC CTTGANTAAT 300  
 TGGAGTTTGT CTTTGNGNGG CAAATTTAGN CCCNNGGNTC ACAAGNTTTC GGGGGTN 357

SEQ ID NO:5242

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06257

SEQUENCE DESCRIPTION:

GATCGGGGAC ATCCTTAGGC TGGTGGCCGG CCGCATCAAG AACACCTTCT GATTGAGCGG 60  
 TTGCCATGGC CGGTCTCCGT GGGGCAGGGT TGGGCCGCAT GTGGAAGGGC TCTGAGCTGT 120  
 GTCCTCCTTC ATTAAAAGTT TTTATGTCTC GTGTCAGAAA 160

SEQ ID NO:5243

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06258

SEQUENCE DESCRIPTION:

GATCAGACTA AAAACNATAA CACCATAGGT CAAAANAAGT TGTCTGAGG TTTTTTGAA 60  
 ACATTAAAGN TCCAAAACAT GACATTTTGA AGAATAAATT TGNAATAGAG TATAATTGNN 120  
 TN 122

SEQ ID NO:5244

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06259

SEQUENCE DESCRIPTION:

GATCTCCCCT CTCACCCCTC CCACCCATTA ATCTCCTCCC AAAAAACAAG TAAAGTTATT 60  
 CTCAATCCAA A 71

SEQ ID NO:5245

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06260

SEQUENCE DESCRIPTION:

GATCTGTTGT AATATATGGT GGATATTTTC CTTTAATTTT AAACATAACC TCTGAAATNT 60  
 GTATCTNTCC TTTTTNATCT TACCATTANT TTAAATCTA GTGGATTGGT TTTN 114

SEQ ID NO:5246

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06261

SEQUENCE DESCRIPTION:

GATCAGACCG CTCAAAGGTC CCCGTNTTCA CTGTTACCCA GAGGCTCTTG TNACTACCCA 60  
 CTTCAATTCCC CACCGCTGCC AGTGCCACTG CCAACCCTGT TCACAGGCGN TTCCAGCCCA 120



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CTCCAGCCAG GGGAGCAGGG AAGAAGAAGG GGCTCCCTCC TCTTCACATT CCCCCGACC 180  
 CCAAAGCCAG AGAAAGCCAG ATGGCACCAG CTGCTCCGGA TGTGCCTGCC CACATTGGGG 240  
 GACAGGGCCG GGCCTGGGCT CGGTTCCNAG GTTTGAGCTC TGCAGNCTGT GTCCTGGNGT 300  
 GAGGGGGCTG AAGTNAGNCC AAAGGAAGAA CTNAGTN 337

SEQ ID NO:5247  
 SEQUENCE LENGTH:168  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06262

SEQUENCE DESCRIPTION:  
 GATCACCTNA TTTTITNAAC AAAATATTN TAACAGGAAT GGGTGGGAGT NCTGGTGAAA 60  
 AGAGGTGAAA TGTGGTTGTA TGAGCCAATC ATATTTGTAA TTNTTTAAAA AAAGTTTAAA 120  
 AGGAAATATC TGTCTGAAA CCCCACTTAA GCATTGTNTT NNTATAAN 168

SEQ ID NO:5248  
 SEQUENCE LENGTH:378  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06264

SEQUENCE DESCRIPTION:  
 GATCAACAAA GAGGACTTTG TGGCACTGGA GAGGCTTACC CAGGGGATGG ACATTCAGTG 60  
 GATGCATGTT NCTGGTCATT CGGGATTAT AGGCAATGAA GAAGCTGACA GATTAGCCAG 120  
 AGAAGGAGCT AAACAATCGG AAGACTGAGC CATGTGACTT TAGTCCTTNG GAGAACTTNA 180  
 GCCAGCGGCT GTCTTGCTGC CTGTACTTAC TTGTGTGGAA AATAGCCTGC AGGTAGGACC 240  
 ATTGCAGTGA TGGGCAGATT GGGTCTTTCA CACGGNGTCA GGCACAGTGG CTTTCTGTNG 300  
 NCATGGTNGT TTTATANANA AATNGGTAA GGTATATAAA TAAAGTNTGG NCCANCTTTT 360  
 GNNAAGGNAN GANATGGN 378

SEQ ID NO:5249  
 SEQUENCE LENGTH:131  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06267

SEQUENCE DESCRIPTION:  
 GATCANCTAC AGGAAAAGTA AATGTGAACG CAAGCAGAAT GAAACACAGT AAAAGCCGGT 60  
 CTAGCCTGCC TGGCCACACT CTCAGCGCCT TGTGAGGATG GGNCANTANA TAAANTCATC 120  
 TTTAGTAGAA A 131

SEQ ID NO:5250  
 SEQUENCE LENGTH:322  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06268

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCATCACT AGCAGATGTC AGTTGCACAT TGAGTCCTTT ATGAAATTCA TAAATAAAGA 60  
 ATTGTTCTTT CTTTGTGGTT TTAATAAGAG TTCAAGAATT GTTCAGAGTC TTGTAAATGT 120  
 TATTTTAATA ATCCCTTTAA ATNTNATCTG TTGCTGTTAC CTCTTGAAAT ATGATTTATT 180  
 TAGATTGCTA ATCCCACTCA TTCAGGAAAT GCCAGGNAGG TATTCCTTGG GGAAATGGTG 240  
 CCTCTTACAG TGTAATNTT NCCTCCTGNA CCTTTGCTAA TATCATGGCA GANTTNNCCT 300  
 NATCCCTTTG TGAGGCAGTT TN 322

SEQ ID NO:5251  
 SEQUENCE LENGTH:215  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06269

SEQUENCE DESCRIPTION:  
 GATCAAAAAT AAGATTACAG TAAAAATATT NCTATATTCA GATGGTTTAG AGACCAGGCT 60  
 GTAGAATCAG ACAGCCCTGA AATTGTATCA CACANGGCTG TGTACCCTG TACAAATAAC 120  
 TTAGCCTTAC TAAGCCTGTA TTTCTCATC TGCAAANTAG GGNTGNTAAT ATACCTGTNG 180  
 NTAAANATGT TTTCATTAAT AANC GTTGGC GCAAA 215

SEQ ID NO:5252  
 SEQUENCE LENGTH:229  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06270

SEQUENCE DESCRIPTION:  
 GATCTAAAGT GCAGCAGAGT GGCTGNTGCT GCAAGTNATG TCTAAGGCTA GGAACATATCA 60  
 GGTGTCTATA ATTGTAGCAC ATGGAGAAAG CAANTGTAAA ACTGGATAAG AAAATTATTT 120  
 TGGCAGTTCA GCCCNTTCCC TTTTCCCAC TAANTTTTN CTTAAATTAC CCATGTAACC 180  
 ATTTNANCTC TCCAGTGCAC TTTGCCATTA ANGTCTCTGC ACATTGAAA 229

SEQ ID NO:5253  
 SEQUENCE LENGTH:219  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06271

SEQUENCE DESCRIPTION:  
 GATCGTGAAA GAGGCTTACC CAGACCACAC ACANGTTTGA GAAAAACAAT CCCCATTATN 60  
 ACCCATCTAG CAAAGAGGAC AACCCTAAGT GGTCCATGNG TGGATGTACA GTTTGTNCGG 120  
 ATGATGAAGC GTTTCATTCC CCTGGCTGAG CTCAAATCCT GTCATCAAGG CNCACAANGC 180  
 TACTGNTGGC CCCTNAAAAA ATATTGTTNT NTGTCACTN 219

SEQ ID NO:5254  
 SEQUENCE LENGTH:144  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06272

## SEQUENCE DESCRIPTION:

GATCACGCTG AAAGAATACC TTGCAGACAC TTAATCTCTG CGGCAAATGC ATGAAAGTAG 60  
 AAGGATGAAG CCAACTTTCC AAAAACTTTT ATGAAATTAC TTCAGTGNGA AAACCTATTA 120  
 AATNAANTNC AGCCNTTCTN TAAA 144

SEQ ID NO:5255

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06273

## SEQUENCE DESCRIPTION:

GATCCCGGGG ACATGATGCG GGAAATCCGC AAAGTNTTGG ACGCCAATAA CTGCGACTAT 60  
 GAGCAGAGNG AGCGCTTCTN GCTCTNCTGC GTCCACGGAG ATGGGCACGC GGAGAACCTC 120  
 GTGCAGTGGG AAATGGGAAG TGTGCAAGCT GCCAAGACTN TCTCTNNACG GGGGTCCGGG 180  
 TNTN 184

SEQ ID NO:5256

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06274

## SEQUENCE DESCRIPTION:

GATCAATGTG GGCACCTAAA AGGGTATGTT AAAATCACCA TTTCTCAGGT CAAAATACTG 60  
 TGAATAAGTC TTCAATAGAA TCACTANTGG TTNNAAA 97

SEQ ID NO:5257

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06275

## SEQUENCE DESCRIPTION:

GATCATATCT ACATGTATGA ACTTAACATG GAAAATGTTA AGGAAGCAAA TGGTTGTAAC 60  
 TTTGTAAGTA CTTATAACAT GGTGTATCTN TNTNCTTATG AATATNCTGT ATTATAACCA 120  
 TTGTTTCTGT AGTTTAATTA AAACATTNC TTGGTGTTAG CTTTTCTCAG AAA 173

SEQ ID NO:5258

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06277

## SEQUENCE DESCRIPTION:

GATCTTTCTG GGAGCTGCGC CGGACAGAGT GGGGAGCTCC TAGTTTNTGG GGGGAAGCTT 60  
 TGATATCCAT GCCACGTCCA TCCACCCAC CCCTNTTCGT CACGAGCACA ATGGTCTTAC 120  
 ATNGATNTN TGTAAAAAAA TANAAATAAA TGGAGACTTT AACTCAAGCA ANNAAN 176

EP 0 679 716 A1

SEQ ID NO:5259

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06278

SEQUENCE DESCRIPTION:

GATCATTGTA ACCTAGGAGT TAGAGGCTGC AGTGAGCTAG AATTGCACCA CTGNATTGCA 60  
CCTTGGACAA CAGAGTAAGA CTCGTCACC AAA 93

SEQ ID NO:5260

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06279

SEQUENCE DESCRIPTION:

GATCAGGAGG CCACCCCTT CTGTGGCACT TCTGAGATGA CAACTTGTTT CACAGTTGGA 60  
TGGGGGTGGG GAAGGAAAGA GCGGCCCAT TATCCAGAA CATTATATCC ACACAGGCTC 120  
AGACACCTG TGATGAAGAG TCCAAGAACA GCCTGAGATA AGGATGTCAT TTTNTTTTCA 180  
CAGNCCCAC GATGGGTTA TTTTGGGA CCAAGACATT GGGTCCCTAC ATGTTTTCCC 240  
CTACCTTCT NNGGGAATAA AATATCAAAC ANCCNCANA GNTGTNNTAT TNNTGN 296

SEQ ID NO:5261

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06280

SEQUENCE DESCRIPTION:

GATCTATTGA CTTGTAGAGG TTTGGGACAA ACAGGAATAT AAAGATTATG GAATTGGGAA 60  
A 61

SEQ ID NO:5262

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06281

SEQUENCE DESCRIPTION:

GATCACTGCA AAACCTCAAGG AGGCCCGGGG CAGAGGAAAA AAATTACCA CCGATGATTC 60  
CATTGTGTG CTGGGAATAA GCAAAAGAAA CGTTATTTT NAACCTGTGG CAGAGCTGAA 120  
GAAGCAAACG GATTTTAAGC ACAGGATTCC CAAAGANCAG TGGTGGCTCA AGCTACGGCC 180  
CCTCATGAAA ATCCTGGCCA AGTACAAGGC CAGCTATGAC GTGTCGGACT CAGGCCAGCT 240  
GGAANCATGT GCAGNCTGG NGTGTCTGAC CCAGTCCCGN CTGCATGTGC CTGCAGCCAC 300  
CGTGGNCTGT CTCTTTTTT TNACACTTAA GTTNTTTT 339

SEQ ID NO:5263

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06282

SEQUENCE DESCRIPTION:

GATCTTATCT ACTTTCTCAT CTCCATATTT TGTAAAGAT AATATTGCCA GATGTAAAGA 60  
 AAATGGTTTA TTCTACCTAA AGAGTGGATA AGGAGAGAA ATTATGATGA AATAAAAATT 120  
 ATAAGCAAAG TTTATTTAAN CTAAATTTAA ATGTGAAACA TCACCTTTT CCTANTCAGA 180  
 TTTGATATTG CTACGGATAT ATNTTGNTGA TATNGTCACT ATATANNCAT ANGGGGANTT 240  
 TNACTNTCTA TTACCCTN 258

SEQ ID NO:5264

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06283

SEQUENCE DESCRIPTION:

GATCTCTCTC CTCTCTGACC TGGATACGCT TTGGTTTCTC AACTTCTCTA CCCCAAAGAA 60  
 AAGATTATTC AATAAAGTTT CCTGCCTTTC TGCAAACATA AA 102

SEQ ID NO:5265

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06284

SEQUENCE DESCRIPTION:

GATCTAGATT TGAAAGTAAA TTTTATGAAG ACATTGCCCA TTTTACTTC CTCATTCATT 60  
 ATTGTACCAG CATCATAGCT TTATTACTCT AATCCCAGGT AAGTCAAGCC TACACTGCCC 120  
 TAGNGGNNGC GTAAACCCAG AANTTCATGC TGGCTTAANT AATCTATTTT TGTCTCTNAT 180  
 CTTTTGAATN TTTAAN 196

SEQ ID NO:5266

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06286

SEQUENCE DESCRIPTION:

GATCAGCCTG GGCAACATGG TGAGACCCTG TCTCTACAGA AAAGACCTGA AAATTTTAAA 60  
 AAAAAGTATA AAGCCAAGCT GTTACCCAGC CACCTTGCTC ACATATTCTC AGGACCTGCT 120  
 GAGGTGGTTT CACAGGTCAT AGTCCTCACA TTTGCTCAGA ATAAATATCT TCAAATATTT 180  
 AAANNNGGN NANAATNTNT GNN 203

SEQ ID NO:5267

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06288

SEQUENCE DESCRIPTION:

5 GATCTGGACT ATCCACGTGC TTTGAACTT TTCCCTCAC CCTCCAGCCC TGGAGGCTTT 60  
 TGCTGGGATG AATGTTTTTA TAGGGTTTTT GTTGTAACAT AAGCTATTTT CTAATATGCT 120  
 GCCAGGTACC CTTAAA 136

SEQ ID NO:5268

10 SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06289

SEQUENCE DESCRIPTION:

15 GATCTNGGAC TACNACTGGA CTACTAGCCT CCAGAACTAT NAAATAATAC ATTTCTAATG 60  
 TCTAAGCCAA A 71

SEQ ID NO:5269

20 SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06290

SEQUENCE DESCRIPTION:

25 GATCGGTTTT TGTGGGGAAT CTCCCTTATA AAGTTGAAGA ATCTGCCATT GAGAAGCACT 60  
 TTCTGGACTG TGGAAGTATC ATGGCCGTGA GGATTGTNAG AGACAAAATG ACAGGCATCG 120  
 GCAAAGGGTT TGGCTATGTG CTCTTTGAGA ATACAGATTC TGTTCATCTT GCTCTGAAAT 180  
 TAAATAATTC TGAATCATG GGGAGAAAAC TCAGAGTCAT GCGTTCTGTT AATAAAGAAA 240  
 30 AATTTAANCA ACAAATTC AATCCACGAT TGANGAATGT CAGTAAACCT AAGCAGGGAC 300  
 TTAATTTTAC TTCCAAAAC GCAGAAGGNC ATCCTAAAAG CTTGN 345

SEQ ID NO:5270

35 SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06291

SEQUENCE DESCRIPTION:

40 GATCTCTGCT GTGCAGGTGC TAAGATTAAG CACTAAAAAG AAAGAGAGAT ATATGTAATG 60  
 TACAACTGAC ACTGCCATTT TNCCTTTTGG GAGGAAATGG ACATAGATAA AGAAGATATT 120  
 TCTNCGGTTA AA 132

SEQ ID NO:5271

45 SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06292

SEQUENCE DESCRIPTION:

50 GATCTTCTGC CAAGTAATTT TTTTGCACAA TTTTCTGTN CCAAANTTTA CTCAGTTAAA 60

55

AGTAAANAA TNCTTTACAC GTTTTAGGTT TTAGGACATT AAAAGTATGT N 111

SEQ ID NO:5272

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06293

SEQUENCE DESCRIPTION:

GATCATCTTA CGATATCAAG CTGAAAATTT CACCACTACC TGGACAGTTN CACATGTTTT 60

ACTGGGAATA TTTTCTTT NTTTNTGTA TGCTCTGTGC TAGTAGGNTT GATTGAN 117

SEQ ID NO:5273

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06294

SEQUENCE DESCRIPTION:

GATCATATTC ATTATGAAAG GTCAAGCAAA GACAGCAGAN TACCAATCAC TTCATCATTT 60

AGGAAGTATG GGAACATAAGT TANGGAAATC CAGAAAGANG CCAAGATATA TCCTTATTTT 120

CATTTCAAA CAACTACTAT GATAAATGTG ANGAGGATTC TTTTTNTTG TGACCTATAA 180

TANTTNTACA NGCTTTCATG CATTACTTG GTCCTAAGCA AATTANNGC AN 232

SEQ ID NO:5274

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06295

SEQUENCE DESCRIPTION:

GATCAAGTAT AATGTTAGCT GCAGGTTTTT AATAAATACC TTAATTCAGT TTGAAA 56

SEQ ID NO:5275

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06296

SEQUENCE DESCRIPTION:

GATCCTGAAC ATGTGCTGAT TTNAATTGTG CTATATAGTA TATAAANTAA AATANTTTTG 60

GTATTTCTGC AACGTGACCT GATAATNAAT CTATTCATCC TGAGNAAGCT ATACTTCTGT 120

CCNTN 125

SEQ ID NO:5276

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06297

## SEQUENCE DESCRIPTION:

GATCATTGGT TCCANNCACA GGTNTAGTAA TNNTGGGTAC TTTAAGGTTT GGAGCACTTA 60  
CAAGGCTGTG GTAGAATCAT ACCCCATGGA TACCACATAT TAAACCATGT ATATCTGTGG 120  
AATACTCAAT GTGTACACCT TTNACTACAG CTGCAGAAGT GTTCCGGNTA GACAAAGTTG 180  
TGACCCGGGG NNCTCTGN 198

SEQ ID NO:5277

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06299

## SEQUENCE DESCRIPTION:

GATCTCAAGT TGTATAAAAC CAATAAATTT GTGTTACTGC AGTAGTAATC TTATGCACAC 60  
GGTGATTCA TGTTATATAT GCAAAGNAGG CAACTGTTTT CTTAGTTACA GAAGTTTCAN 120  
GCTTCACTTT TGTGCAGTAG AAACAAAAGT AGGCTACAGT CTGTGCCATG TTGATGTACA 180  
GTTTCTGAAA TTGTTTACA AGACTTTGAT AATAAAACCC TTAANCTTAA A 231

SEQ ID NO:5278

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06300

## SEQUENCE DESCRIPTION:

GATCAAGNGC CATAGCCTTT ATTCAGGGGG CCTATAAACC CTTCCAGTTC TTGCCCCAGG 60  
GCTGGCCTGC TAGCGTTTCA AATTCACAGG TGTCCTAAT TTNAGAAGTA ACCTTTTGGA 120  
ATAGCATTAG ACCCTGGCTG TCCCCTCCCC ACCAAATAAA CATGATATTT CATTCTNAAA 180

SEQ ID NO:5279

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06301

## SEQUENCE DESCRIPTION:

GATCAAGNNT ANTGCAGCCN TTCTTTTCCT ATTTCTTTTT TTNAAGGGTT AGTATTAACA 60  
AATGGCAATA AGTAGAAAAG TTAACATGAA GATTTTAGAA GGAGAGAACT TACAGGACAC 120  
AGATTGTNA TTCTTTGACT GTNACACTAT TGGATGTN 158

SEQ ID NO:5280

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06302

## SEQUENCE DESCRIPTION:

GATCGAACAT NACGTGGTGA TGAAAGCCAN CAGCAGCCTA CCCAAGAAGC TGGCACTGCT 60  
GAAGGCCCCA GCCAAGAAGA AAGGGGCAGC TGCCGCCACC TCCTCCAAGA CACCTTCCTG 120



EP 0 679 716 A1

AGGACGCTGG CCCCAGTGCA GGCCAACATC NCACCCCTA CCTCCATATG GGACCTTGCA 180  
GGTAATCCCA CAGGCTGCAC TGTCAGGGGG GGGACCCTGT CCCCAGCAC TGGGCTTCAC 240  
CTAGAACTTC AGTGGGGGCC AAGGGTGCTG AGAACCAGC AATGNCCAGG ANGATACAGT 300  
CACTAACTT CATCTGTCCC CGTGCCCTT CCCAGGTCCT GNTTCACAGG TTTAACCCAG 360  
NACANTAAAN CCTNN 375

SEQ ID NO:5281  
SEQUENCE LENGTH:272  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06303

SEQUENCE DESCRIPTION:  
GATCAGGATG AGATTTAATG CCCATATCTT ACCAGTTCAG TAATCTCCAG AGCCATTTC 60  
CCCTTTAGAG TGAGTCACAT GCAGGGAGTG TGAATGTCAG AGGTGGTTTA TTATCCAGTC 120  
TGCCTTACCC TTAATCTGTT CACAGATATT TATTTACTAA TGCTTTTTTT TTCTTAAGAG 180  
TTATGGGATA GGAAAATGAA GTGTTTGCTC TTCATTACT AAATGATTGT AAAC TTGAGT 240  
TTTTCATCAA AATAAAATTC CATTGTTTTA AA 272

SEQ ID NO:5282  
SEQUENCE LENGTH:379  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06304

SEQUENCE DESCRIPTION:  
GATCCAAGGC CACAAGTAAG GCTATGGCTC TAATTCTAGA AGACAACCTT CCAAGATGCC 60  
TGGCAAAACC ACCTCCCTGT GCCACACAGA CACACTAGGC CTGTGTATTT ATTTCCCTT 120  
CAAAGCAGAC TGAGGAGGGA GGAGACGAGG TTCTCTTGGC ATCACTTTCT CCCTGGCTGC 180  
AGAACTAGAC ACCCTTGAAG ATTTGGCCTG GGCCAGTNAG ACTGAAATCA AGAAAAACAG 240  
AAGGGATGTG CAGGGTGGGG GGGTNCATT CCTGCTCCCA TGTCAACCCC CAGGGCCTCC 300  
AGCGTGCAGA CGCGTGTCTT ANTTNATCTG CTCCCACGGA TGANCCTGGT CTCAATGGG 360  
TTAGCAGNNG NGAGATNTN 379

SEQ ID NO:5283  
SEQUENCE LENGTH:377  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06305

SEQUENCE DESCRIPTION:  
GATCCTCTGA AAAGGCCAG AAAAATAGCT CAGTTCAAAT ACAATGTTCT AGGACAATTG 60  
GAATATAAAT ATTGTCCAAA AATATAATTA AAAGAAAAA GTTTAGCACT GTGTAAAGTA 120  
AGTGTTAACT GAGGAAGTCC CAAAAAGGTG CTGTCACTTT AAGTTCTGGA CTTGGGGTTC 180  
TTTGATTTG TAAACAGCAA NGCATTGTG TTTGTTGTC TATTTGTAAA GCANCCACCT 240  
TCCTTATTGG NAGGNGANAA NNNGGGTNC ATNCATGTNA NTACTTGCTG CAGCATTNA 300  
TATGTTTAT TTTGTGTAN GCTTTTGTG GCATCGTGNN CACATTATTT GTTACCAATG 360  
GACATGGGTT CTTTGTN 377

SEQ ID NO:5284

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06306

SEQUENCE DESCRIPTION:

GATCGTAGTG TTTTAAATA AACACAGTCC AGACTCAAAC GGAGGAAGCC CACATATTCT 60  
 ATTATAGATA TATAANTANT CACACACACA CTTGCTGTCA ATNTTTTGAG TCAGTGCATT 120  
 TCAAGGAACA GCCACANAAT ACACACCCNN N 151

SEQ ID NO:5285

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06307

SEQUENCE DESCRIPTION:

GATCAACTGA GGAAACTCCA GGCCATGGTG ATTGANATAT CAAACAAAAC CAGCAGCAGC 60  
 AGCACCTGCA TCTTGGTCCT ACTAGTCTCC TTCTGCCTCC TCCTTGTAAC TGCTATGTAC 120  
 TCCTCTGACA CAAGGGGGAG CCTGCCAGCT GAGCATGGNG TGTTGTCCC G CAGCTTCGT 180  
 GCCCTCCCCA GTGAGGACCC TTACCAGCTG GAGCTGCCTG CCCTGCAGTC AGAAGTGCCG 240  
 AAAGACAGCA CACACCAGTG GTTGGACGGC TCAGACTGTG TACTCCAGGN CCCTGGCAAC 300  
 ANTTCTGCGC TGCTGCATNA CNGAN 325

SEQ ID NO:5286

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06308

SEQUENCE DESCRIPTION:

GATCTGCCTC CTGGGAAGGG AAGGGGCCAA TGTCAGCCTC CAGGTGATTT CTTAATCTG 60  
 ACATTACAAA GAGACCAACA GACTGCCAAT TCTACCACAT TCCCCTGGTG GGTACTCGAC 120  
 TATGTAGTTT TNTCTATGCT TCTGGTCAAC TCTGACACAT CTTGGAATTC TTGTAATAAG 180  
 AAAAGAAATT TTTATACTTT TAAA 204

SEQ ID NO:5287

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06309

SEQUENCE DESCRIPTION:

GATCCTCAAA CAGTCGGACC AGATGACAGC CAAACTCTGC TAACCCGGGA CTCCTTGCCA 60  
 TGGACTTTTC CTGTTGTTGT ACACACACAA CAGAACAAAA TGANGCAAAA CAAAACAAAA 120  
 AAACCCACAA AANTTTGTAA AATGTAATTA ATATTCAANG AAAAGGNGGA AANTCTTCAT 180  
 TTGTTGGA AAA TGAAANCGTT CTAGCAACTG TAANNANN 219

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SEQ ID NO:5288  
SEQUENCE LENGTH:259  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06310  
SEQUENCE DESCRIPTION:  
GATCTTAAAA TTCATCTAGA TTTCAAGCAT TCAGCTGACT TGCCTCATAA ATGTAGTGAC 60  
TGCTTGATGA GGT TTGAAA TGAAAGGGAA TTAATAAGTC ACCTTCCAGT CCATGAGACA 120  
ACTNGATTAT TCTCTNTAAC TTACAGAATG TTAGTNTAAA ATAATAAATN CATCCTTNTT 180  
TTGGAGATGA TTAAATGGAT GATTGTAAAC ACAACTTATG AAATCTGCCT NTAACAAGTA 240  
NCTTTNTTAA ATNNTANN 259

SEQ ID NO:5289  
SEQUENCE LENGTH:99  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06311  
SEQUENCE DESCRIPTION:  
GATCTTATTG GCTGATGGTG TTGTTGAATT CTATATCCTG TTGATTGCT GTCTAGTTGT 60  
TCTATCAATT ATTAAAAGAG GAATGTTAAT GTTTCCAA 99

SEQ ID NO:5290  
SEQUENCE LENGTH:81  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06313  
SEQUENCE DESCRIPTION:  
GATCAAATAC TTTAAAGGAA AAAATGTTGG ATTTATAAAT NCTATTTTTT ATTTTACTTT 60  
TATAATAAAA GGAAAAGCAA A 81

SEQ ID NO:5291  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06314  
SEQUENCE DESCRIPTION:  
GATCTGAAGG CCGTTCCAAG CGAGGGTGCT TCTGAGGACA CTGAGAAGAG TTTTGCCATT 60  
CTGAAGAGGC GAGCCTGTGG AACTNTTTAA GGTCTGTTC CCAGAAGAAT AAAAGTTTCT 120  
CATTATGGCA AA 132

SEQ ID NO:5292  
SEQUENCE LENGTH:102  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS06315

SEQUENCE DESCRIPTION:

5 GATCACTCTC CCGACATCC ACCTGTATGA CTTTGTACC AAATGCTGTC TTCTCTTTCT 60  
 CCAATCAAGA AATAATAATC CCTCGAGTTT ACAAACACA AA 102

SEQ ID NO:5293

SEQUENCE LENGTH:196

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06316

SEQUENCE DESCRIPTION:

15 GATCTCANCT TCATGCCAGG CCTTGGGTTT GACAAACATG GCAACCGACT GGGGAGGGGC 60  
 AAGGNCTACT ATNATGCCTA TCTGAAGCNC TGTTTGAGC ATCAGGAAGT GAAGCCCTAC 120  
 ACCCTGGCGT TGGCTTTCAA AGANCAGNTT TNCCTCCAGG TCCCAGTGAA TGAACACGAC 180  
 ATTGAAGNTA GATGNN 196

20 SEQ ID NO:5294

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06317

SEQUENCE DESCRIPTION:

25 GATCAAGAAG TTTGTGTACA CATAATCTCA TTTNAGATA TATAACTATT TTTNTCTTTC 60  
 AGAAGTGAAT CAAAATATTT CAAAATGCTG TCTTATGAAA CTACAATATT CTCACAGATT 120  
 AGAAAAGTTT TNCTGTAAAA GTCAGATAGT AAATATTNA GGTTTTGCAG TGTCTNTTGC 180  
 30 ANCTNCTCAA CTTTCCTACT GTNGCACANG NGTAGCTGTG GTACTGTGCA AATNAAN 237

SEQ ID NO:5295

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06318

SEQUENCE DESCRIPTION:

40 GATCACTACC TTTTCTCTC TNATCTGCTG CCAATNTGAGA TGTGGCTTTC ACCTTCCGCC 60  
 ATGATTGTAA GGCCTTCCCA GCCCGTGGN CCGTAAAGTC CANTAAACCT CTTTGTAAA 120  
 TAAA 125

SEQ ID NO:5296

SEQUENCE LENGTH:198

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06319

SEQUENCE DESCRIPTION:

50 GATCTTACAG ACTGTATCAG TCTAATTTTT AAATTTTAAG TTATTTTGTA CAGCTTTGTA 60  
 AATTCTTAAC ATTTTATAT TGCCATGTTT ATTTTGTGG GGTAATTTGG TTCATTAAAGT 120

55

ACATAGCTAA GGTAATGAAC ATCTTTTCA GTAATTGTAA AGTGATTAT TCAGANTAAA 180  
TTTTTGTGC TTATGAAA 198

5  
SEQ ID NO:5297  
SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10  
CLONE:HUMGS06320

SEQUENCE DESCRIPTION:  
GATCTAATTT CCCTNTTCAC ACAAACTTTA CACTTTAATC TGATGATTGG ATATTTAATT 60  
NNAGTGAACA TCATCTTGT AGCTAACTTT AAAAANTGGA TGTAAGATGA TTAANGGTTG 120  
GTATGATNN 129

15  
SEQ ID NO:5298  
SEQUENCE LENGTH:143  
SEQUENCE TYPE:nucleic acid  
20  
TOPOLOGY:linear  
CLONE:HUMGS06321

SEQUENCE DESCRIPTION:  
GATCTGTGCC ACTGTGTCA GAGAAGAAGA AACACGTAGN GCAAGTTGTA AAATAATTGG 60  
TATTCCTAAC AATCCTGATG TATAATTNTT TGTTACTTTT GNTTGTAGAA CTCTACANAT 120  
25  
AAAAGTGTG GACTAGATT AAA 143

30  
SEQ ID NO:5299  
SEQUENCE LENGTH:334  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06322

35  
SEQUENCE DESCRIPTION:  
GATCTCTTCG ACTCCTACGA CCTTGGGGAC CTGTTGATTA ATTGAGTGGC CCTGCCTGCC 60  
CCCAGCAGCC TGCCCCGAC TCTACCTCCT CACAGACAGG CTGACAGCCC CTCTGCCTGC 120  
ACAGGGACAT TGGACACTAG GTGCTGCCCT CAGGGCATGG GGTCTCCTCG CCTTTCCTGC 180  
CCCAGCCGGC AGAAGCTGTG TGGGGNGNNA TGAATGGTAC GGGTGAGGAG TGGATAAGGG 240  
GTGGTCCTCA CCTTNCTAAT GGAAGCTGGG CCTAGGGAGG CCCATNCAGT CTTCTGACTT 300  
40  
CTNGACCTCT NACAAGAAGG NTGCAGGTGA GGTN 334

45  
SEQ ID NO:5300  
SEQUENCE LENGTH:337  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06323

50  
SEQUENCE DESCRIPTION:  
GATCTGGAGC CAGCTGGCTT TGCTCCGTTT CCTGGCTAGT CTGTGCCTGG TCACCAGGGA 60  
GGCTGAGTGA GGGGCTGTGA ACAGTTGCCG GAAGCACCCC CTCCCTCCCC GGCCCGTGCA 120  
GCAGTGCTG AGCTGTAGTG AAAGTTTCAG GGCCTGCAAA AGAAGAGGCT TGGGCACAGG 180

ACTGACCATN GCTCCAGGGG TTTAGGACCC CCAGGNCNGT GAAGGTGGGA GCAGCTCACC 240  
ACCTTTNACG CAGGCTTTGG TATGTTCTCT NAGGCTTAGT TGATTTTGGG CCCNAAANCA 300  
AATNCAAAAG GTTCTGGGC CAACCTTTTG TTAANTN 337

5  
SEQ ID NO:5301  
SEQUENCE LENGTH:326  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10  
CLONE:HUMGS06324

## SEQUENCE DESCRIPTION:

15  
GATCACAGCT CCAGGACCAG TGCAGGCTGG CTGCCCTCTT TTGSCCGCGT CTGGAATAAT 60  
GGACGCCGCT GGCAGTCCAG ACATCAATTC AAAACTGAAG CTGCAGCAAT GAAGAAGCAG 120  
TCACATACAG AAAAAAGCTA ATCATGCTCT CTACCAACTA CCATGAGGCT AGNAAGCAAA 180  
GTCAACAAAC CCCTATTATA CCTTCCACCA AATTCTTTAT CATTGTCTTT CTTAGGAAAC 240  
AGNCATACTC ATTCATTGA TTTANTAAGG TTTTATTTT CCAANGTNTG NTGTGGNTGN 300  
TTNGGNNNNN TTGTGGTGGT TGNGNN 326

20  
SEQ ID NO:5302  
SEQUENCE LENGTH:174  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25  
CLONE:HUMGS06325

## SEQUENCE DESCRIPTION:

30  
GATCTTTNAT TTACCTGTAC AGGAGTGTAA ACTTTTTNGT GNTTTTATTT TTCAATTGTG 60  
AGAACCACTG ATTGGTATGT TCAACAAATT TGTGTATACA AAGAAATGGA TAAATCACTG 120  
CTATATANGG GAAACTACCT TAGGAAAGAN TGTTTACTGA ATGTTTATNN NATN 174

35  
SEQ ID NO:5303  
SEQUENCE LENGTH:104  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06326

## SEQUENCE DESCRIPTION:

40  
GATCAGTGAT ATTTGATGTT AGTGTGTGAC TATAGGGTGC CAATAACTCT GCCTATACAA 60  
GATGGTGTAC TTAATCAATA AACGTGTATT CTGACTGCCT TAAA 104

45  
SEQ ID NO:5304  
SEQUENCE LENGTH:238  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06327

## SEQUENCE DESCRIPTION:

50  
GATCCTTCCG TCTCAGCTCC CCAACCCAG TAGCTGGGAC TACAGTTGCA CATCATCATG 60  
CCTGGCTAAT TTTTNNATTT TTGTAGAGGT AGGTTTCACT ATGTTGCCCT GGCTGGTCTT 120  
GAACTCCTGG GCTCAAGTGA TTCACCTGCC TCGGNCTCTC AAAGNGCTGG TGTTTACNGG 180

CATGAGCCAC TGTGTCCGAC CCANACCTAC TANTGTTAAT NGANNTTTTN TTAACNN 238

SEQ ID NO:5305

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06329

SEQUENCE DESCRIPTION:

GATCAACAGA GTGAGACCCC TGTCTATATA TTNNTTAAAT TAAAAAATA AAAGANTAAA 60  
ATTGTGTAGC TCAGTATAGT ATCAAGATTA ATCTGCCTAC TCACATTTCT ACACTTTATA 120  
NNANTGTAAAT AN 132

SEQ ID NO:5306

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06330

SEQUENCE DESCRIPTION:

GATCCAGCCA TNACTAACCT ATNCCNNTT TGGGGAAATC TGAGCCTAGC TCAGAAAAAC 60  
ATAAAGCACC TTGAAAAAGA CTTGGCAGCT TCCNGATAAA GCGTGCTGTG CTGTGCAGTA 120  
GGANCACATC CTATTTATTG TGATGTTGTG GTTTTATTAT CTTAAACTCT GNTCCATACA 180  
CTTGATATAA TACATGGATA TTTTATGTA CAGAGGTATG TCTCTTAACC AGTTCACCTA 240  
TTGTNCTCTG GCAATTTAAA NGANNGTCAG TAAATTNTT TNCTTGTAAG AGN 293

SEQ ID NO:5307

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06331

SEQUENCE DESCRIPTION:

GATCAAAACC CAGCAGAGTG CAAGCAGCAG TGAAGCAGGA TGTATGTGGC CTTGAGGATA 60  
ACCTNCACTG TAATAGCCTA AACACANCTC TAATTTACTT ACAGCCTTAT GTTTTTGTAT 120  
TGNCTTGGTA GACTAGGTAA TTTTTTTTA AAGGNCAGGN GACGGNTATT TTAAAGNCCA 180  
ATTTGTTCTA CGTAGCATNT TAACTAGTTT TNNTGCCAGC NATGTTGN 228

SEQ ID NO:5308

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06332

SEQUENCE DESCRIPTION:

GATCCCTGAA GTTGCCCTGG TCTCTGCACC TTCTAAACCT AGTTCTTAAG AGCTTTCCAT 60  
TACATGAGCT GTCTCAAAGC CCTCCAATAA ATTCTCAGTG TAAGCTTCTG AAA 113

SEQ ID NO:5309

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06333

SEQUENCE DESCRIPTION:

GATCTGTCAC TGTCTCCCGT CACCCNCAGA TGGGGCTGTC TAGTTGCAGG AAAACAAGCT 60  
CAGGGCTCCC ACTGAGTCTC TGTGATNGTG AGTTGTAGAA TTATTAAANN ATATGTTACA 120  
ATGTAATANT AGTAGAANTA AAGTGCACAN TAAN 154

SEQ ID NO:5310

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06334

SEQUENCE DESCRIPTION:

GATCTCTTTC CCTGTCTTGG AGGTGAAAAG TNATATCTAA GGNTNTGTTT GCAGTGACCC 60  
CTAGTTTGGG GTACACAGAC CAGTGTTCCT NATTGACAGT GTTCAATAAG GCCCGTCAT 120  
TCTGCCAGT NTNTTGTGT NCTTAATGGG CTCCTCCTTG AANTGTGTGT GTGTTTGTGT 180  
CAAGAGGAGT TNGTGTCTT GGTAAATAAA GNTN 214

SEQ ID NO:5311

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06335

SEQUENCE DESCRIPTION:

GATCTCTNCG ANTNAATTC AATCTAGGGA AAAATGGCAG AGAAGTAAAT GGATGTNCTG 60  
GTGTCAATAG ATATGAAAGT GTTGGTTGGC GACTTGCAA TCAACAAAGT TAAAAAATC 120  
GAATNNN 127

SEQ ID NO:5312

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06337

SEQUENCE DESCRIPTION:

GATCGAGAAT NACNATNTTT TGTAATGGA AATACCACTA CTAAAGACAG AATGCTATAA 60  
ATAGAAA 67

SEQ ID NO:5313

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06338

SEQUENCE DESCRIPTION:



GATCTTCTGT ACTTCTGTCT TCCATAGGAC AAATNATAAG TACTACATAC CTCATCTCTT 60  
GGGTTATNAT TGTA GTCTTG CATTTCATGAT TATNAATTA AAAATAAATA CCAATTATGG 120  
AAATTGTAAA 130

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SEQ ID NO:5314  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS06339  
SEQUENCE DESCRIPTION:  
GATCTACATN AGGAAAAGTA TAAGCCCCCT CCCTAATGGC CGCTGGGNGG TGAGGGCGGT 60  
GTGTTGTATG TCTTGGGTG TTTGTTNNTT NATAAAGCAT ATAATN 106

15

SEQ ID NO:5315  
SEQUENCE LENGTH:195  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS06341  
SEQUENCE DESCRIPTION:  
GATCTNAAAA AGAGAGAAGA AAATAAAAAG TATTATTTAT ATGTCAGTGC CAACTTTGAA 60  
GGTAAACAG TAGTAGTAAC TTTTGGGAGA AATTCTAAAA ACTACTTTAA AAAGAAGCGT 120  
GCACATAAAA TAANTATCTT TCTATCCAAG GCTTGTCAAT TNATATGCTT TNNTTGTA 180  
TTTAANATNN NGCTN 195

25

SEQ ID NO:5316  
SEQUENCE LENGTH:136  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS06343  
SEQUENCE DESCRIPTION:  
GATCTAATTA CTTATAGATT CTGTAGTCTN GNGAAGGNGT GGGTGACGTG ATGAGAGGTT 60  
TGAGAAATGG GTGAAATGAA ATGGGGGGAT ATGTAGGTCA AATCANATNA AAGATGATTT 120  
TTTTNATGTG AATAAN 136

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SEQ ID NO:5317  
SEQUENCE LENGTH:180  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS06344  
SEQUENCE DESCRIPTION:  
GATCAGCTTA AGGNTTTAGC GCTGGTGGAT AGACACTCGA GACCAGAAAT CATATTTTNN 60  
CTGAAAGTAG ATGATTTACC TGAGGATAAT CAGGAACGTT TTAATAGCCT TTNCTCTCTA 120  
AGGGGAGAAGT GGACAGAAGA AGATATTGCT CCATATATTC AAGATTTGTG TGGAGAGAGN 180

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SEQ ID NO:5318

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SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06345

SEQUENCE DESCRIPTION:

GATCGCGGTA TATAGAGATA TGCATTTTAT TTTACTTGTG TAAAAATATC GGACGACGTG 60  
GAATAAAGAG CTCTTTTCTT AAA 83

SEQ ID NO:5319

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06346

SEQUENCE DESCRIPTION:

GATCTCCTTA GGTGATGCAC AGTCCAATA CCTGCTAACC ACCGCCGAGA ACGAGCTGGG 60  
AGTGGTGGTA GCCACAGTG AGTCAGGTAT CCAGATGGTT CCCATCAGCT GGTGTGAGAT 120  
GCAGTGCCTT AAGACCCACA CTAAAGAATT CCGGAAAGTA GCCCGNGTAC AACCCGAATN 180

SEQ ID NO:5320

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06347

SEQUENCE DESCRIPTION:

GATCAGAGAA TCACAAGAGC AGCAAATGTG GTTTCATCAA GTGGGAAGAA AGCAGCAATT 60  
TAAAATANCT TTTTGGGNGA CTGANTTGAG TAATAATAAA NCTTCAGTCT TTCGCTAATN 120  
ATANTN 126

SEQ ID NO:5321

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06348

SEQUENCE DESCRIPTION:

GATCTAGACG CCCCCAAATC CTTGAGATGT GGGTATAGCT CAGGGTAAGC TGCTCTGAGG 60  
TAAAGGTCCA TGAACCTGC CCCACTCCTG TCAGCCCCTC ATCAGCCTTT TCAGCAGGTT 120  
CCAGTGCCTG ACTTGGGATA GGAAGTGTG GTAGGAGGAG GGGGAGTGGG GGGGCATAGC 180  
CTTCCCTAA TTCTGCCTTA AATAAACTG CATTGCTGAT TCAAA 225

SEQ ID NO:5322

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06350

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCAGCAAA TTGTTATNTT AAAAAGTTTT CTTGTTTAGG CAATTTGGTA AGTGGTTTCT 60  
AGTTATAAAC TAGCCACTGT TGATTAACCT GAGAAGGTGA AGCAGGGGAG TTCTGAAGAG 120  
ATTACCTAGA GCTACTTAAC CCTAAGTTAA GTAAAATTTT CACTTTCATT CTTTTCATT 180  
TCTCATAAAC TGGTTGAAAA AACACTGTAC TACCAACAAA GGTGTCAGTT GCTTGTGCTG 240  
CCCTGTCTAT GTTATGCTCT GAATAGGTCT CGGTAAAGAT TATATGGAAA TACTATAAAG 300  
NNTACATAAG GTAAAATACT AGTCAGANAG GGTTCAGGTT N 341

10 SEQ ID NO:5323  
SEQUENCE LENGTH:157  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06351  
15 SEQUENCE DESCRIPTION:  
GATCTGAAGT NCTTCCATTA TATCTATATC TGTATATGNA CATATATGTG GGTGTGTATA 60  
TATATGNGTG TATGTATATA TATACAATTN CCGGAGAACT CACTNTTTTT TGTGAATTN 120  
CAATAGTGTT CGCCATGTTT TCCACCAGNA TGTATAN 157

20 SEQ ID NO:5324  
SEQUENCE LENGTH:94  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06353  
25 SEQUENCE DESCRIPTION:  
GATCAAGTTT TGATGAAGAT GTGAAAAACN GTTGGGCAGT ACTACTCAAG CTGAACCCCA 60  
TGCATCAGAG AAATTACACT TTTATATNTC CAAA 94

30 SEQ ID NO:5325  
SEQUENCE LENGTH:128  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06354  
35 SEQUENCE DESCRIPTION:  
GATCTGCCCT NCTCAGCCTC CCAAAGTGCT GGGATTAGAG GCGTGAGCAC CATGCCTGGC 60  
CAGGTCTTNC TAACTAAAAA ATAATAATAA TAATAATAAA AAANAAAAGA NGATACTTGC 120  
AAAAATAAA 128

40 SEQ ID NO:5326  
SEQUENCE LENGTH:117  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06355  
45 SEQUENCE DESCRIPTION:  
GATCAAGAGT ATTTNCTNTA GCTAGCTTAA AAAGAAAACA TATATTTAAT GTAAAANCAC 60  
ATACATGGCC AAATGCAATA CTGANGAGAC AATCATCCTG TATCTTTNAT GGTTTTN 117

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SEQ ID NO:5327

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06356

SEQUENCE DESCRIPTION:

GATCAATGCG CTAGTGCAGG AGCTCGGCTT CTACCGCAAG GCGGCGCCCG ACGCGCAGGT 60  
GCCCCCGAG TACGTGTGGG CGCCCGNAAA GCCCCAGAGG AAATTCGGA CCACGCTGAC 120  
CTNTAGGTCC GGGGGCGCGG CGGANCTGGG ACCTACCTGC CTGAGTCCTG GAGACAGAAT 180  
GAAGCGNTCA GCATCCCGGG AATACTTCTC TTGCTGAGAG CCGATGCCCC TCCCCGTGGC 240  
CAGCAGGGAT GGGGTTGGGG AGGTTCTTCC AACCNGACTT TTTTCCTTC CNCAAGNTCC 300  
ACTAAAATTT CCCTTCTGCN TTAATAAAAA AANN 334

SEQ ID NO:5328

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06357

SEQUENCE DESCRIPTION:

GATCAGCCAA ATTGGGCGGC CACCCCGNC TCCACCACTT TCCACCATCA GCTGCCAAAC 60  
TGGTCCCTCT GTCTCCCTGG GGCCTTGGGT TCTGTTTGGG GGTGATGACC TTCCTAGTTT 120  
CCTGACGCAG GGGNATACAG GGGAGAGGGT TGTCTTCCC CCCAGCAAAT GCAATAATGC 180  
CCTCACCCCT CCTGAGAGGA GCCCCCTCCC TGTGGAGCCT GTNACCTTCG NATTTGACAC 240  
GAGTCTGCTG TGAACNCGC ANTCTGCTC NCACCTNCNA TCTNTCTNC CAGGGCCATN 300  
CCTGGGCCAG AGCAGGAGGG GAGGGAGGTN 330

SEQ ID NO:5329

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06358

SEQUENCE DESCRIPTION:

GATCAAAAAT NTGTGGGTTT ATTTCTGGAG TCTCTGTTCT ATTGGTCTAT ATGTCCGTCT 60  
TCATGCTGGT ACTATGCTGT TTTATTTACT GTAGCTTTGT AATATATTN GAAATCAGAA 120  
GGTGGGATGC CTTAGCTTT GTNCTTTT TNCTCAAAATAA AAAATNCTTT TGAAA 175

SEQ ID NO:5330

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06359

SEQUENCE DESCRIPTION:

GATCAATCA GAGTAATTTG GATATTCATC ACCTCGAATA TTTATCTTC CTTTGTGTTG 60  
GGAACATTAT AATTTCTC TGCTAGCTAT TTTAGAATAT ATAATAAATN ATNGTCCCCT 120  
AAA 123

SEQ ID NO:5331

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06360

SEQUENCE DESCRIPTION:

GATCAAAGCC AGCCACCCCC ACCCCAACAC ACTCGGTGTC CCTTTCATCC TGGGCCTNTG 60  
TGAATCCCAG CCTNGGCCAT ANCCTCAACC TCAGTGGGCT GGAAATAACA GTGGGGNCCC 120  
TGTAGCAGTG GCAGAATAAA CTTAGATGTT NTNACAGGAA A 161

SEQ ID NO:5332

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06361

SEQUENCE DESCRIPTION:

GATCNTCTCA GNGANGNCGC TTNGGTCGCA GTTTTAGGGG GTTCTCGGT TGCAGGAACC 60  
CTGGGTGCAG GTTCGCAGCC CTGTCAACCA GCTCCGAGCC GGCAGCGAAA CCTGAAGTGG 120  
ACCCTGTGGA AAATNAAGN 139

SEQ ID NO:5333

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06362

SEQUENCE DESCRIPTION:

GATCTNCTCA CCCTCGGTGA NAACAGTGTC AGCCATGCAA GCAGGACAGA ATGGTGACTG 60  
GGTGCCCTTG GTGAGCTGTG TATTTCTAG NAGGTAGAAA ACTGTGGGAA ACTGTGGCTA 120  
ATAAAAACTA AGTGTGAGCG TCAAA 145

SEQ ID NO:5334

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06363

SEQUENCE DESCRIPTION:

GATCTTAAAT NACCTATTTT TAATGTGATT CATAACGTT TTNACTTAG TGGTTTAAAA 60  
TATGAAAGTA TATAAACACA TTACCAACA CTTTGGGGTA GGAGAAGTAC GCTTAGCATG 120  
TCTGTGTCAT ACCTAATTTT TTAAAGCTA TAATGAACTG ATACACATCA ATTTANNNGC 180  
NGGTTTTATT CTTCAATGA ACACTGTATC AAAATTTTTT NATGANGTAA TGTTAGTCTT 240  
TGTGGTCAAT AGTTATTGGT AATACTACTA GTAATATGGG TNCATGGCTA TAAGATGCTT 300  
TAGCTTAGTG GTCAGTTGTT ATNCTAAGGG GTTTNAATCN AATTNGGTNG N 351

SEQ ID NO:5335

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06364

SEQUENCE DESCRIPTION:

GATCACAAGT AGAGAACTTG TTTCTTTTCA CCCCTCTTGC TCCTCCCCGG AGTTATGAAA 60  
AATTTCAAAC CTGCCAAAAG TTTGAAGTTT ACAACAAATA CCCTCCAACG TTTGGNTTGC 120  
CTCCCTCCCC CTTCTCTCCC TTNCTCCCTC TGATTTCTTA CAGAACCACG CTTTCATGAC 180  
CATGCCCGGG AACTTCACGC TGGCGCGGTG AGGTCCTGCG CCTCCGNTTN CNGCACACAC 240  
GTGCTTCTNA ATAGCTGCAG GCTATTTTCA GAGAGGAATT TGCTCACGTT AACATNGCTG 300  
TTCCCAAATG CCAGGCTGNT TTTAAGTGGT TTCCTAATTT ATAAAGGN 348

SEQ ID NO:5336

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06365

SEQUENCE DESCRIPTION:

GATCTCAATA GTCAGTTACT GATGCTCCTG AACCCTATGT GTCCATTTNT GCACACACGT 60  
ATACCTCGGC ATGGCCGCGT CACTGCTCTG ATTATGTGCC CTGGCCAGGG ACCAGCGCCC 120  
TTGCACANGG GCATGGTTGA NTCTGAAACC CTCCTTCTGT GGCAACTNGT ACTGAAAATC 180  
TGGTGCTCAN TAAAGANGCC CATGGCTGGT GGCATGCAAA 220

SEQ ID NO:5337

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06366

SEQUENCE DESCRIPTION:

GATCCCAGCC ATAAAGTACC TGGGATGAAA GAAGTTTTTT CCAGTTTGTC AGTGTCTGTN 60  
AGAATTACTT ATTTCTTTNC TATATTCTCA TAGCACGTGT NTGATTGGTT CATGCATGTA 120  
GGTCTCTTAA CAATGATGGT GGGCCTCTGG AGTCCAGGGG CTGGCCGGTT GTTCTATGCA 180  
GAGAAAGCAG TCAATAAATN TTTGCCAGAC TGGGTGCAGA ATTTAAA 227

SEQ ID NO:5338

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06367

SEQUENCE DESCRIPTION:

GATCTTNACT CTTGTTTCCT TTGTCCTTTT NTTCAGACAG AGTTGTACCT GCAGCAGACA 60  
ACTCTGAATT AAAGCATGAA AACACAGCAA A 91

SEQ ID NO:5339

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06369

SEQUENCE DESCRIPTION:

GATCTCTCCC CACACAGAGG CCAGCAGACC TCTTCCTGAG GACTTCTGTT TAAAGGAGGA 60  
 CGAGGAGGAG GTTGGTGACA GTCAGGCCTG GGAGGAGCCC ACAAAGTGA GCACAGAGAC 120  
 ATGGAACCTA GCTACTTCCT GGNAGGTGGG GCGGGNACTA CGGAGAAGGT GCAGCCAGGC 180  
 TGTGGCAAAG GGCCCCANTC ACAGCCTTGG CTGGGAAGGN GGGNNGACA GCTGANGGTC 240  
 GACTAAACA AAGTCTGTTT TCATGNAAA 269

SEQ ID NO:5340

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06370

SEQUENCE DESCRIPTION:

GATCTCTTGT NATGGGGCCA ATAAGTCAAT TGAATTCATG GGCCAAACAG TTCCCATTTCT 60  
 CTTCAAA 67

SEQ ID NO:5341

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06371

SEQUENCE DESCRIPTION:

GATCCTNATN ACGNAGCTGA TGCCTGCCTT GGTNCCTACC ACTCTGGTGT AGACAGAGGA 60  
 CTTTNTCCAA GTGTCACACT AAACATGCCC GGGCTTCGAT GTGCCTGGAG GATTCCCCA 120  
 CAGGGACCCA CGCACCTCCC TGTATCTGCG CAGTTGCTCG TGTGGCTGGA AGCGCTGTCTG 180  
 ATAAGCTTCN NGGCGCTGNN TTGCCAGTTC TTCAGCTCTA GGACTTGTAG CTTTAAGCAA 240  
 ACGGTGTGGC ATGGGNTTGA NGTNTGGCCA CCTGGCAGNG NTGTGCAGGG TCTTGCCTTA 300  
 NNAAGCTGG CTN 313

SEQ ID NO:5342

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06372

SEQUENCE DESCRIPTION:

GATCAAAAAA TATATGAAAG TTCCTTGTAG ATACATATCT ATAGATATAT ATGTNTATGT 60  
 ATATAAAGAT AGATATATAC ATTGAAA 87

SEQ ID NO:5343

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06373

SEQUENCE DESCRIPTION:

5 GATCTTTTTA TATTCTTCTA CCACACCTGG AAACAGACCA ATAGACATNT TGGGGTTTTG 60  
 TAATGGGAAT NTNTATAAAG CATTACTCTT TTTNAATAAA TTGTTTTTNA ATTTAAAAAA 120  
 AGAAA 125

SEQ ID NO:5344

10 SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06374

15 SEQUENCE DESCRIPTION:

GATCAGGTGG AAATGTTTAA GCTAAATAAA TCTAGGGGTT NTTTNAACAA A 51

SEQ ID NO:5345

20 SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06376

SEQUENCE DESCRIPTION:

25 GATCTGAAGA AACAACGCAG TGTNCACGCA AGCCACTCAG ACAAGCCCAG GGGTTCCTTG 60  
 GCCTTCTCAG TCAGCTAACT TTCCTGAGTT CTCCTTTGAC TTCACTAGGG AACAGTTGAA 120  
 CAAGAGATTT TTCAATCAAG NCTTTGGAAC TACGAAGATG GAAGAGATTT GAAGAGGGAT 180  
 ATNGAATGAG TAAATTAAGC AACTTTTTAN TATCCTATTT CTNTAAATNT CCAGATTTTA 240  
 AAACATTCCT GTATTATANT ATCTAAAAAC AAA 273

30

SEQ ID NO:5346

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS06377

SEQUENCE DESCRIPTION:

GATCTAGATA TTTTCTCTT TTTCTGAAGN TACTTTCTTA AAAAATAAAT AAAATGTTTA 60  
 TAGCATTCTT NGTAAA 76

40

SEQ ID NO:5347

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS06378

SEQUENCE DESCRIPTION:

50 GATCAATTCT CCTTTGCGAG GNGACCACCA ANGGACTGCA GAGCTGNCCG GGCATTTCGTG 60  
 CGTGTTTCATG ACCGAGAACT TTNCACACAG AGAGGACTTC TGTCTGACG AAGGAGCGCA 120  
 GAGCTGGCCG NGCATTTCGTG CGTGTTTCATG ACCGNGAACT TTTCACAGCT AGGACTNCTG 180  
 TCCTGACGTC TTTATNGGTA TAATAGTTGC GTTTAAGNCT GCAGACTTCA AGTTTATATT 240

55



TCTCTTTATT GTAACACTCT GTGCANNNTT TGATTNCTAG TTTATTTNCA TTGTN 295

SEQ ID NO:5348

SEQUENCE LENGTH:416

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06379

SEQUENCE DESCRIPTION:

GATCGACCTG AGCACAGTGG ACCTGAAGAA GCTCCGAGTT AAAGAGCTGA AGAAGATTCT 60  
 GGATGACTNN NNGGAGACAT GCAAAGGCTG TGCAGAAAAG TCTGACTACA TCCGGAAGAT 120  
 AAATNAACTG ATNCCTAAAT ATGNCCCCAA GGCAGCCAGT GCACGGACCG ATTTGTAGTC 180  
 TGCTCAATCT CTGTTGCACC TGAGGGGGTA AAAACAGTTC AACTGCTTAC TCCCAAANCA 240  
 GCCTNTTTGT AATTTATTTT TTAAGNGGGC TCCTGACAAT ACTGTATCAG ATGTGAAGCC 300  
 TGGAGCTTTC CTGGATGATG CTGGNCCTGC AGTACCCCCA TGAGGGGATT NCCNTTCCTT 360  
 CTGTTTGCTG GTGTACTNCT GGGGGNGNGA AGTGTGTCTG GGGNNTTTTT TNNTGN 416

SEQ ID NO:5349

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06380

SEQUENCE DESCRIPTION:

GATCTGAAGA AGTGGTTAAG ACCAAGAGTT TATGTACCTT TTAAACAAA GATTAATAAA 60  
 TTTTGAAGA AGTGATGAGA CAAAGAAA 88

SEQ ID NO:5350

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06381

SEQUENCE DESCRIPTION:

GATCAGAACA TGAACTTTTT TTTTAAAAGA AGATTTGAGC ATTTTCCTGT AATCACATCA 60  
 AAATNATGTT TTCTGTGTAA AGCGAGATAC ATATTNCTNA TAATGCAGCA TTGTGAGAAG 120  
 TCAGTTCGGC CCACTGCACC ANCACTGTCG TATCCTTGTT AAAATGGTGT GTACCTTACA 180  
 ANTTATAATT TATGTGCCAG GTTCGTTTTG TNCTTAATTT GCTATTATTG TGCTGTGTNT 240  
 ANCCCTGTN NNCTNGGTN 259

SEQ ID NO:5351

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06382

SEQUENCE DESCRIPTION:

GATCTTATAA AGTACTTGTG TGGAGCTTTG ATTCCACAGA ATAAAAGATA TTTTGTGTGT 60  
 AGAAA 65

SEQ ID NO:5352

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06383

SEQUENCE DESCRIPTION:

GATCTCAGCC CAGGACAAGG TGGGAATNAG TCAAGCCTGG ACTCTGGCCC CCCTGCCTGG 60  
CCAGTAAGAA GGGCAAAGTC CAAGGGGAGG GATGAGGNAG GGGCCAGATG GGGTCCTGGA 120  
GGAAGAATTN CCTGGCAAAA GCCATTGGAG CTTGTNTGTG TGTCTTTGGT GATGACATNT 180  
GTTGTGAGGG TAGATGGGAA CCATNTTAAA AGGATGAAAT GTGAAA 226

SEQ ID NO:5353

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06384

SEQUENCE DESCRIPTION:

GATCCTTTTG TAAGNCCTT CCTGAAGAAG AAAGGTGGCA AATACAGTNT TCAGTTCAAG 60  
TTGCCCAGC TGTATGGTGT ATTCCAGTTT AAAGTGGATT ACAACCGGCT AGGCTACACA 120  
CACCTGTACT CTTCCACTCA GGTATCCGTG CGGCCACTCC AGCACACGCA GTATGAGCGC 180  
TTTATCCCCT CGGNCTACCC CTACTACGGC AGCGGCTTTC TNCATGATGC TGGGGGCTCT 240  
TTTATCTNTC AGCATCGGGC NGGCTTTGCA CATGNAGGGN GAATGNTGGA NGTCCGANTT 300  
TTNGN 305

SEQ ID NO:5354

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06385

SEQUENCE DESCRIPTION:

GATCTACATT CTTCAAAAAA AAAAATTGGC TTAAGTGTTC CATCTTNAAG TAGCATTITG 60  
CTGCCATTG TATTGGGCTG AAGAANTCAC TATTGTGTAT ATACTCAAAGT CTTTNAATT 120  
TCCCNCTTTT CATAAATNCT CTTGGNCATN ATTGGGCTTG CAGAGTTCCC TTATNCTGGG 180  
GATTACAATG CTTTATCGT TTCAGGCTTC ATTTNNGCTT CAAANCAAGC TGGGCACACT 240  
GTAAANCAAT GATTTTGCAG ANCCTTTGGT TTTGGACAGT TTCATTTTTT NGGATTTGGG 300  
ATAGATTNCA TAGGAGTATG GAGTATGCTG TAAATAAAAA TNCANGCTAG TGCTTN 356

SEQ ID NO:5355

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06386

SEQUENCE DESCRIPTION:

GATCTTTAAC AGTCCTTTA CTTGCNCTTT GTAAAAAAA ATAAAAATTAG NTTGAATTAT 60

TCTACCTTTG TAAA

74

5

SEQ ID NO:5356

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06387

10

SEQUENCE DESCRIPTION:

GATCCTGCTG GCCGAGCTCG AGCAGCTCAA GGGCCAAGGC AAGTCGCGCC TGGAGCAGCA 60

GAATAAGNTC CTTAACTTAA AATAAATTAA TTTTTCAAA AAACATAAAT CTGGAAGTGT 120

TGTTTCTATA TTNATAACA AATACAGTAT ATNTNATNTA TAAGCCATGG TCTACTGATA 180

15

CTGTATGAGG ACTTNCCTGA N 201

SEQ ID NO:5357

SEQUENCE LENGTH:409

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06388

20

SEQUENCE DESCRIPTION:

GATCAGAACG TTAACATATG AACCTGCAGA AATCTGGTAA GACTTAAATT CAGTGTGAGG 60

25

AATAACTCTA GTTCTCTCCT ATGAGCATT CTTAAAAGCC ATCTGATTG GCATTCTTAC 120

TGGAGCTGCA GACAGAAATC TACAAAGNCN NAAGTAAACA AAATTAAGTT ATTATTCCAC 180

TGTTAGGAAT GGAAATAAAC TTGTGAAGTC TGTTTATTTT GAAGTATTGG TGAAGTAGGC 240

TTGCTAATNG GGAGCTGCAG CAGTTTGTGT TTAATCCAGT TCATCAGCTT AGGTCATTTG 300

AAAGNTATAA GAGCTTAAGG CAAGAAAGGA ATACCATGGG ATTCTATTN AGGGCCACCA 360

30

GNCCATTCTT GGNAAGCAGC TCCNGTTTGG TTTTCCAGCT GTCAAACTN 409

SEQ ID NO:5358

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06389

35

SEQUENCE DESCRIPTION:

GATCTGCCCCG TNCGGCCTC CCAAAGTGCT GGGATTACCG GCATGAGTCA CTGCGCCTGG 60

40

CCGACAAAGG CTTTGATATC AGAATGAAGT GTCAAGGGAG GTGCTGGAGA GGGATTAACC 120

TGTGCAGAGN CCAANNNGTA TGGAANNAAG ANTGGGATTG GGAAGAGGTG NTCTN 175

SEQ ID NO:5359

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06390

45

SEQUENCE DESCRIPTION:

GATCAGGCTC AGGCGGCCCC ACTCACCCAC AGCATCCGCC GCCACCCCTT CGGGTGTGAG 60

50

CGCTCAATAA AAACAACACA CTATAAAGTG TTTTAAATC CAAA 104

55

SEQ ID NO:5360

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06392

SEQUENCE DESCRIPTION:

GATCTTTCCC AAGAGAAGGG GAAGCACTCG TGTGCAACAG ACAAGTGACT GTATCTGTGT 60  
AGACTATTTG CTTATTTAAT AAAGACGATT TGTCAGTTAT TTAA 106

SEQ ID NO:5361

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06393

SEQUENCE DESCRIPTION:

GATCTACGCT GCCTTCAAGG AAGTGCTGGG TTCGGGCATG CACCACCACC TCCAGAACAA 60  
TGAGCTACTC CGTGACATCT TTGGCCTGGG CCTGTGCTG TTGCTGGATG CCACTGCCCT 120  
GAAGGCCTGC AAGGTTCCAC GCTTTGAGAA GCACCTGTAC AATGCTGCTG CCTTCAAAGC 180  
CCGGACCAAG GCTCGAAGCC GTGTGCGGGA CAAGCGGGCA GACATCCTGT GAAGCAGGAC 240  
CTGCTGAAGA GGAGACTTTC TATGCCCTTG GTCCGTATT TTAACAGAAG ACAGTGCAAC 300  
AACTGGTCTT CACCAGTATT TGTCACCTTA TTTT TTTTAA TGTCAAAACC AAAACAGAC 360  
ATGGGGTTGG GTAGCTGGGG GN 382

SEQ ID NO:5362

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06394

SEQUENCE DESCRIPTION:

GATCCNATCA TTCCTTAAAC ATANTACCCT TNGTCTTGGA GTAGAATACT AAGTTAGAGT 60  
TAGTGGATTT CTAGTTTAGG AGAGGAGCTC AAAACTATAA TCTNTAACAA ATTGAAAAAT 120  
GAAATAGGGT GTTTTCCCTT TTTGTGCACA CCTACATNAC CTTAAGAAAT NNCCTTCCAT 180  
AGACAGCTGC CTCAAAGGGA AATCCTCTTT AAACCGTAGT TGGCGCAGAG GTCAGTCCTA 240  
GTCGGAGCTT AGGAGGTGCG GNGACGCTCA CATCGTCTGG ACTTGAGTCG NCACTGGATT 300  
GTGGCANCAN NTTTNGCTCA TGNGTCAAAA ATTTNGGCAA TTTCTTTTGG ATTN 354

SEQ ID NO:5363

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06395

SEQUENCE DESCRIPTION:

GATCCAGGGC CTCCTCGCCT TCCTTCTTCC TTTTATATA CAATTGTGTA TTGTCAAATA 60  
AAAGTAGGAA ATATTCAA 79

SEQ ID NO:5364

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06396

SEQUENCE DESCRIPTION:

GATCTTTGTG GCCAAGGAGC TGCTATAGCC TGGGGTGGGG TCATGCCCTC CTCTCCCAT 60  
GTCCCTCTNC CCCATCCTCC AGCAGGGAAA ATGCAGCAGG GATGCCCTGG AGGTGGCTGA 120  
GCCCCTGTCT AGAGAGGGAG GCAAGCCCTG TTGACACAGG TCTTTCCTAA GGCTGCAAGG 180  
TTTAGGCTGG TGGCCAGGA CCATCATCCT ACTGTAATAA AGATGATTGT NAAATAAA 238

SEQ ID NO:5365

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06397

SEQUENCE DESCRIPTION:

GATCCTTGTC CGTGGCAACC TTAAACGTGT GCTGCAGTGC TGATGTATTT ATAGGCTTAG 60  
CATGTCTGCT TTATTAGTTA TCCTGGAAAG AATGCTATTC AGTTTTTTTT TTAATGTCTA 120  
CATCANGGAA TGAATGCTAA ATNAGCCCAT TTAGCAGCCT GAAATCAAAT NCTGCATTN 180  
TTTTTTNAAA CTCTTGCTAG CAAAAGAAAA AGCTGATTAA ANTATGATTG TGTTACAATG 240  
ACTAAAGGGT TANCTNCTCA TTAATTCTAA ATNCTTCAAA ATGNACAAGC ATCATAATAA 300  
AGGCTTTTGA TGNGAANTAA A 321

SEQ ID NO:5366

SEQUENCE LENGTH:409

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06398

SEQUENCE DESCRIPTION:

GATCTACAAG TCAGTGCCCT GTATGCTCTC CAGGTGCACT GCTATAACAG CAACTTCCCA 60  
AAAGGCATGT TACTTCGCTT TTTTGTGCAC TTCTATGACA TGGAAATTAT TGAAGAAGAA 120  
GCTTTCCTTG CTTGGAAAGA AGATATAACC CAAGAGTTTC CGGGAAAAGG CAAGGCTTTG 180  
TTCCAGGTGA ATCAGTGGGC TAACCTNGTT AGAAACTGCN GAAGAAGAAG AATCAGAGGA 240  
NGAAGCTGAC TAAAGAACCA GCCAAAGCCT TAAATTGTGC AAAACATACT GTTTGCTATG 300  
ATGTAACTGC ATTTGACCTA ACCACTNGCG NAAANTNATT CCGNTGTAAT GTNTTCACAA 360  
TATTNAAAAG CAGANGCACG TCAGTTTNGG NTTTCCTTCT GCANAAAGN 409

SEQ ID NO:5367

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06399

SEQUENCE DESCRIPTION:

GATCCTCAGT ATAGCCGGTG AACCCCTGATA CCAGGAGCCT GGGCCTCCCT GAACCCCTGG 60  
CTTCCAGCCA TCTNATCGCC AGCNTCCTCC TGGACCTNTT GGCCCCCAGC CCCTTCCNA 120  
CACAGCCCNA GAAGNGTCCC AGAGCTGACC NACTCCAGG ACCTAGGNCC AAGCCTN 178

SEQ ID NO:5368

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06400

SEQUENCE DESCRIPTION:

GATCATGTGA ATATATTAN TTGTATATNA AGCATGACTA CTTTAAGTNT TAAATAAACT 60  
GCAATAATCC TAAA 75

SEQ ID NO:5369

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06401

SEQUENCE DESCRIPTION:

GATCAGTGNC TGGCACCAGA CACTTCTGGG GATGGTACAG GGTGTGACAA CATGACCTGC 60  
ATCATCATTT GCTTCAAGCC CCGAAACACA GCAGAGCTCC AGCCAGAGAG TGGCAAGCGA 120  
AAACTAGAGG AGGTGCTCTC TACTGAGGGG GCTGAAGAAA ATGGCAACAG CGACAAGAAG 180  
AAGAAGGCCA AGCGAGACTA GCAGTCATCC AGACCCCTGC CCACCTAGAC TGTTTTCTGA 240  
GCCCTCCGGA CCTGAGACTG AGTTTTGGTC TTTTCCTTT AGCCTTAGCA GTGGGTATGA 300  
GGTGTGCAGG GGGAGCTGGG TGGCTTCACT CCGGCCATTC CAAAGAGGGG TCTN 354

SEQ ID NO:5370

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06402

SEQUENCE DESCRIPTION:

GATCACTGGA ATGTGGGGAT TCTGAAACAG AAATGAACT GTCCTTTTGA CAACTCTCTT 60  
ATATAATAAA GTATCACCGG CTTGTGTATG AAA 93

SEQ ID NO:5371

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06403

SEQUENCE DESCRIPTION:

GATCATGCAT TATCTTTATA ATTCAAAAGA ATTTATATAT ATGTAAAGGA GGAGAAAATA 60  
AAAAAATA TAATCTTAAA 80

SEQ ID NO:5372

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06404

SEQUENCE DESCRIPTION:

GATCATNTTG ATAATGCTCG GAATATTTTN AAATGTCCAT TCCGCTGTGT TGATTGAGGA 60  
 CGTTCCCTTC ACGGAGAAAG ATTTTAAGAA TGGCCCCCAG AACATATACA ACCTTTACGA 120  
 GCAAGTCAGC TACAACTGTT TCATCGCTGC AGGCCTTTAC CTCCTCCTCG GAGGCTTCTN 180  
 TTTCTGNCAA GTTCGGCTCA NTAAGNGCAA GGANTACATG GTGCGCTAGG GCCCCGGNGN 240  
 GTTCCCCCGN TCCAGCCNCT TCTCTATTTA ANGACTGCNN GCACCGTGTC AN 292

SEQ ID NO:5373

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06405

SEQUENCE DESCRIPTION:

GATCCTNCTG GCCGAGCTCG AGCAGCTCAA GGGCCAAGGC AAGTCGNGCC TGGGGGACCT 60  
 CTACGAGGAG NAGATGCGGG ACTGCGCCGG NAGGTGGACC AGCTAACCAA CGACAAAGCC 120  
 CGCNTCGAGG TGGAGCGCGA CAACCTGGCC GAGGACATCA TGCGNCTCCG GGAGAAATTN 180  
 CAGGNNGGAG ATTN 194

SEQ ID NO:5374

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06407

SEQUENCE DESCRIPTION:

GATCCTGGAT TCACTCACTC ACTCATTCCT TCACTCATCC AGCCACCTAA AAACATTAC 60  
 TGACCATGTA AA 72

SEQ ID NO:5375

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06408

SEQUENCE DESCRIPTION:

GATCACGCAC GAAGTGACG AACTGACCCA GATTATCGCC GACGTGTCCC AGGACCCAC 60  
 GTTGCCGCGG ACCGAGGACC ACCCGTGCCA AAAGTGCGGC CACAAGGAGG CTGTGTTCTT 120  
 CCAGTNACAC AGTGCGCGGG NCGANGACGN CATGCGCCTT TACTACGTGT GNACAGCCCC 180  
 ACANTGNNGC CACCGCTGGA CCGAGTGNCC TNCTNTGTN 219

SEQ ID NO:5376

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06409

SEQUENCE DESCRIPTION:

5 GATCCAACAA GAACATTTC AAAAGTATCT AGGTGTTCTC AAATAAAAAG CTTTCTTTGC 60  
ACAAA 65

SEQ ID NO:5377

SEQUENCE LENGTH:97

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06410

SEQUENCE DESCRIPTION:

15 GATCTGCTAA TGCTTTTCTAG GAGTCTGCCT GGAAACTTTG ACATGGTTCTN TGTTTTTACT 60  
CAAAATCCAA TAAACAAGG TAGTTTGGCT GTGCAA 97

SEQ ID NO:5378

SEQUENCE LENGTH:206

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06411

SEQUENCE DESCRIPTION:

25 GATCCCAGAG AGCANCTTCA GTGACAAACA TATCCTTTCA AGACAGAAAG AGACAGGAGA 60  
CATGAGTCTT TGCCGGAGGA AAAGCAGCTC AAGAACACAT GTGCANTCAC TGGTGTCAACC 120  
CTGGAATAGG CAAGGNATAA CTCTTCTAAC ACAAATAAG TGTATTATGT TTGGAATAAA 180  
GTCANCCTTG TTTCTACTGT TTTAAA 206

SEQ ID NO:5379

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06412

SEQUENCE DESCRIPTION:

35 GATCACTTAA ATGATTTTNT GGTGATTCGT GCCATTGCTT TTTTATTAA AAGAAAATTT 60  
TGTAATTAAA TGCCTTTTTC TAAA 84

SEQ ID NO:5380

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06413

SEQUENCE DESCRIPTION:

45 GATCACACCA GAGTACATGT CTCTGCCTCT NTTTTAGTG TGGCTTTGGA CAGGAATATA 60  
TGAATAANTC ACTGCCATAC AGGTTTCCA ATACACAAGT GCTAGAAAAT ACACACAATT 120  
CCCCAAA 127

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SEQ ID NO:5381

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06414

SEQUENCE DESCRIPTION:

GATCAAAAAT GCAACTGAGA AAATNATGGC TCTTGTGTCT GAGCTGTCCA TGAAACAAGC 60  
CCTAACCATT GAACTCCAAA AGGAAGTCAG GGAGAAAGAA GACTTCATCT TCACTTGCAA 120  
TTCCAGGATA GAAAAAGGTC TGCCACTCAA TAAGGAAATT GAGAAAGANT GGTGAAAAGT 180  
CCTTCGAGAT GAAGAAATGC ACGCCTTGGC CATCGCTGAA AAGTCTCAN 229

SEQ ID NO:5382

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06415

SEQUENCE DESCRIPTION:

GATCCCTAAC TGTTCCCTTA TCTGTTTTCT ACCTCCTCCT TTGTTTAATA AAGGCTGAAG 60  
CTTTTTGTAA A 71

SEQ ID NO:5383

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06416

SEQUENCE DESCRIPTION:

GATCACTTAC AAATTTTTTG AATAACACAA AATCTCATT CACCTGCAGT TTAATTGGAA 60  
AGATGTGTGT GTGAGAGTAT GTATGTGTGT GTGTGTGTGT GCGTGCACGC 120  
ACGTCTTGAG CAGTCAGCAT TGCACCTNCT NTGGAGAAGG GTATTCCTTT ATNAAAAATCT 180  
TCCTCATNNN NGNTTGTCTT TCAGTTGGTT TTCAATTNC TCACTGGCCA GAGAN 235

SEQ ID NO:5384

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06417

SEQUENCE DESCRIPTION:

GATCTTCCCT CTTCTGAACA GCAACTCCCC CCAACTCATA CACTGCCGTT TTCAGGGTAA 60  
GCGGCCTTCA CCCCTAAGTG AAAATGTTAG TGAAGTAAAG GAAGGAGCCA TTCTTGGAAC 120  
TGGACGACTT CTGAAAACG GAGGACGAGC ATGGGAGCAA GGCCAGGACC ATGACAAGGA 180  
AAATCAGCAC TTTCCCTTGG TGGAGAGCTA GGCCCTGCAT GGCCCCAGCA ATGCAN 236

SEQ ID NO:5385

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06418

SEQUENCE DESCRIPTION:

5 GATCCAGTAC TTGGCAGCCA TAGTTTAGAC AATATTGTTT AGTGCTGTGT TGCTNNCATG 60  
TTAACAACAA AACCTTTT TAG AGGNCCCACA AATCATNGGT ATNGGACACA GGTCCGAGGN 120  
ATTCCAGAGC ATCAN 135

SEQ ID NO:5386

SEQUENCE LENGTH:261

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06419

SEQUENCE DESCRIPTION:

10 GATCAGCTCG CACAGAGGTT GTCTGCAAGC AGTGTGAAGC TCATCTAGGT CACGTGTTTC 60  
CTGATGGACC TGGGCCCAAT GGTCAGAGGT TTTGCATGAA CAGTGTGGCT TTGAAGTTCA 120  
ANTCAAGGGA AACTGACCA TCTCAAGAG TCCCGTTCCC TTGCCACCCC TTCACGTGCA 180  
20 CCCTCAATTT CCACAATTCA CTTGAATGAC TTGTNTTATT NGCAATAAAA CTGGGCTGAA 240  
TTTGCTGCTG TCTCCAAANA N 261

SEQ ID NO:5387

SEQUENCE LENGTH:300

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06420

SEQUENCE DESCRIPTION:

30 GATCATAGAC ATGATTATAT GTGAGTATCA TTAATCATT A GTTTATAGCA NTTNCTCTTT 60  
ATTCCAATAT TATAATAATC CNCACTCTAC AATCATAACC TAGGAAAAAC CAGGCCATAC 120  
AGAGATAGGA GCCGAGGGGN CATAGTGCGA AGTGGCCAGA AGACAAGAGT GTGAGCCTTC 180  
TCTTATGCCT GGACAGGGCC ACCAGAGGGC TTGGTCTAGC AGTAACACCA GTGTCTGGGA 240  
AGATGCCTGT TGCAAGTGG ACCATGGTCT AGCGGGGGGC ATCAGTGTCA NGGTANNGAN 300

SEQ ID NO:5388

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06421

SEQUENCE DESCRIPTION:

40 GATCAACAGT GGCAATGGAG CTGTGGAGGA CAGAAAGCCA AGTGGACTCA ACGGAGAGGC 60  
CAGCAAGTCT CAGGAAATGG TGCATTTGGT GAACAAGGAG TCGTCAGAAA CTCCAGACCA 120  
45 GTTTATGNCA GCTGATGAGA CAAGGAACCT GCAGAATGTG GACATGAAGA TTGGGGTGTA 180  
ACACCTACAC CATTATCTTG GAAAGAAACA ACCGTTGGAA ACATAACCAT TACAGGGAGC 240  
TGGGACACTT AACAGATGCA ATGTGCTACT GATTGTTTCA TTGCGGAATC TTTTGTGAN 299

SEQ ID NO:5389

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06422

SEQUENCE DESCRIPTION:

GATCCACCTG CCTCGGCCTC CCAAGGTGCT GGGATTGCAG GTGTGAGCCA CTGTGCTCGG 60  
CCTTATTTAT ATTTTATATA TTGTTGATAT GGTGAATTT ATGTATGCCA TTAAATTATT 120  
TGTTCCTATT TAAA 134

SEQ ID NO:5390

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06423

SEQUENCE DESCRIPTION:

GATCAACGTC CTCCATGAGC ATGGNATAGT CCACCGTGAC ATTAAAGGTG CCAATATCTT 60  
CCTTACCTCA TCTGGTTTAA TCAAACTGGG AGATTTTGA TGTTCACTAA AGCTCAAAAA 120  
CAATGCCAG ACCATGCCTG GTGAAGTGAA CAGCACCTG GGGACAGCAG CATACTGGC 180  
ACCTGAAGTC ATCACTCGTG CCAANGGAGA GGGCCATGGG CGTGCGGCCG ACATCTGGAG 240  
TCTNTGGGTG TGTGTCATA GAGATNGTGA CTTGGCANGA GGCCTTGGCA TGAGTATGAG 300  
NAN 303

SEQ ID NO:5391

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06424

SEQUENCE DESCRIPTION:

GATCCAGAAG AAGTGACCTG AAGTTTCTGT GCAACACTNC AACTAGGCA ATGCCATTTT 60  
AATGCATTAC TAAATNACAT TTGTAGTTCC TAGCTCCTCT TAGGAAAACA GTTCTTGTGG 120  
CCTTCTATTA AATAGTTTGC ACTTAAA 147

SEQ ID NO:5392

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06425

SEQUENCE DESCRIPTION:

GATCAATTCG ACAGACAGAT GGNGTGTATG CCCCTCCCAN GTTTGACTTC ACACACACTC 60  
ATAACTTTCC AAATGAAGCC CCACAGTATA GCGCATATTT TNGATATTTT TGTGAATNCC 120  
ANNAGGAN 128

SEQ ID NO:5393

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS06426

SEQUENCE DESCRIPTION:

5 GATCCCTAGG AGCTGNCCTN CTTCCAGCCA NTGCCAGGAA CCAGCACTCC ATGAAGATAA 60  
ACTCTGGGCC CGACCACCAG CAGGNCCTGA CGACCTGAGG TGACCCTNGG CCTTTCCCCC 120  
NN 122

SEQ ID NO:5394

10 SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06427

15 SEQUENCE DESCRIPTION:

GATCACAAAT TTTGATATGT GCTATACAGG AAATAAAGTG TTATGATTGA GAATAAA 57

SEQ ID NO:5395

20 SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06428

SEQUENCE DESCRIPTION:

25 GATCTGAAAT CTTCACTAGG TTGATGTGGT TTCCTCTGCA GTGATTTTCC TAGGAAGTTC 60  
AAATTTGACA GCGAGTTTCA CTCAGCTGTG GCCCTCTGCC CTTCCAGCTG TGCCTAGCAA 120  
GCAAAACCCA GGNAAGAAGC AGTNGCCTCC TGGCCTTACA TACAGAATGC CTGGACAAGA 180  
GAGAACTTGC TCGGNCCTGC TTTGTATTTT AAAACACAGC TTGNGAGTTC AGAGTTGGTG 240  
GTTTGCTCAC TTAGCGGTTG TTANGNTGGC TTGAAAAGTT TTCATTATGA TACACTGGGT 300  
30 ACCCTGGGCT TNGAATGTTN NCAACTTNGG NNNATCTNAT GGTTACCTNT GATTANNAN 359

SEQ ID NO:5396

35 SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06429

SEQUENCE DESCRIPTION:

40 GATCTACCCA CCTCAGCCTC CCAAAGTGCT GGGATTACAG GCATGAGTCA CCACGCCCGG 60  
CCCTGNTTAT CAATCTTCAA TATTTTGTAT TTTGAGCACT TTGTTGGATT TGTTATTTAG 120  
CACATGTATA CATTGTTTTA TTATAATATT GTGTGTAATT TATTTCTGAT TAATTTTATA 180  
TCCTTCCTTC ACATTTCAA TACTTCTAAT TAAAAGCAGA CTGTTCAAAA AANNNNNGNN 240  
NGNNNN 246

45 SEQ ID NO:5397

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06430

50 SEQUENCE DESCRIPTION:

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GATCTGGCTG AGGGCTCAGG ACACAGGCCC AGCCACCCCC AGGGGCTCC ACAGNCCGCT 60  
GCATGACAGC NATACAGTAC TTAAGTGTCT GTNTAGACAA CCAAAGANTA AATGATTCAT 120  
GGTTTTTTTT AAA 133

SEQ ID NO:5398

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06431

SEQUENCE DESCRIPTION:

GATCCTGAAC CAAATTATA GCAATATAAT TAGTGTTTNT CTAAGGCATT ACTCATCAAA 60  
AAAATTGCTG CAGTCTTTAC AGTTGAATAA ATAAAAACAA CTGCATAAAT ATGCCCAAA 119

SEQ ID NO:5399

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06432

SEQUENCE DESCRIPTION:

GATCACCACC TGTAGAAACT GTTCTTCCTC TGTGAAACTA ACGGCCTGCT GGTAATAAAA 60  
GTAGCTACCA TTTCTTGAAA 80

SEQ ID NO:5400

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06433

SEQUENCE DESCRIPTION:

GATCACTCAT TGCTAATTTT GTCCTGTACA GCTTATGTAA TATTNNATG GTGGAGACGG 60  
ACTCTGTGTG CTCAGGGCCT TGTCTCTAGG AAGATTTTGT CAATCCAAA TACAGTTTG 120  
AAGATTCAAA 130

SEQ ID NO:5401

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06434

SEQUENCE DESCRIPTION:

GATCAACTGA TAAGTTGCCT TATGTCACCA TGGGTTCTGG CTCCTTGGCA GCAATGGCTG 60  
TATTTAAAGA TAAGTTTAGG CCAGACATGG AGGAGGAGGA AGCCAAGAAT CTGGTGAGCG 120  
AANCATCGCA GCTGGCATCT TCAACGACCT GGGCTCCGGA AGCAACATTG ACCTCTGCGT 180  
CATCAGCAAG AACAAGCTGG ATTTCTCCG NCCATACACA GTGCCCAACA AGAAGGGGAC 240  
CAGGCTTGGC CGGTACAGGT TGTGAGAAAG GGGACTACTG CAGTCCTCAC TGTGAAANTN 300  
ACTCCTCTNG AGATTGAGG TTNTTGAAG AACANGTCC AAACAATGGA CCACTTCCTG 360  
AATTGGCATC ANTGGTNNN 379

SEQ ID NO:5402  
SEQUENCE LENGTH:297  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06435

## SEQUENCE DESCRIPTION:

GATCTGTAGT AAACAATGGT GATTTTATTT ATTTNACTC TCTGGAAAAG GAGATAATAC 60  
AATTCCAGAA AGTGAAC TCA TATTTCTAAG GTTAAGATT CTTTTTATTG CACCTAGAAT 120  
AGTGCTATGC ACAGAGCGGG TGCTTGAGTT GTTGTCGTTT TNTGTTTGT TTTTAAATGT 180  
AAACTGGTAA ATNTTGTGCT TATCTTCAAG GCTAGCTTAN GTATAAAATN GTTTTTTAAA 240  
CACTTGNAAT ATTAAGGAT TTGTTTTAAN NANCANNAG GGGNGGTGGT TNGGTNN 297

SEQ ID NO:5403  
SEQUENCE LENGTH:294  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06436

## SEQUENCE DESCRIPTION:

GATCAAATAG TTGCATAGCA GTATATGTNA ATTTGTGTGT TTTTAGCTGT GACACAGCTG 60  
TGTGATTAAA AGGTATACTT TAGTAGACAT TTATAACTCA AGGATACCTT CTNATTTAAT 120  
CTNTTCTTAT TTTTGTACTT TATCATGAAT GCTTTTAGTG TGTGCATAAT AGCTACAGTG 180  
CATAGTTGTA GACATGGTAC ATTCTGGGGA AACAACTTT NTNTGTNGCC TTTACTGTTT 240  
GATATACCAN ATNANAANAA AATTGGGTCT NATNCTNAT GCTGGGGCAC CNTN 294

SEQ ID NO:5404  
SEQUENCE LENGTH:103  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06437

## SEQUENCE DESCRIPTION:

GATCCTCACC NCTTGGAATT AAAATNCTTG TTCCTCAGG CAAGCCTACA GTTTGCAACC 60  
AAGTCTAGGG TTTCTGTAA TCAANGNCGT TTTTCANTT AAA 103

SEQ ID NO:5405  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06438

## SEQUENCE DESCRIPTION:

GATCTGCTGG ACATCATGCC CCATGTCATA GAGAATAAAG CTGATGATTG TACCAGTAAA 60

SEQ ID NO:5406  
SEQUENCE LENGTH:91  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06439

SEQUENCE DESCRIPTION:

5 GATCATACCN ATAAAAATAA TNCCAAACAC CAAATATGAA TTTTATGAAT GTACACTTTG 60  
TGCTTNACAT TAAAAGAAAN AACACACAA A 91

SEQ ID NO:5407

SEQUENCE LENGTH:108

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06440

SEQUENCE DESCRIPTION:

15 GATCGTCGCC TGCTGGCTAA GACCAGGGAG CTAAAACTT NAGGAAGGGA ACCTGCCTGG 60  
TTGGNTGCTA CTTCTGATTC ATTGTCCTTN TCCCTNTCAT AAGTNCCN 108

SEQ ID NO:5408

SEQUENCE LENGTH:321

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06441

SEQUENCE DESCRIPTION:

25 GATCTTATGT TTAAAGAGAT TCTGTTATTA GCACCATGAA CTCGTACTAT GAAATNTTTA 60  
AGCCTTTTAT TTTTCTAACT ATATTACTGT AGGACTGGAT ATTAGGTGTC ATATAGGAAA 120  
CACAAAAGTT ATTGCTGTTT GCTAAAGCAA AGTAGCAGAA AATTTTGTAT ATGCAAAACT 180  
GTTGAAGGNC CATAGAGAAA TGTGTACTAC TGACGGGGCT TTTACTAGGC TTCCTGCGTG 240  
TGTANAAGTC GAGGTTTTGG CTTGGCATT CAGGGTGACAT GGTGGTGCTA AATTGTTTTT 300  
30 CNTTTAAAAG GCNTTCTATT N 321

SEQ ID NO:5409

SEQUENCE LENGTH:390

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06442

SEQUENCE DESCRIPTION:

40 GATCCGCAGC AGAAGCTCTT CCCTTCTGTA TCCTATGTAT GCAGTGTGCT TTTNCTTGCC 60  
AGCTTGGGGC ATTCTTGCTT AGACAGTCAG CATTTGTCTC CNCCTTTAAC TGAGTCATCA 120  
TCTTAGTCCA ACTAATGCAG TCGATACAAT GCGTAGATAG AAGAAGCCCC ACGGGAGCCA 180  
GGATGGGACT GGTCGTGGTT TGTGCTTTTC TCCAAGTCAG CACCCAAAGG TCANTGCACA 240  
GAGACNCCGN GTGGGTGAGC GCTNGCTTCT CAAACGGNCG AAGTTGCCTC TTTTAGGNAT 300  
CTCTTTTGGA ATTTGGGAGC ACGATGNCTC TNGAGTTTGA GCTATTAAAG NACTNCTTGG 360  
45 CACATTAAANA AAANANAAAT GNGGTNNGNN 390

SEQ ID NO:5410

SEQUENCE LENGTH:197

50 SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS06443

SEQUENCE DESCRIPTION:

5 GATCCCAGGG AAATATCAGC CTTGGGCAAC TGCAGTGACC AGGGGCACCG GCTGCCCACA 60  
 GGGAAACACAT TCCTTTGCTG GGGTTCAGCG CCTCTNCTGG GGCTGGAAGT GCCAAAGCCT 120  
 GGGGCAAAGC TGTTTTTCAG CCACACTGAA CCCAATTACA CACAGCGGGA GAACGCAGTA 180  
 AACAGCTTTC CCACAAA 197

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SEQ ID NO:5411

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS06444

SEQUENCE DESCRIPTION:

GATCTTCAAG TGAACATCTC TTGCCCTGAT TGAAGGCTTT GCCACATGCT GGAAGGCCCC 60  
 CTCCCAGGAA GATGGGGGTC ATTAAAGGAA ACTNAACATT GAAA 104

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SEQ ID NO:5412

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06445

SEQUENCE DESCRIPTION:

GATCACCTGA ACAATCTAGA TGTGGACAAA ACCATTGGGA CCTAGTTTAT TATTTGGTTA 60  
 TTGATAAAGC AAAGCTAACT GTGTGTTTAG AAGGCACTGT AACTGGTAGC TAGTTCCTGA 120  
 TTCAATAGAA AAATGCAGCA AACTTTTAAT AACAGTCTCT CTACATGACT TAAGGAACTT 180  
 30 ATCTATGGAT ATTAGTAACA TTTTCTACC NNGNNGTCCG TAATAAACCA TACTTGCTCG 240  
 TAAA 244

35

SEQ ID NO:5413

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06446

SEQUENCE DESCRIPTION:

40 GATCTNAGAA AANGCACCAC GTNAGCTTAC TAANTNATAA TATCTGTTTC TACTACGGAT 60  
 TTAGGCAACA GGACCTGTAC ATTGTCACAT TGCATTATTT TTCTTCAAGC GTTAATAAAA 120  
 GTTTTAAATA AATGGCAAA 139

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SEQ ID NO:5414

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06447

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SEQUENCE DESCRIPTION:

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GATCGGGGTC CATGGGCCCCA CCACCCCTG CAAGGAGGTC TCCATGAAGC ATGTAGGCAA 60  
CCAGCAATAC AACGTCACAT ACGTCGTCAA GGAGAGGGGC GATTATNTNC TGGCTGTGAA 120  
GTGGGGGGAG GAACACATAC CTGGCAGCCC TTTTCATGTC ACAGTGCCTT AAAACAGTTT 180  
TCTCAAATCC TGGAAA 196

SEQ ID NO:5415

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06448

SEQUENCE DESCRIPTION:

GATCCATTAA TCTGCTAATT GGTTCCTAT GAAATCACAT TGTCTGTTAT TAAAGCTTTT 60  
TACCATAAA 69

SEQ ID NO:5416

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06449

SEQUENCE DESCRIPTION:

GATCTAGTAA AGTGTTTATAG AACCCCTTTT TATCCCATGC ACCATTCAGT AAACATAAAA 60  
ATCACAATTC TGCTAATGTC ATTTGGAAT TCAAAATAAA TATCTTGTCT AAAAACAAA 119

SEQ ID NO:5417

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06450

SEQUENCE DESCRIPTION:

GATCATTGCA TGAATAGAAT CAAGGAGCTC ACTCAGAGTG AACTTNAATT ATNACTTTNN 60  
AGGCTCATT GTACTCTCTT CCCCTCTCAT CGTCATGGTC AGGCTCTGAT ACCTGCTTTN 120  
AAAATGGAGC TAGAATGCTT GCTGGATTGA AAGGGAGTGC CTATCTATAT TTAGCAAGAG 180  
ACACTATTAC CAAAGATTGT NGGTTAGGCC AGATTGACAC CTATTTNTNG NCNNTATGCG 240  
TATATTTNCC TGTGCTATAT ATGAAAANTA ATTGCATGAT TTCTCATTCC TGNGTCATT 300  
CTCAGNGN 308

SEQ ID NO:5418

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06451

SEQUENCE DESCRIPTION:

GATCTGAAGG GAGAAGGTGA TATTCATGAA AATGTGGACA CAGACTTGCC AGGCAGCCTG 60  
GGGCAGAGTG AAGAGAAGCC CGTGCCTGCT GCGNCTGTGC CCAGCCCGGT GGCCCCGGCC 120  
CCAGTGCCAT CCAGAAGAAA TCCCCCTGGC GGCAAGTCCA GCCTCGTNTT GGGTTAGCTC 180

TGACTGTCCT GAACGCTGTC GTTCTGTCTG TTTCTCCAT GCTTGTGAAC TGCACAACCTT 240  
GAGCCTGACT GTACATNTT TGGATTGTG TCATTANAAA GAAGCACTTT AAA 293

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SEQ ID NO:5419  
SEQUENCE LENGTH:180  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06452

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SEQUENCE DESCRIPTION:  
GATCCTGGNA CATTTCATAA GCTTGGGTAA AAAAATTTT TGTATNNTC CATGCACAAT 60  
AAGGGAAATG TTTAATTGG CTTTGNCCCT CTGCTTTAC AACAGTTCTG GCCTCAAGTT 120  
ACCAGGTAGC CTGAACCTTG NTTTTATTTT ACCATTAANT TGCTTTAATA CCATNGTAAA 180

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SEQ ID NO:5420  
SEQUENCE LENGTH:99  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06453

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SEQUENCE DESCRIPTION:  
GATCACTGA GCCCANGTG AGGTTGAGGC TGCAGTGAAC TATNATTGTA CCACTGCACT 60  
TCAGCCTGGG CAACAAAGGA AGACCCAGT TCTGGGAAA 99

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SEQ ID NO:5421  
SEQUENCE LENGTH:209  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06454

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SEQUENCE DESCRIPTION:  
GATCCCTGCA TTNCCTGAAG ATNTTTAAAC GTGAGAGTNT GGTAGGCAAA GCAGTCTGAG 60  
AAAGAAATAG GAAATGCAGA AATAGGTTTT TTTTGGTTGC ATATAATCTT TGCNCTTTTT 120  
AAGCTCTGTG AGCTCTGAAA TATATTTTNG GNTTACTTCA GTGTGTTGA CAAGACAGCT 180  
TGATATTNCT NTCAAACAAA TGACTNNGN 209

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SEQ ID NO:5422  
SEQUENCE LENGTH:246  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06455

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SEQUENCE DESCRIPTION:  
GATCCAGTGG ACAAAGAGG GGAACTATG GGAGTTCCCA ATTAACAATG AAGCAGGTTT 60  
TGATGATGAT GGTTCAGANT TTCATGAACA TATATTTNTG GAGAAACACC TGGAGAGCTT 120  
TCCAAAACAA GGACCAATTC GCCACTTCAT GGAGCTGGTG ACTTGTGGCC TTTCCAAAAN 180  
CCCATATCTT AGTGTTAAAC AGNNGGTTGA NCACATNGAG TGGTTTAGAN ATTNTTTTNA 240  
TGNNAN 246

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SEQ ID NO:5423  
SEQUENCE LENGTH:105  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06456  
SEQUENCE DESCRIPTION:  
GATCTGCTCA GAAAGGAAGA GGCAGGCGCC AGGGNGAACC CCCTTCCGTG NTTTGTAACC 60  
CTCCCTNTAA GGTGAAGCCC TTTNCTTGC TAAAACCGGN AATTN 105

SEQ ID NO:5424  
SEQUENCE LENGTH:159  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06457  
SEQUENCE DESCRIPTION:  
GATCCTGGGG GTCGTGGCTA CCCCCTCCTC GTGGCCGNNC TCCTTGCTGC TCCTGTCAAT 60  
AGTGAGCTTG TGCCGTCCCN CTAGGATGGG GGCATGGCCN TGGGCTGCCA GATGCCACA 120  
GCACCCTGGC ATGACCTNCC ACCTNGGGTT CCANACCGN 159

SEQ ID NO:5425  
SEQUENCE LENGTH:211  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06458  
SEQUENCE DESCRIPTION:  
GATCACCTAT CCCCTGTTTC AACAATGAAT AAGGAACAGC AAATNTTTGA GACGTGCCCT 60  
GAAACTGAAC AGAGATGCAC TCTCCAGTGA CTCCCCAGCA AACACAAGGT GCAGCAGGGT 120  
CCCAAAGGTA GCTGGNTGGC TGANCTGCTG GNTATGGGAG ATACATGACG CGAAGACGGN 180  
TTTNACATCC ACAGGGCGGT NTTNANGAAA N 211

SEQ ID NO:5426  
SEQUENCE LENGTH:66  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06459  
SEQUENCE DESCRIPTION:  
GATCCACCAC AGGGTTAGGG GACAGGAAGC CTGTTCTATT CTCAATAAAT CTTACAAAAT 60  
TCCAAA 66

SEQ ID NO:5427  
SEQUENCE LENGTH:189  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06460  
SEQUENCE DESCRIPTION:

GATCATTATT TCCATTCTTA ATGTGAAAAA AAGTAATTAT TTATACTTAT TATAAAAAGT 60  
ATTTGAAATT TGCACATTTA ATTGTCCCTA ATAGAAAGCC ACCTATTCTT TGTGGGATTT 120  
CTTCAAGTTT TTCTAAATAA ATGTAACCTT TCACAAGAGT CAACATTAAA AAATAAATTA 180  
TTTAAGAAA 189

SEQ ID NO:5428

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06461

SEQUENCE DESCRIPTION:

GATCTAGACA TGCCTTAGGT AACTGCAGAA ATAGCAAATT AAATNATTAA TGAGCTTATT 60  
AGTCATAGTA AACATACAGA TTCCTANTTC TATGACAGTG TACATNTATG ANAATAAATG 120  
ATGAAAAAAG AACTATAGTA TTTTAAAAA TATGCTTTTA TTTNTATTNC ACATAGTGNA 180  
AAGTTCTACA NAN 193

SEQ ID NO:5429

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06462

SEQUENCE DESCRIPTION:

GATCACATTT CTGGGAAGAT GAGANCTNNT TTCCAGACCA GCATCCAGTG GCCATCAGGT 60  
CTTGTGGCCC AAAGGCTATG CTTGCCTCCG GCTGAGTGCC TGGNATAGGC CTTNCTATG 120  
TCTCCCAAG GCTGGGGTGC TGAGCCTGCC TTCCTACCA CCTAGCCATA GTCTCAAACC 180  
TGTGGGAAG GNGGNNTTCT CCCTGCCCGG GAAGAGGACA GATAACTGAT TTCCGTTCTT 240  
TTGACTGTGT TTAAAATTC TCTTTCTAAA 270

SEQ ID NO:5430

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06463

SEQUENCE DESCRIPTION:

GATCTCCTGG GACTCCGAGC AAGGCCTGCA CGAGAGAGGG CTGAAAGGCT GCTGGGGCTG 60  
CCACCTCGCT ATTCCCGCAT AAGCATCTGC CCCCACCCC TTTGACCTTC ATCTGATGGA 120  
CATTTTATA CAGAAAACAA TAAAGATTTC CCTCTCAGCA AA 162

SEQ ID NO:5431

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06464

SEQUENCE DESCRIPTION:

GATCAGTTGT ACTAGAGGAA CATCATAGAA GAGAAAAATC CAACTCTTTA TATTAATAAT 60

NAATACAATA AGAAAATTGC AAA

83

5

SEQ ID NO:5432

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06465

10

SEQUENCE DESCRIPTION:

GATCTGCAAG CCTGCTGTA CAAGAAAATC ATTAAGGAAC ATTTGGAGAG TTAGCTACTA 60

GCTGCCTAAG TGTGCACTT CAATCTAACT GTGAAAGAAT CTTCTGATGT TTGTATTATC 120

CTNCTTATAT TATATTANCA AAATAAATCA AGTTGTGGTA TAGTCAAA 168

15

SEQ ID NO:5433

SEQUENCE LENGTH:357

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS06466

SEQUENCE DESCRIPTION:

GATCCACCCA CCTTGGCCTC CCAAGGTGCT GGGATTGCAT GCATGAGCCA CTGCACCCAG 60

CCAAGATACA TTGTTGACGT GAAAAAAAAA TTCAAGATA TATAGAACAG TGTAACATG 120

25

CATCCAATTG TGTTTTTCAN GGAGAAAATA ATGTATACTT GTATTGGTTT ACGTATGAAA 180

CAAAANTATC TAGAAGGATG AATAAAAAATC TAGTAACTGA TTNTACACTA GGGCAAATTG 240

GAAACAANTG GGNGACTTCA TGGATGACTT TTTTATATTT GTAAAGTGGA NGTGANTGTN 300

TTACTTATTC CACCAGTTAN GTTGAAACCT TTNNNNGGNA GGTTNGTGGT GNTTNTN 357

30

SEQ ID NO:5434

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06468

35

SEQUENCE DESCRIPTION:

GATCAGATGG CTTAGAGAAA TTNCTGGAAT ATTCACATTC GAAGATTCCT TATTAATNAA 60

TGTCTTTNAC TTAAATCTAA CCAAAAACTG CAACATTATT CTTTGTACAT TTNCATTATA 120

TAGTGTTAAC AAGCTTAGTT GCANACAANT AAAATACTTA AGCTATTTGT TTAAA 175

40

SEQ ID NO:5435

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45

CLONE:HUMGS06469

SEQUENCE DESCRIPTION:

GATCTGGTGA AACTNGCTAA ACGNCTCAAG AAGGAGAAAAG TTAATNTTGA CATTATCAAT 60

TTTNGGGAAG AGGAGGTGAA CNCAGAAAAG CTGACAGCCT TTGTAAACAC GTTGAATGGC 120

50

AAANATGGAA CCGGTTCTCA TCTGGTGACA GTGCCTCCTG GGCCAGTTT GGCTGATGCT 180

NTCATCAGTN CTCCGATTTT GGCTGGTGAA GGTGGNNN 218

55

SEQ ID NO:5436

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06470

SEQUENCE DESCRIPTION:

GATCACAGTG GGCAGCCGGC ACCCNGCACC ACTTTGGCGA GCGTCCTGCT TCCGNCCTCG 60  
CCCTCATCTA CGCTGCTCCG CTTTCCTCAG ACCCCTTTT GCCGTGCAAA GGGAATTCTT 120  
GACATTAAAT AAAAGGTATC CAGNTTGCAG AAA 153

SEQ ID NO:5437

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06471

SEQUENCE DESCRIPTION:

GATCAGTTGG GTGCACGAGT GGGTTACATC GAACTGGATT ATAGGAAGCT TATAACAAGA 60  
ATGGAAGATT CTAAATAAC TCACTTTCTT TGGNATCCAG TAACAGTAGA TGTTCAAAAAT 120  
ATGTAGCTGA TTAATACCAG CATTGTGAAC GCTGTACAGC CTTGTGGTTA TTAATAAGCA 180  
AGTTACTACT AGCTTCTGAA AAGTAGCTTC ANAATTAATG GTTATTTNTA NACTGCCCTT 240  
CCNTGGCTGN TACTTNNCCC TAAGNTNAAT CTNCGAGAAT CTGAAATGNT TNCTNCANTT 300  
NTCAGGGAGN 310

SEQ ID NO:5438

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06472

SEQUENCE DESCRIPTION:

GATCACATTN GATNAAAGAG CAAAACCTGT TAAGTCCAAA ATAAATTCTT ACTGTTTATA 60  
TCCTAAA 67

SEQ ID NO:5439

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06473

SEQUENCE DESCRIPTION:

GATCCACAGA AGGTCCTGGT GGTATTTGTA ACTTTTGTCA AGGCATTTTT TTATATATAT 60  
TTTTGTGCAC ATTTTTTTT ACGNTTCTTT AGAAAACAAA TGTATTTCAA ANGTATATTG 120  
ATAGTCGANC AATTCATATA TTTGAGGTGG AGCCATATGA ATGTCAGTAG TTTATACTTC 180  
TCTATTATCT CAAACTACTG GCAATTTGTA AAGCNATATA TATGNTATAT AAAGGTGATT 240  
GCNGCNTTNC ANTGTTAGCC CCNGTGNN 268

SEQ ID NO:5440  
SEQUENCE LENGTH:306  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06474

## SEQUENCE DESCRIPTION:

GATCCAGGCT CAGAACTTCT TCTCCAGCTT CACCCTGATG AAGCTGAGGC ACTCCTCCGC 60  
TCTGGGTGGG GCCAGCCTAG GGGCCAGGCA CATCGGGCAC CTNCTCCCA TGGACTATAG 120  
CGCCAATGCC ATTGCCTTCT ATTCCTACAC CTNTTCCTAG GGGGCTGGTC CCGGGCTCCA 180  
CCNGGTCCAA GCTCAGTGGA CACTGGGTCT GAAAGGAAGG AGTCTTTTGN TTCCTTTCTC 240  
CTNTTTACAN GAACAAACAT AGATGGTAAA TAAATNNACT TTNTCCNCT CCCAGAANN 300  
NAATNN 306

SEQ ID NO:5441  
SEQUENCE LENGTH:111  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06475

## SEQUENCE DESCRIPTION:

GATCAGCTAC ATAAACGGC CTGAGTGCTG TTTTAAACAG CNCTTGGGTG ATGGTACAAC 60  
ATNACTTTTT AAGATAATNA NGTAGAAAA GTTCTAGTG GAAACATGAA A 111

SEQ ID NO:5442  
SEQUENCE LENGTH:255  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06476

## SEQUENCE DESCRIPTION:

GATCCCAACA TTTTGGCAG TGAGCATTAC GATGTTANCC GTGGGGTGCA AAANATCTGA 60  
ATAAAATTTA CAAAAGGAGA ATTCAGACAG ACCAACCTGG GTNATGTGT TCAAGCTCTG 120  
CCCCAGGAGC TTGAATGTCT NTNCCTNGTG GCAGGAGCAT TCCTAGAGAC TGGTGCATCA 180  
GGTTTTATGT TGTGTCTCT CTGCTCCAGC TCACCCNTNA AANCTCTNCC CTNGGATGTT 240  
GGAATCANA TTCTN 255

SEQ ID NO:5443  
SEQUENCE LENGTH:313  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06477

## SEQUENCE DESCRIPTION:

GATCCCATAA AGCTACGAGG GGGACGGGAG AGGGCAGTGC AATGGGAAGT AAAGAGATAT 60  
TTNCCAGTAG GAAAAGCAAT GCTTCTTGT CTTTAGACTC AAATGCTTAG GGAACGTTTC 120  
ATTTCATT CATGGGAAA GGCAGCCTCC TTAAATGTTT NCTGAAGAGC GGTAAATCT 180  
AGAAGCTTAA GANTTTNCAG TTCCTTCAAT AACCATGATG ACCTGAAGTN CACCTATCCC 240  
ATTTAGCAT CTNCTTGTTT TNCCCATCTC TNCCTTTCCA ATTTTNCCTA TNCCTGCTGA 300

ATATTTTGT AAA

313

SEQ ID NO:5444

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06478

SEQUENCE DESCRIPTION:

GATCAGCTCA CACCCAGTCT CTCACAAGTN TTCATTCCAT AAAAGTGGTT GACTAAAGTG 60  
 AATATGTCCA TAGTGGGGTC TTTAATCCC TCTGGTCTTA CCANGGGTTA GANGTCTNTN 120  
 GGTNTAACT TTTCCATATT GTTAGAACAT CATGGNGACA TCATGTNCAT CTGTTCAAAA 180  
 TTACAAGAGG CTTTNCAG CTCTACCATG CTTTGNAN 218

SEQ ID NO:5445

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06481

SEQUENCE DESCRIPTION:

GATCATTGTG AAGGCAGGGG AATGTATGTG CACATCTGTT TTGTAAGTGT TTAGATGAAT 60  
 GTCAGTTGTT ATTNATTGAA ATNATTTCAC AGTGTGTGGT CAACATTTCT CATGTNGAAA 120  
 CNTTAAGANC TAAATGNTC TAAATATCCC TTGGACATT NATGTCTTTC TTGTAAGGCA 180  
 TACTGCCTTG TTTAATGGTA GTTTTACAGT GTTCTGGCT TNGANCAAAG GGGCTTAATT 240  
 ATTGATGNNT NGGATN 256

SEQ ID NO:5446

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06482

SEQUENCE DESCRIPTION:

GATCCGGAAG CGAATTCATC TCCGAGCTGA GGATNCCTTG TTTTNTTTG TCAACAATGT 60  
 CATTCCACCC ACCAGTGCCA CAATGGGTCA GCTNNACCAG GAACACCATG AAGAAGACTT 120  
 CTTTCTCTAC ATTGCCTACA GTGACGAAAG TGTCTACGGT CTGTGAAGCT GCTGCCCCTG 180  
 AGCTGGAGGG GGGTCTCATT CTACAAAGAG AGAGGTGGCC CCCCTTTCTT GACCTGCTCC 240  
 TCCTCAAGC TTAACANCA CCTCCTTATT CAGGACCGGC ACTTCTTAAT GTTTGTGGG 300  
 CTTTCTNTCC AGCTNTCTTT NGGNGGGGTA ATGGGTNGGA GTTN 344

SEQ ID NO:5447

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06483

SEQUENCE DESCRIPTION:

GATCTTTCTA GGAGGGAGAC ACTGGCCCCT CAAATCGTCC AGCGACCTTC CTCATCCACC 60



CNATCCCTCC CCAGTTCATT GCACTTTGAT TAGCAGCGGA ACAAGGAGTC AGACATTTTA 120  
 AGATGGTGGC AGTAGAGGCT ATGGACAGGG CATGNCACGT GGGCTCATAT GGGNCTNAGA 180  
 GTAGTTGTCT TTCCTGGCAC TAACGTTGAG CNCCTGGAGG CACTGAAGTG CTTAGTGTNC 240  
 TNGGAGTATT GGGGTCTGAC CCCAAACAAC TTTCAGNTTC NNTAACATAC TGGGNCTTGA 300  
 CTGTTTTNTC TNGGTNCCNN ATGGGTCCTG GTTN 334

SEQ ID NO:5448

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06484

SEQUENCE DESCRIPTION:

GATCTAGAAA GCCCTAAGCT CTCACCACTG GCTACCTTGA GCCTCTACAG AATNAGGAAG 60  
 TAAAGTCTAA GGCAGTTAAA 80

SEQ ID NO:5449

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06485

SEQUENCE DESCRIPTION:

GATCGCANCT CCGAAGACGG AGAGGAGGGA AATGGGGCCC TTCCCTCT ATTGCATCCC 60  
 CCTGCCCGNC TCCTTCCCG CACCCACGTG CCCTAGATTC ATGGCAGAAA ATGNCCAAAT 120  
 CCNGNGTATT TGTGTANAT ANTTAAN 147

SEQ ID NO:5450

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06486

SEQUENCE DESCRIPTION:

GATCATTGTA TATNACACAC ATGTATCAAA GTATCACATG TACTCCAAAT GTTTGTACAA 60  
 CTATNATATA TCATTAAAAA AATACAAANT AAAAAATGTA GCTATGAAA 109

SEQ ID NO:5451

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06487

SEQUENCE DESCRIPTION:

GATCCAGTGT GCAGAAGAGC CAGCAGGGAA CCGGAAGCTC TNATGTCAAG GCCAGAGCAG 60  
 TTGAGANTGG GNCCCAGAGT AGATGCTGAC CTGGGCACTC CACCATTCCG GGGCCACCAC 120  
 AGAGATGCCA GCAGGATGCC ACTTTNCCAG CCCGACACAC GGACCTTNT AAAGANCAGC 180  
 AACAGGCAGG AGAGGCAGCG TNTGNCCAGA TTGTTTCCCG TCATTGGGTG GCATNTGTTA 240  
 NCTAGCTGNC AAACANCTTC ANCCCGTGTA ATTN 274

SEQ ID NO:5452

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06488

SEQUENCE DESCRIPTION:

GATCACGGCT CTTTAAAGC CCTGGCAGCA TTTTGGTCCC TGCTCCTTGC CCATAGTAAA 60  
ACAGCTTGAA ATATCCCATG CAAGAGAGTA GTTCAAGTG GGCAACTCTG CTCTCTATTT 120  
AAAAGCGTGC ACAATCAAAA GTACTATGCA ATTTAGGAC AATAAAGANC ATACAGTTTT 180  
AAA 183

SEQ ID NO:5453

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06489

SEQUENCE DESCRIPTION:

GATCACCAGT GGGCACTAGA TGATGTNGAA GAAGAGCTCA TGGCCAAANA CCTCCACTTC 60  
GAAGGCATGT TCAAAAAGGA ATTACAGACC TCTATTTTTT GAAGACCGAG CAGGGATTAG 120  
CTGTGTCAGG AACTTGGAGT TGCACCTAAC CTTGTAAGTT TGTGTTGGAGC TGGCACCTCT 180  
TGAAATAAAA AGGGAGGNTG CACGAGCTGG GCAAAA 215

SEQ ID NO:5454

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06490

SEQUENCE DESCRIPTION:

GATCAAAAAA TTCAATTTC TACAAGTTCT NCTATCTGAA ATAAATAACA GACTCATTTT 60  
TGACAATAAA 70

SEQ ID NO:5455

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06491

SEQUENCE DESCRIPTION:

GATCANGNTA GTGGTGTCTG TCAGCTGTCT AAGAGGTTGG AGAATNAACT ACTCAAGATA 60  
GTCACGAAAA NACTGAAAGT TTNATTTTCC TTTCCATATT TAAN 104

SEQ ID NO:5456

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06492

SEQUENCE DESCRIPTION:

5 GATCCCAGTT ATCCTTGNAT CCATGTAATT TCAGATGAAT TATTAAGCAA ACATTTTAAA 60  
 GTGAATTCAT TATTA AAAAC TATTCATTTT TTTCCTTTGG CCATAAATCC NCTAATTNTC 120  
 ATTA AAATTC TAAGGTCATT TCAACTGTTT TAAGCTGTAT TNCTTTAATT CTGCTTACTA 180  
 TTTCATGGAA AAAANTAAAT TTNTCAATTT TAAA 214

SEQ ID NO:5457

10

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06493

15

SEQUENCE DESCRIPTION:

GATCCAGAAT AACTTCTCCC ACTCATATCT NCAGTTCACC NAATGAAATN AATGGATAGC 60  
 AAGAGCCCNT TGTTCACAGG ACTTTAAGGC AAAATATTAA AANTN 105

SEQ ID NO:5458

20

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06496

25

SEQUENCE DESCRIPTION:

GATCCTTTTA TAAATTTAAA AAATTTAATG TTAATAAAGC GAGGTGTAAT TGTA AA 56

SEQ ID NO:5459

30

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06498

35

SEQUENCE DESCRIPTION:

GATCCGNGAA AGGCTGAAAG GCCAGGAAGA CAGCCTAGCC TCTNCAGTGG ATGCTGCCAC 60  
 CGNACAAAAG ACCTGTNACT CCGACTGAGG CATGNCCTGC CCN 103

SEQ ID NO:5460

40

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06499

SEQUENCE DESCRIPTION:

45

GATCNTGGAT NTAGAAGAGG TNACATTGCA CAATGTTTGA ATAAGGAAAC TATTGGAAAG 60  
 TTTTCCAAG CTGACATTGC AGAAAATGCT TTGNAAAATT CCTCAGAAAC AGAAATACCT 120  
 ACTGTCAGCG TTTAGCTGA TGAAGANTTC CTTCCCTNCA AAGAAAATAC ATTTGACCTG 180  
 GTGGTNNGCN 190

50

SEQ ID NO:5461

55

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06500

SEQUENCE DESCRIPTION:

GATCCCGCCC ACTCAGAAAA GCGGAGAAGG CTTTGTAAAT TTCTACATGA ATCAAACACA 60

GAAACAACTT TTGGAGAAAT TAAATTCTGA GTGTNACTTC TGAAA 105

SEQ ID NO:5462

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06501

SEQUENCE DESCRIPTION:

GATCTTCTTC ACACCAAGCT CTGTTTACAT TCCGAGAGTT GTCATGAAGA AAGTNCTNNT 60

CAATAAGNTT TTGGAATGTT AAA 83

SEQ ID NO:5463

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06502

SEQUENCE DESCRIPTION:

GATCAGGACA CGAGGAAGAG TAAATGTGAG ACAGTCAATG TGA CTCTCTGC GATAAACAGA 60

TTTTTAAACC CCGAAATTTT GCAAAATTTT GGTGAACCTG ANCTTNCTTC GTTG CATATG 120

CTGGCACTAT CTGTACCATC ATACANCTGT CTCACATTAA AGCTATTTTC CTTGGGCAAA 180

SEQ ID NO:5464

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06503

SEQUENCE DESCRIPTION:

GATCATCTCC CCTGGCAACG TGA CTCTGTT TTTTGTGTGT GTTTC CATGC TGA CTAGTCC 60

CCTACTGTTA ATATCACTAC TAATTAGGCT ATAACCAGGT CTTTCCTGGC CTGAGAAATA 120

TTCTCTTAAA ATNACCTTG TTTTAATCTC ATTCATGATG TTGATTTTTT TTCAATGTGG 180

TGCAATATAT ACANTAAAAAN TNGTCATANC TAAA 214

SEQ ID NO:5465

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06504

SEQUENCE DESCRIPTION:

GATCTGTCCA GGGAGGTGGC TGAAGAGTGG GCATCTCCCT TAGGGACTCT ACTCAGCACT 60

CCATTCTGTG CCACCTGTGG GGTCTTCTGT CCTAGATTCT GTCACATCGG CATTGGTCCC 120  
TGCCCTATGC CCCTGACTCT GGATTGTNA TCTGTAAAAC TGGAGTAAAA ACCTCAGTCG 180  
TGTAAC 186

SEQ ID NO:5466  
SEQUENCE LENGTH:117  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06505

SEQUENCE DESCRIPTION:

GATCTTTGCT TCCTTNCAT TATGTTTGT CACAACACCT AAAACCAGTT TTGCTGCTAT 60  
ANTTCTATAC TGTTGATTCT TCTGCNANNT ATCTGTAACC AAATAAACAT AATAGGN 117

SEQ ID NO:5467  
SEQUENCE LENGTH:309  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06506

SEQUENCE DESCRIPTION:

GATCCAAACC AAAGACTGTA GAACCTGGG GTGTGGCTAA CTGGCCNTN CNGCACCCGT 60  
AGCCAGGTCT TCCTGGCCCT TNAGGCTGGG CTGGCGGACA GGCACCTNCC TGTTCTTAA 120  
GCTGAAGCTC CCACACTGTC TTCCAGGGCT GAGGAGATGC TCTCCTTTT TACTGACCAT 180  
CTTGATACTT ATTTATACGA GAGNCAGTTG CTGGACGGGG TAGTACTGGG AAGCAGGAGG 240  
CAGAATGGCT CTGCTGAGCC TNCNACCCAT GGNCAACANC CTAATAAAAC AGANCATTTC 300  
AGAGCCAAA 309

SEQ ID NO:5468  
SEQUENCE LENGTH:97  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06507

SEQUENCE DESCRIPTION:

GATCCCATAC CAGAAGATGA GAAAAAAGAA TAAGTGTTC CTTGTTTTGT GTGTTCTAAA 60  
TACTTTTTNT AATGAAAAAA TGNTTTTNG TTTTAAA 97

SEQ ID NO:5469  
SEQUENCE LENGTH:67  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06508

SEQUENCE DESCRIPTION:

GATCATCTAA ACTAAGTCCA GCTGCCTAAT TCTAGATATA TATATATATA TAGAGNTCCA 60  
CCATAAA 67

SEQ ID NO:5470

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06509

SEQUENCE DESCRIPTION:

GATCTTGGGA AGTATTCCCA AGGAAAACAG TCCTGGGCAC AGTCTCCAAA ATAAATTCTN 60  
AATTTTGGGA AA 72

SEQ ID NO:5471

SEQUENCE LENGTH:467

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06510

SEQUENCE DESCRIPTION:

GATCCCATGG CTTTCTTTAC TGGGCTCTGG GGCCCCTTCA CCTGTGTAAG CAGAGTGCTG 60  
AGCCATCACT GTTTCAGCAC CACTGGGAGT CTGAGTGCGA TTCAGAAGAT NACGCGGGTA 120  
CGAGTGGTGG ACAACAGTGC CCTGGGGAAC AGCCCATACC ATCGGGCTCC TCGCTNCATC 180  
CATGTCTATA AGAAGAATGG AGTGGGCAAG GTGGGCGACC AGATACTACT GGCCATCAAG 240  
GGACAGAAGA AAAAGGCGCT CATTGTGGGG CACTGCATGC CTGGCCCCCG AATGACCCCC 300  
AGATTTGACT NCAACANCGT GGTCTCATT GAGGNCAACG GGGAACCTN TNGGNGACAN 360  
GTATTNAAGA CACNGTNCCC ACCTAGGCTG TGGNAGGGTG AAGGGCGAGT TTTCCCAAGN 420  
TGGTGGGCCT TNGTTNAGAN CTTTGTGTTG NGTTGGNNC NNGNTAN 467

SEQ ID NO:5472

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06511

SEQUENCE DESCRIPTION:

GATCTTAACT NTCTTGACTG ATTTAAAAAG CTAATCAATT TATTAAAGCC AGANATGTNC 60  
TCCTCTGGGA AAGCAATTTT TATCTATTTA TCTACCAATC CCCACTCACA TATATATGTT 120  
TGNTTTTACA TAGAGATAGA TGGTTTTAAG GGTTTTCTTA TTGTTAAATT ATTTCTTAAG 180  
ACATTGTGGG NTGGAGACCA CTAAACTTAT AAAAAACCAA GGAAAGTAAA GTTTTNCAAA 240  
TGTTTATACT GTTTAAGGTG TTTATTTATN TAANCCATGC ATGGGGTNNC ATGCATAANT 300  
NNNGNGGTTT AAATTCACC AGTGANN 327

SEQ ID NO:5473

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06512

SEQUENCE DESCRIPTION:

GATCAAGGAA CTTGTGCCTG TCTATAGATT TTATTTCCCC TGTACAAATA AACTTGGCTG 60  
CAATCCCAA 70

SEQ ID NO:5474

SEQUENCE LENGTH:414

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06513

SEQUENCE DESCRIPTION:

GATCTTGCAA GACTAAAATT GGCCATTAAG TACCGTCAAA AAGAGTTTGT TGCCCAGCCC 60  
 AATTGTCAAC AGCTGCTGGC ATCTCGCTGG TACGATGAGT TTCCAGGCTG GAGGAGAAGA 120  
 CACTGGGCAG TGAAGATGGT GACATGTTTC ATAATAGGAC TTCTTTTCC TGTCTTCTCT 180  
 GTGTGCTACC TGATAGCTCC CAAAAGCCCA CTTGGACTGT TCATCAGGAA GCCATTTATC 240  
 AAGTTTATCT GNCACACAGC CTNCTATTG ACTTTTTTGT TCCTGNTGNT GCTTGCCTCT 300  
 CAGGACATAG GCAGGTCAGG NNTGANCNGG GAAGGTCCAC CANCACCATC GTCGAGTGGA 360  
 TGATATTGNC NTGGGTNCTN GGNNNATGTG TTANNTAGGA AATGTNATAA ANCN 414

SEQ ID NO:5475

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06514

SEQUENCE DESCRIPTION:

GATCAACAAT NAGCATCAAA TCTATGGCTC CTGGCTCCAG CANCAAGACG CAAGAAGACA 60  
 GGANGAGAAG CANGAAGTGA GACTGGAGGG AAAGGGAGCT GAGTCTNCTA GN 112

SEQ ID NO:5476

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06515

SEQUENCE DESCRIPTION:

GATCATTCTT TTATAGAGCA TATTTGCCAA TAAAGCTTTT GGAAGCCGGA AA 52

SEQ ID NO:5477

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06516

SEQUENCE DESCRIPTION:

GATCTAACTT TGCACTCTTT GATAATAATG TTTTAGATAA TGTGCGTAAT CCAAATTGGT 60  
 ATTGTAGCCT CTGTTAACAC AGACAGTATA TGTTTAAAC TTTGATGTAA ACCTTTTNAG 120  
 ACCCAAATT GTGGAAGTAT CATGTGTTAA GTNCTCTGTC TCTGTTTCTT TGTTTATTTA 180  
 TTAATAAAAT GAAGTTGTTA TTAAAGTATA TGCAAATNTG AAA 223

SEQ ID NO:5478

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06517

SEQUENCE DESCRIPTION:

5 GATCCGGGGN AGCTGTATCC CCAGTAGAAA AACATTTTA ATCACTCTAA TATAACTCTG 60  
 GATGAAACAC ACCTTTTTTT TTAATAAGAA AAGAGAATTA ACTNCTTCAG AAATAACTAA 120  
 TAAATGAAAA ACCTTTAAAG GAAA 144

10 SEQ ID NO:5479

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06518

15 SEQUENCE DESCRIPTION:

GATCTTTTGA CGNNTATANA AATGTACTAA TGTNATAAGT TAATGCTGGN CATTTCATTT 60  
 ATATATATTT TTAAGAGGCT AGAGGCTTTT AGCTTTTTAA AACTCCATTA TATACAN 117

20 SEQ ID NO:5480

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06519

25 SEQUENCE DESCRIPTION:

GATCTTTTCAT TCTCATGCAG ATATTTCTAT TGTGGGCTTA TACATTTGNT CACCTATTGT 60  
 TGATGGNACT TGNGACTTTC CATTTTGGCG CTATTACAAN TAGGCACTAT GAATGACTGA 120  
 TGNACCACTT ACTTGAGCTT TATGNCTTAT TNTCAAAGCN GCAAAATN 168

30 SEQ ID NO:5481

SEQUENCE LENGTH:395

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS06520

SEQUENCE DESCRIPTION:

40 GATCAGTTAT GAAGAAGGGA AAGCTTTGGC AGAATCTTGG AATGCAGCTT TTTTGAATC 60  
 TNCTGCTAAA GAAAATCAGA CTGCTGTGGA TGTTTTTCGA AGGATAATTT NGGAGGCAGA 120  
 AAAAATGGAC GGGGCAGCTT CACAAGGCAA GTCTTCATGC TCGGTGATGT GATTCTNCTG 180  
 CAAANCCTGA GGACACTGGG AATATATTCT ACCTGAAGAA GCAAGCTGCC CGTCCTCCTT 240  
 GAGGATAACC TATGCTNCTT TTTNCTCCTG TTAACCTGNA AGATATCATT GGGNTCAGAG 300  
 CTCCCTNCCT TCAGATTATG TTACCTCTGA GTCTGTCCAA TGAGTCACTT CCATTTCAA 360  
 TTNNNNGCAT CNNTTNCAN TGTGTATGTN GNATN 395

45 SEQ ID NO:5482

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS06521

55



## SEQUENCE DESCRIPTION:

GATCTTCCAG AGAAGGGAAC ATCTGTCACA GACAATGACT GTATCTGTNT AGATATTTCT 60  
TATTTAATAA AGACGATTG TCAGTTAAA 89

SEQ ID NO:5483

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06522

## SEQUENCE DESCRIPTION:

GATCAGAAAT GCCTCCTTTA CCTACCAGAG CCTACAACAC TACCTGCCAC TAATAGTTAT 60  
GTCAACCCTCT TATTAATCAT CATCTAGCCC TAAGTCTGGN CTATNAGTGA CTACAAAAGA 120  
TTAGCTGAGT GAATAAA 137

SEQ ID NO:5484

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06523

## SEQUENCE DESCRIPTION:

GATCAGGGGA AGAATACCAA CCTGCATAAG TGTACTAANT CTACGTCTGG TTAATGTATG 60  
TACTCTCCTG GACTGAATGC AGTGTATAAT TCCTGTCTAC ANTAGAAGTG TGCCCCAGTT 120  
CCACATTTGA TTACACATGT GAGATTTGCT GCTGTTGCAT ATAACACTAG GNTAATAGNT 180  
TTGNATNCAT GCAGTCATAA AAATTGGAAT GAGAATTAAN CTGCAGGAAC ATTTGNACGN 240  
TNTCTNCNCN 250

SEQ ID NO:5485

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06524

## SEQUENCE DESCRIPTION:

GATCAGAACC AGAAAGAACT NTGCTTNACC GAGAAAATAT CTAAACATCG AAAAAGTTAA 60  
ATATTATGGA AAAAAACAT TGCAAAATAT AAAGTAANTA AAAAAAGGAA GGANCNN 117

SEQ ID NO:5486

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06525

## SEQUENCE DESCRIPTION:

GATCTAATGC AGGATGTCAG ACTTNTNTCT ATCCAGGAAT AAAACCAGTT ATGCCAGAAG 60  
TAACTATTAT NCACCTNTCT CCTACTGAAT TAAATACTA TCAGTTGTAT ATNAAATN 118

SEQ ID NO:5487

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06526

SEQUENCE DESCRIPTION:

GATCACAGTT TTCAGCANNT CAGACATGGT CTTGNGTAGT TGTTCACAG TGTTTGCCAG 60  
CTACAGAGGA AANGNCAGAC TCACAGAAGG GTGTCATTTA GAAGAAAGAA CACTAATN 118

SEQ ID NO:5488

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06527

SEQUENCE DESCRIPTION:

GATCCTCAAC GAAATCAATC TCACAATAGG NAAGGAAAAG NCAATACAAG GAAGAAACCA 60  
TTGAGAAGAT GCAGAATAAA GTAATCTTAT ATACANGCTT TGATTAAAC TTGAAACAAA 120

SEQ ID NO:5489

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06528

SEQUENCE DESCRIPTION:

GATCGCCATC ANTTGGGTAG TGACAGNGTA TTAATTTGCT TATACANTTN CTTTACTNTC 60  
CTTTTTTCCT TTCTGGAGCA TCACATGCTG GTGCTGTGTC TTTATAATGT N 111

SEQ ID NO:5490

SEQUENCE LENGTH:422

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06529

SEQUENCE DESCRIPTION:

GATCCTACAG ATACAAGTTG CTAAANGGGC ATATCAACAG TCCAACAAAT AAAGAAGATG 60  
CCTGGATTGA GCATGATGTT TGGAGATGGA GATTTATGTG TCTCTGGGAT TGTGGGTTGG 120  
ANTACTGGTC TGTGGCTGTN ACANCTATTC CTCGTGAGT GACTCTTGCA TGGAGAGATT 180  
CATATATTCA GGCAGCTAGG ATTGTTTCCTT CTA CTGTTGAC ATACACGATT GANTTTNCTG 240  
AATANGGGTA GTTAANCATT GTATGTTACN CNCACITTTG TGCTTTTCCT CCATTGTGCC 300  
NTATTAACGC TCTTTTCGNT CTGNGAGAGT CTGAGTTAGC TGGTGGAGCG CCAAATACAA 360  
CTGGTTGTCC GTGTGTNCTT TCCCTTTGTC ANTGGTTTGC CACATCAGTT TGTGNTGTAT 420  
GN 422

SEQ ID NO:5491

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06530

SEQUENCE DESCRIPTION:

GATCCCCCAG ATACCAGCTC TTCTGGNTAT ACACAGACCA GCTATAATTN GCTAAGCATA 60  
AANTATTNCA GTGTATTAGC CAGCNGTGGC TCCAGAGTCT GTGCCCTTGA CCACCGTGCC 120  
CAACTGTTTC ACATGCTGTG TTTGGTAGTT TNNCCTAGTG CTCTCCTTAA TAATGGTGGT 180  
GTNTAGCAAA NN 192

SEQ ID NO:5492

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06531

SEQUENCE DESCRIPTION:

GATCATTAGG TCAGAGTTTA CAGCNCCTCT CGTCACTAGA ATCCACCCAG CCCACGAATC 60  
ATCACCCNCT TGAAGGACAT TATTACTACT GNAANTTNGA ACAAACNT 108

SEQ ID NO:5493

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06532

SEQUENCE DESCRIPTION:

GATCCATCCA GAACAGCGGT ATCTGAAGCC CAGGCCATAC TCCCTGCCTC CTTNCTTCTG 60  
CCTACCAGAG GCTCCANAGT TGAGCTTGTC CNTTATCTAG AAACATGTGA AGATGCCCAA 120  
GAGCCTGGAG GCACTGCTGT CCTTCCTNCA GAAACAGTTT CTCCTCCTNC CCTCAGCCTT 180  
GTGGCCANTT CCNCTTCACA TGAAGCCCCT TGGCATTTC TNGGGAAGGG ACTNGCCTGG 240  
TACTTGCTGT TAGGGCAGGA AGGGGCAAAN GGNNGACTTT GGGTAAGTAA TCTGGGGGGT 300  
TTAGATGGGN AGCANTAAGC CAGCTNGGN 329

SEQ ID NO:5494

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06533

SEQUENCE DESCRIPTION:

GATCATGCTT GTTNAGGCA ATCATGGTGG CATCACCCAT AAAGGGAACA CATTAACTT 60  
TTTTTNCCTA TATTTTAAAT TACTACANGA TTATTAAAGA TAAATNATT TGA AAAA ACTC 120  
TTAAA 125

SEQ ID NO:5495

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06536

SEQUENCE DESCRIPTION:

GATCATGAGA CTGAAATTGG TCAGAATTGT GTCCAGAATG TGCTCAGCTA ATTCAGTATT 60  
CTTCCCCATT CTGGGTTGGA GTTTACTGCA GAGTAATTCT TACAGTGCTG ATGTCAAGAC 120  
TGTTACTGTT CTTGACTTTT GATTCTTGC TCATGACATG AGTAGGGTGT GCTCTTCTGT 180  
CACTTCACAC AGACCTTTTG CCTTTTTTAG CTGCAAGTCA AGGACTAGGT TGATGATGCN 240  
CATGACCTGT AATTGTAAAG ANGCTTGGNC ATCTGCAAAT GATATTNAGA CCATCTNGGC 300  
TTGTGCTTNN ATTCAAATA ATGTGAACCA ATANGTN 337

SEQ ID NO:5496  
SEQUENCE LENGTH:194  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06537

SEQUENCE DESCRIPTION:  
GATCCATGAT GATAATTAAG AGAAGAGAAA AAAAGATATT ATTTTGTNA GGACAAACCA 60  
TTGTAGGTTT TTAGCAATGT GTATCTGTGT GTCCCTCACA CCTTTTCTA TTCTACTTTT 120  
TTTTCTTTT TTTAAAAATA TTATGTACTA TATTTNAGT CTCAAACACA CTATATATTA 180  
TATATNTNNN NNNN 194

SEQ ID NO:5497  
SEQUENCE LENGTH:207  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06538

SEQUENCE DESCRIPTION:  
GATCATTCTT AGGCAAAATT GTGAAGCTAA TGACCAACCT GTTCTACCT ATATGCAGTC 60  
TCTTTATTTN ACTAGAAATG GGAATCATGG CCTCTTGAAG AGAAAAAAGT NACCATTCTG 120  
CATTTAGCTG TTTTCATATA TTGCATNTCT GTATTTTTTG TTTGGATTGT AAAAAGTTCA 180  
CATAATAAAC GATGGTTGTG ATGTAAA 207

SEQ ID NO:5498  
SEQUENCE LENGTH:320  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06539

SEQUENCE DESCRIPTION:  
GATCCAAGTG ACCAAAGGAG TTCAAGGCC AAAATTTAGT TATGCTGGAT TAATTCTGAG 60  
AGTAACAAGC ACATAGATTA TAATCTAAGA AAACCTTTG TAGCTATGCA TNGTCGGGAG 120  
AGCATCTAAC ACTAATGGTG ATGTTTCCCA TGCAGAGACT CAGATTACAG TGACTCTTCC 180  
AGTGAAGACA GATGAAAGCC ATTGGGCATT GTNCCTTTNT TAATCCAAGC TAAACTANCC 240  
AAGGATATAG GGGTGTGTAT GTGTCTGNGT GTGTGTGTTT GTNTGTGTGT GCACATACAT 300  
NTNTAGGTAT GGTGTTTGGN 320

SEQ ID NO:5499  
SEQUENCE LENGTH:115  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06540

SEQUENCE DESCRIPTION:

5 GATCTGTCTT GGTCTTTGT GTTATAAAAC CAAAGTTCTC TACAGACTTT ATTTTGTAC 60  
AATATCATTT TGTAACTTT TACAAATAAA AACTCATTTT TATTGCTCTC TGAAA 115

SEQ ID NO:5500

SEQUENCE LENGTH:314

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06541

SEQUENCE DESCRIPTION:

15 GATCACTTAC GGAGAAACAG GAGGAAATAG CCCTGTCCAG GAGTTCCTG TGCTGGGTG 60  
CAAGTCTACA GCTACCATCA GCGGCCTTAA ACCTGGAGTT GATTATACCA NNACTGTGTA 120  
TGCTGTCACT GGCCGTGGAG ACAGCCCCGN AAGCAGCAAG CCAATTTCCA TTAATTACCG 180  
AACAGAAATT GACAAACCAT CCCAGATGCA AGTGACCGNT GTTCAGGGNA GCAGCATTAG 240  
20 TGTCAAGTGG CTGCCTTCAA GTTCCCCTGT TACTGGTTAC AGNGTANCCN NCGCTCCNA 300  
AANTGGGCCA GGAN 314

SEQ ID NO:5501

SEQUENCE LENGTH:312

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06542

SEQUENCE DESCRIPTION:

30 GATCTGGGTT TAGAGTGTGT ATGATTAATA AATATACCTT TCCTCTTTTC AGGGAAAATA 60  
ACAACCACCC NTAAGTATAG TTGGGAAAAG AAGATTGGGT TATTTNCCA TATCATTTAG 120  
CTGGAAGTGA CATTTAAAG CACCCTGCAT CACTAGTAAT AGTGTATTN NCTATTCTGC 180  
CCTTGTAATC GGTGTCCCTG TAAAACANTC CCCACAGATT ACTTTCAGAA ATAGATGTAT 240  
TTCTCTNCGT AAGGGCCAGG TTTATTTCTT CCTTTTTTGN GATNNNNGGN GGAAANTGCT 300  
35 GCTTGCACAT TN 312

SEQ ID NO:5502

SEQUENCE LENGTH:217

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06544

SEQUENCE DESCRIPTION:

45 GATCATCCTG TAAACATTTT ATCATGTATT AATCATCCCT GCCTGTGTCT ATTATTATAT 60  
TCANATCTCT ACGCTGGAAG CTTTCTGCCT CAATGTTTAC TGTGCCTTNN NTTNGCTAG 120  
TATGTGTTGT TGAAAAAAA AACATTCTCT GCCTGNGTTT TAATTTTGGT CCAANGTTAT 180  
TTNAATCTNG TACAATTAAG AGCTTTTGCC TATCAAA 217

SEQ ID NO:5503

50 SEQUENCE LENGTH:334

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06545

SEQUENCE DESCRIPTION:

GATCAGGTTG AATGAATGGA ACTCTTCCTG TCTGGCCTCC AAAGCAGCCT AGAAGCTGAG 60  
GGGCTGTNTT TGAGGGGACC TCCACCCTGG GGAAGTCCGA GGGGCTGGGC NAAGGGTTTC 120  
TGACGCCAG CCTGGAGCAG GGGGGCCCTG GCCACCCCT GTTGCTCACA CATTGTCTGG 180  
CAGCCTGTGT CCACANTATT CGTCAGTCCT CGACAGGGAG CCTGGGGCTCC GTCCTGCTTT 240  
AGGGAGGCTC TGGNAGGAGG TCCTCTCCCN NATCCCTCCA TCTTGGGGCT CCNCCAACCT 300  
NTGCACAGCT CTGCGGGNGC TGAGATATNA ATTN 334

SEQ ID NO:5504

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06546

SEQUENCE DESCRIPTION:

GATCTTTTAA AGGTTTTNAC CATTTTGTNA TGAGGAATTA TACATGTATC ACATTCACTA 60  
TATTAATAATT GCACTTTTAT TTTNAAA 87

SEQ ID NO:5505

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06547

SEQUENCE DESCRIPTION:

GATCCATCCC ATGATTTGTN CCTGTCTGAG GCATAGAGGC AGGCAAGCCG TGGATTTTNC 60  
ACATGGTGAC TTTCCCACTG TGCCATGATA CAGTGTGCAT CTTATAGCAG TGCCTTTNTG 120  
TCAGGGTCTC TGCTGGCAGT CTAGACCTTT TGGGCAGAAA GGAGCTTCAA ATGGCTGTGA 180  
TAAGGAATAT TAAAAATNGT GTTTCTACTT TAATTGTATT GGCTGTTCAT GTATGTAGGA 240  
GTAAAAATAG GCCAAACTGG AGAAATAAGC GCATTCTGTC CACCANAAAN GTGGNTTGGN 300  
TGGTNNNTGT NNGNTTNGGN GGN 323

SEQ ID NO:5506

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06548

SEQUENCE DESCRIPTION:

GATCAAGTTG CCATGAAAAA CCATCTACTA TATGTNAGAC ATGACATTCT NTTTCTCTCC 60  
TTCCTGAAAA ATAAAGTGTG GGAAGAGAAA 90

SEQ ID NO:5507

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06549

SEQUENCE DESCRIPTION:

5 GATCTTACTT TCTTGCTGCT TTTCCAACTA TAATCATTTT GCTCTTGCTT TAACAAAAGN 60  
NGNGGCACAG NAATTTAGTA AATTTGTGTA ATAACATTTA AA 102

SEQ ID NO:5508

SEQUENCE LENGTH:64

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06550

SEQUENCE DESCRIPTION:

15 GATCTCACCA CTGCACTATA GCCTGGGCGA CAGAGCAAGA CTCCCCTCC AAAAAANGGA 60  
GAAA 64

SEQ ID NO:5509

SEQUENCE LENGTH:360

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06551

SEQUENCE DESCRIPTION:

25 GATCCACAAA TCGCTAGGAA TGTGTATACT CTGGGTAGTA AGTTTGTAGT ATTAGAAGGT 60  
TTAATGACAA GTATTTGAAG AGCTGAAGTT AAGTGTGGG AGGCCATCCC TTATGAAGGA 120  
CAATGAATGG CAAGTAAAAG ACCAAGTTCT GTTCCTGGGT CCATTAATTT AGTAAAAANG 180  
GCAAAGTTCT TTCAGCACAC ATATCTGCAT GCAGTCACGT GCTGCCTAAG GNTGCTTCAT 240  
TCAACANTGA GCCTCACAGC CGTGCTACAC ANTAGGATAN TACTGTATTT TTNCTGTACC 300  
30 TTTTAACATT GTGTTACAAT GGCCTACAAG AGGCTTGTGT GGNTGGCTTT NNNTGTGGGN 360

SEQ ID NO:5510

SEQUENCE LENGTH:357

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06552

SEQUENCE DESCRIPTION:

40 GATCATCCTC ATTAGCACAC AGATTTTNAA AAATCAATTC TCTNGCCATG CCTCCTATGT 60  
GTTACATCT CTGCATACAC TACAGATATA AGTGCATAAT CATTATATA NACATCTGGT 120  
AGGTATTCTG TAAAACTGTG TTTACTTTAG TGCATGTNAT TGTCATGTNA TGATGTGACT 180  
GGGGTGTTTC TTTGTGCATG AAACCTTTGCT TCTNCACAGA NTTAGATTAC TGCTCTCTCT 240  
ATATNGANCT NCATATACAG CGTTTTCTTG TTATCAGCCC CCCNAAGTCT GGGATGCCCG 300  
45 GTGGTTGGTG NTGACATGTG AGTGGTGNC TGGGNGGTCT GNTNCACATA GGGGCNN 357

SEQ ID NO:5511

SEQUENCE LENGTH:138

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

CLONE:HUMGS06553

SEQUENCE DESCRIPTION:

5 GATCTTTTCA GCTGCTATTT TGAATAATG ACTATCATAT ATCATAACAG TGA CTGATGT 60  
TGGTTGTAAT GGTGGGTTT AGGATGAACC ATTTAAGGA TGCCAAATNA AATATTAGTA 120  
TTGTACACA GTAAGAAA 138

SEQ ID NO:5512

10 SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06555

SEQUENCE DESCRIPTION:

15 GATCCCAGCA GGGNTTCTGC TCTGGGGCTG GCAGGTTGCC TGGTATTATG CCCAAGGNCG 60  
NTCTGCCTGG GGGAAAGGGC AGCCAGGCAG AGGCCAGTG TCTAGTAGGC NGCTGAATTT 120  
CCTGGAAGGG GTGATTGGTT GGAAAGNGGN CAGNAACCCC AGCCTNN 167

SEQ ID NO:5513

20 SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06556

SEQUENCE DESCRIPTION:

25 GATCCCTTGG AGCACCTNA TGCCTGGGGT TTCTCTCCCT AAAGCTTCTT GCAGTCTAAG 60  
CCTTATCCCT TATGTNCCCC ATTAAAGGAA TTTCAAAGA CATGGAGAAA NTTGGGAAGG 120  
TTTGTNCTGA CTGCTGGNNG CAGAATAGCC GTGGNAGGN 159

SEQ ID NO:5514

30 SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06557

SEQUENCE DESCRIPTION:

35 GATCTGGACA AATGGCAAAT AATTTGGGGT TGAATTATGG CCCAGAGAAG TAAGCAAATG 60  
NAAACTAAA CANTTATAAA TGTATCTGGG AAGCAAAGGT ATTCATANTA NGTCCCATGG 120  
CCAGCTGCGA GCAGTATTTA ACTAGACATG CTGTTGTCAA TANNNNN 167

SEQ ID NO:5515

45 SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06558

SEQUENCE DESCRIPTION:

50 GATCGTCCCC CTTTNTGGGC TGGAAAAGCA GGTGAGGNTG GGGTGGGCTG AGGCCATTNC 60  
CGCCACTATC TGTTTAATAA AATCCGTGAG CACGAAA 97



EP 0 679 716 A1

SEQ ID NO:5516

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06559

SEQUENCE DESCRIPTION:

GATCCTCCGG AAGTAGTCTC TNCCCTCGGC AGCGGAAATA CTGATTCCCA CTGCTCCTNC 60  
CTCTAGGGTG CAGTGTCCGT ACCTNCTGGA GCTGGNCCCT CCTTCCCCAN CCCAGACATT 120  
GAGAACTTG GGAAGAAGAG AGAAACCTNA AGCTCCCAA CAGCACGTTG CGGGAAAGAG 180  
GAAGNGAGAG TNTGAGTNTG TGTGTGNTT TTTCTATTG ANCAN 225

SEQ ID NO:5517

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06560

SEQUENCE DESCRIPTION:

GATCATTAAAT AAAGCTTTTC TTGGTTCCTT CAGTGGTGTT GGTAGTAAAA TGGAAGNGT 60  
CTTGCTGCAG GTAACATAATG AAGANGTGGT CAACCACAGA GTCTCAAGA AATAAGAAAT 120  
TCTGTACCAN CTGAAAGTAG TGCTTGTTGG TGCCTTCNTT TAAAAAGCAC TCTTTTAAAT 180  
AAAAGGGAAA TGTTTTCTGA TAAACCAAAC ATTTAGTTGA GGTTCCTGAT ATAAACATT 240  
TACAANNTGA GTGTTGTNTG TAAAGCAGTA GCCNTCATT TGGCTAGNG AGNTAAATGN 300  
GTCANGTTTT ANCTAGGTTT TNGTGAGTNG NCAGGTTTNN 340

SEQ ID NO:5518

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06561

SEQUENCE DESCRIPTION:

GATCAAAGCC AGTNTTAAAT GGGAGACCGA GCGAGCGCGG CAAGTGCTGG AACACCTGCT 60  
GAAGGAAGGG TTGGCGTGGC TGGACTTACA GGCCCCAGGG GAGGCCCACT ACTGGCTGCC 120  
AGCTCTCTTC ACTGACCTCT ACTCCCAGGA GATTACAGCT GAGGAGGCCA GAGAAGCCCT 180  
CCCCTGACTG CATGTGGAAG GGCACACAGC AGCAGGCAGG GAGGAGGCGG AGGTGGCAAA 240  
TAAACCTGGG CAATTTTGT TATACAAAAA ATAGAAGAAA AGTTCCAAGT TTTTCTTTCT 300  
TCCCTCATT TTTNTTTTTT GAAAAAAGAN 330

SEQ ID NO:5519

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06563

SEQUENCE DESCRIPTION:

GATCTCATGA TGATTANAC CACAGNCTGG GNTAAAGATG TCTTGACCTC TGAGGCTAGC 60  
ATAACATATA TNAGAATACA NCTTGCCTAT TTCCAGAAAA TCTGTATATT N 111

SEQ ID NO:5520

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06564

SEQUENCE DESCRIPTION:

GATCAGCTTA CTGAAAAGAA GCCTCCNNAG TATTCCAAAT ACAGATTACA TCCAGCTGCT 60  
TAGTGAAATT GCCAAGGNAC AAGGNTTTAA TATAACATAT TTGGATATAG NTGAACTGAG 120  
CGNCAATGGN 130

SEQ ID NO:5521

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06565

SEQUENCE DESCRIPTION:

GATCNACAAT NTGAATATGT GTTACTTAAT AAGGCTAGGC TGGCCATCAG TNGCTTANTT 60  
CAGATGTGTC ACTAAATTC CCNTCTAGAT GGTCTTGAG CAAAACCTAA TAN 113

SEQ ID NO:5522

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06566

SEQUENCE DESCRIPTION:

GATCATCACA GTTTGAGTTT GACCCCAATG CCAGGATGGT GACACACATA TTAAAGAGTA 60  
ACAGCTGGTT ACATTGCTAG GCGAGATAGG GGGAAGACAG ATATGGGTGT TTTTAATAAA 120  
TCTAATAATN ATNCATCTAA TGTATTATGA GCCAAATGG NTAATTTTTC CTGCATGTTC 180  
TGTGNNTGTN GAAGATGAGC CTTGCAGATA TCTGCATGTG TCATGNNGAA TGNTTCTGGA 240  
ATNCTTNACT TGCTNTTGA NTTGCACTGG N 271

SEQ ID NO:5523

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06567

SEQUENCE DESCRIPTION:

GATCTCACTT TCCCCTTGTT GGGTAGGAAC CGATGCCAGT GGGAGGGATG TGCCCCTGAC 60  
CATTACGAC TGTTTTTTTT TTTTTTTTAA AAAAAATGGN GTTNTTGGGN GGGGNAATNC 120  
ACANAN 126

SEQ ID NO:5524

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06569

SEQUENCE DESCRIPTION:

5 GATCACGGGA ATGCTGCTGG AGATAGACAA CTCTNAGTTG CTGCACATNT TAGAGTCCCC 60  
CGAGTCTCTC CGCTCCAAGG TGGATGAAGC TGTAGCAGTT CTACAGGCTC NTCATGCCAA 120  
GAAAGAAGCT GCCCAGAAGG TGGGCGCTGT TNNNNN 156

SEQ ID NO:5525

10 SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06571

15 SEQUENCE DESCRIPTION:

GATCCTTCTA GACCAAGGAC CCATTGTAA AAGCATGGAT TCTGCCTGAN TTACTTCCCT 60  
TTTGAGAAAT CATATCTCAA ATACATAACC TGGTAATATA ACTGAAAAA TAAAAGTGAT 120  
TGCTCCTTCC AAA 133

20 SEQ ID NO:5526

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS06572

SEQUENCE DESCRIPTION:

GATCCCTGCT TCATAGATTT GCATCATTCA AGCATATCTT GTAAAACAAA CACATATTAT 60  
GGGACTAGGA AATATTTATC TTTCCAAATT TGCCATAACA GATTTAGGTT GCTTNCCTTN 120  
CITTGAAGGA AAGTTTAATT ACATTGCTCT NNNNNN 156

30 SEQ ID NO:5527

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS06573

SEQUENCE DESCRIPTION:

GATCCTAGCT GCAGATTGCA TCCCACAATG CGAGAATAAT AAAATAAAAT TNGATATTNG 60  
AAA 63

40 SEQ ID NO:5528

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS06574

SEQUENCE DESCRIPTION:

GATCNATGGT GTGACTCAAG CTCNCCTTA CCCAGGGGGG GTAAGGGCAG GCCTCTAGCT 60  
ACTTGGAGTT GTCTGTAATA ATCTNGAAAG GCCCAAGGGC CTGTGCCCAT CCTGACTNAA 120  
AGGNATCTCC TTCCCTGTTT CATATCACAT GACAGAGAAA CCTGTTCTCA TGGCATGNAA 180

55

CATCCCTGTN AAGAGAGCGT TGNCNNN

207

SEQ ID NO:5529

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06576

SEQUENCE DESCRIPTION:

GATCTTGCAC ATGAAGCTAC AAAACTGGTA AGAAACAAAT GGCACATGTG NTGGGAATGG 60  
 AAGTCAACCT TTTTGAATTT TTCAAATGTA AGTCAGTCTG GAAAATCCCA GTAAATTGGT 120  
 ATATTTGTTT TGGGTTATTT TTGAAGACCT CTTTAAAAAT TTGCCTAAAA TAAATNCTCG 180  
 GTATGCTAAA 190

SEQ ID NO:5530

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06577

SEQUENCE DESCRIPTION:

GATCCGCCGC CAGAAAGGTT ATGCATCATG TGCCACAGCC TCCAAGGTGC CCATCATGGA 60  
 ATNTCGTGGG GGCTGTGGGC CNANTGCTGC CAGCCCACCC GCAGCAAGCG NCGGAAATAC 120  
 GTCTTCCAGT GCACGGNTGG CTCCTCGTTT GTAGAAGAGG TGGAGAGACA CTTAGAGTGC 180  
 GGCTGCCTCG CGTGTTCCTA AGCCCCTGCC CGCCTGCNTG CCACCTCTNG GACTCCAGCT 240  
 TGATGGAGTT GGGACAGCCA TGTGGGACCC CCTGGTGATT CAGCATGAAG GANATGAAGC 300  
 TGGAGANGAA GGTAAAGGAG GAAGAGANTA TTANGTATTT N 341

SEQ ID NO:5531

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06578

SEQUENCE DESCRIPTION:

GATCTNTTCC AACAGTTCTN TGTAACCAA ATGCTATTTT TCANTGCATT TGGACTGCTG 60  
 ACCATTTAAA AGCAGCCTAT GATTGCTTCT TTTGTAAAG CAAGCAACCN GCCTCCACTT 120  
 TAGCTGTTTT NACTATNGA TNTN 144

SEQ ID NO:5532

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06579

SEQUENCE DESCRIPTION:

GATCCTAAAA CGAAGAGAAT TTTGACTCTC CAGAAAGCTA ATAGCTGGTT CAACTGCAGG 60  
 AAAAATTGAA CATTACTAAT TTGAATGGAA AACACATGGT GTGAGTCCAA NGGAGGTGTT 120  
 TTCCTGAAGA NCTGTCTATT TCCTCAGTCA TTTTAACTT CTAGAGTCAC TGATACACAG 180

AATATAATCT TATTTATACC TCAAANNGAN TNANANGGGG NNNN

224

SEQ ID NO:5533

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06580

SEQUENCE DESCRIPTION:

5  
 10  
 15  
 GATCTNCCTC NACACCTNGG GCAAAGTCTA TGCGAAGATG GTTCTTAGC TCTCCATTG 60  
 CCATGATTTT CCTCCCATTC ATCATGAGGG AGTTTCTCAA ACCAGGAGTT NATATTTATT 120  
 TNTNAGAAAA TACACACTTT TCAGGAGAAA CCTGAGCATG ATTTTGGATT CTCCACCTCC 180  
 CCCAGTCTC GGNNCTGGG ATTCAGCTCA AGGNTTCAGT GTCTTCATTT TTACAAAAGT 240  
 TCCCCAAGA AATCAGCAAC CAGCCTCTGT TTCATCTGGG AGCCCCTCCC TNGGNCCCT 300  
 GGGTTTGGG GGGTGCTGNC CTA CTACTGGGGG AACAGCGGGG GGTGN 345

SEQ ID NO:5534

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06581

SEQUENCE DESCRIPTION:

20  
 25  
 GATCATNTTG GAACCAGACA AGAATCCAAA GAAAATAAGA ACACAGACCA CCAGTGCAAA 60  
 ACAAGAAAAA GCACCAAGTA AAAAGCCAGT GAAAAGAAGA AAAAGAAGA GAGCTGCCAN 120  
 TTAAAGCTAA CAGTTGTATA TCTGTATATA TAACTATTAA AAGGGATATT TATTCCAAA 179

SEQ ID NO:5535

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06582

SEQUENCE DESCRIPTION:

30  
 35  
 40  
 GATCAAAGTT AAGNTTATAT CCTGTTTGTA GTATCAGATA TNTTCCTGTG TACAATTATA 60  
 GGATTGTAAT CTACACTGGA ATTTNAGGC AGTAAGTCAC CACAAAATGT TTTAGATAAG 120  
 ACACAATAAA ATTATTATAA ATAAAAGCTT AATGTTTGTA AAAANTCTCT TTTTATGAT 180  
 TTCTTTTTTC ACATGNAAGN NGTGGTGGCT GCTAAANAAA NAGCTACAGT GTTTATTANG 240  
 GGTCTGTTTG ATTTNTGTNA NTCTTTGTAA ATTGGTCAGT GCCTGTN 287

SEQ ID NO:5536

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06583

SEQUENCE DESCRIPTION:

45  
 50  
 GATCCCAGAG GCTCTCCTCA CCTCANCTGA GCTCCTTTAA AAGTAATTCA AGGGACTATG 60  
 TCACTCAGCC TCATTNCTG GACCAAATCT GGAGGGAGAA CCCCTAAAAC CCCTAAGTAA 120

GGTTGCCAG GGGGTTGTCC CCAGGTGGGG GGAAGCAGGG GAGAGAAAAT GGTAGCCATT 180  
TTAACATTGT TTTGTATAGT ATTTATTGAT TCAGGAAACA AACACAAAAT TCTGAATAAA 240  
ATGACTTGGA AACTGAAA 258

SEQ ID NO:5537  
SEQUENCE LENGTH:248  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06584

## SEQUENCE DESCRIPTION:

GATCGCTTGA GGCCAGTTCA AGACCAGCCT GGCCAACATG GCGAAACCCG TCTCCACTAA 60  
AAATACAAAA CTTAGCCAGG CGTGGTGGCG CGCGCCTGTA ATCCCAGCTA NTCGGGAGGC 120  
TGAGGCAGGN GAATCGCTTG AACCCGGGAG GTGGAGGTTA CAGTGAGCCA AGATTGCACC 180  
ACTGCACTCC GGCCTGGGCA NCATNGCGAG ACTCTGTCTC AGNNAGGAGG GGGGGGTTNN 240  
NNTANTNN 248

SEQ ID NO:5538  
SEQUENCE LENGTH:198  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06585

## SEQUENCE DESCRIPTION:

GATCCTGAAA GAGGACAAAC TACATTGCCT TTAGACCTN TGACTCAAGA AGAAGATGAT 60  
GACCAAAGGT GATTTGTAAC TTAACATGCC TTNTCCTGAT NTTGAAGGAT TTGTGAAGGG 120  
AAAAAAATTC TNGGCTCTTT GTATATAATA AAATGAGACT ANANGCATTG TNNAAAAAAA 180  
AAAAGATTAA NTTTAGAN 198

SEQ ID NO:5539  
SEQUENCE LENGTH:188  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06586

## SEQUENCE DESCRIPTION:

GATCCCCACA CTTACTCTAC CCTCTNGGCA AATTGGCATT CCGGTGGTGG GTTTGTNTC 60  
CTTTAACACA TTAAATAAAT NAGTATATAG GATGTGAGGG GAGGGGTGAG ANCAACTAGC 120  
TGTAGCATGT NTAGGCTATA TACTTTACCA NTTGACTTCT TTCCTGTTTT TTTTNAAAA 180  
NAAAAAAN 188

SEQ ID NO:5540  
SEQUENCE LENGTH:138  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06587

## SEQUENCE DESCRIPTION:

GATCTGGGTG TGCTCTATGG GGAGTNTCTGA CGTCAAANAG CAAATGTCTA TAAGGGGCC 60

TTTTAAATN AACATTTTCC TCATTGAGCA AGCNTGGATT CTCTAATGTA GAAATCAAGC 120  
CATCTTNATA ATTNCACN 138

5 SEQ ID NO:5541  
SEQUENCE LENGTH:332  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS06588  
SEQUENCE DESCRIPTION:  
GATCCTCCCA CCTCAGCCTG CTGAGTAGCT GGGTCTACAG GTGCACACCA CCATGCCTGG 60  
CTAAAGGCAT GTCTGCATTT ATGCGAGGTG TGTTGACCGG GTGGGGAGGG AGCTAGGACT 120  
GAGATTCCGC TGTNTAAAT GCACAAAAG GGTTCGCTAA GCAAATTGAT ATTTGAACTA 180  
15 AAAGATGGAT TAGGGTGAGA GACTTAGTTT ANTCAGGAAT AGTNGCAGAG NCANCCACAN 240  
CAANAANTGN ATTTCCCTGN GACAGCCGTT TGTACGTACA GCAGGGNNCT GGTTCACAGN 300  
TTTCACGGAG GGNNGNTAGG GTTCTTNTAC TN 332

20 SEQ ID NO:5542  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06590  
25 SEQUENCE DESCRIPTION:  
GATCAATNA TTTGACTATT GCTAGACATT TCTATACTCT GTTGTAACAC TGAGGTATCT 60  
CATTTGCCCA TGTTAATTTT TTTCTAAATA AATTGACAAA AACAAA 106

30 SEQ ID NO:5543  
SEQUENCE LENGTH:268  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06592  
35 SEQUENCE DESCRIPTION:  
GATCACAGCC TCCAGGGCCC CCCAAATCCC AGGGAAGGAC TTGGGAGAGA ATCATGCTGT 60  
TGCAINTAGA NCTTTCTGCT TTGCACAGGA AAGAGTCACA CAATTAATCA ACATGTATAT 120  
TTNCTCTATA CATAGAGCTC TATTTCTCTA CGGTTTATA NAGGCCTTGG GGNTCCAACC 180  
AGGCAGTAAG ANGTGCTTCT GAACCGCAAG GGGCGNACGA CTGGAAGTAA AATAGTTTGT 240  
40 TTTTCNCANT TCGNGGGNAG GGGNNGGN 268

45 SEQ ID NO:5544  
SEQUENCE LENGTH:177  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06593  
SEQUENCE DESCRIPTION:  
GATCCAATTA ACAAATCTG CACTGTGGCA ACTNAACGAN ATTATGCTTT GGACAGCTTT 60  
50 ATGTGTGAAT GTAAGAACAT ATTCTNAAGA AATGCTGTAA CTTTATCCCA TATANCTTCA 120

55

TANGAATTTTC TCTATAGGCT TGGNATTTGC AATAAAAAATA GAGGATATGT TGGCAAA 177

SEQ ID NO:5545

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06594

SEQUENCE DESCRIPTION:

GATCANACAG CCTACANCCA GCGCCGAGTG TGCATCANGG TAAAAGAGCT GAGGGCTCTC 60  
TNCAGGGAGC AGCCCATTTA GGTCTCTGTN GTTGTGTGTA GGGAN 105

SEQ ID NO:5546

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06595

SEQUENCE DESCRIPTION:

GATCATATNA GACGAGNAAG AGGAAGACCT AAAAGTGCAT CTGCCAAAAA ACATGAGGAA 60  
GAAAGTGAGA AACAGGAAAA GGAAATTNAC ATCTATGCTA ACCTGTCTGA TGAAAAGNCT 120  
TTCGTGTTTT CAGTCGCCTT NGCAGCNNN 149

SEQ ID NO:5547

SEQUENCE LENGTH:411

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06596

SEQUENCE DESCRIPTION:

GATCAGTGTG AGTCCTGAAG CACTTTNAGN GCTGTGNGAA CGACATCCAC TTTGGGTTTC 60  
ATTGTTTTGT AAGCAGAGGA GCTGTCAGTC ACTCGTGCTT GTCGGTGGCC TCTGAGCCAT 120  
GGTGTGAGT GAAGAGTAGT TCTTGTGTTGT TACAACCTTT GTGAGTCAGC CATGCCCGCA 180  
AAGCGTGCTG TGTTTTAGTC CTGGTAGGAA TATTTATNAG AGTTCACACT ATGTAAAACC 240  
CAACNGCTTC ANCTATTGCC CTTTCAACAG TTTTGCCACT GACCGGATAG AACCGGTTTC 300  
AGTCTCTGGA TGGGTGTGTT TGGTGGGTTT GTAACCATG ACGGGTTTAA ANCCATGGGT 360  
TTNAAGATTT GGCCCAAATA ACCAGNAATT TTGTTCCGGG GAGGGGGTTN N 411

SEQ ID NO:5548

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06597

SEQUENCE DESCRIPTION:

GATCATAAAA GGCTATTATC TATNCTGGGG AACGATTATA ACTTAAATAA TTATTTTAAT 60  
AAAAATACTA AGCTNNAAA 79

SEQ ID NO:5549



SEQUENCE LENGTH:102  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

5

CLONE:HUMGS06599

SEQUENCE DESCRIPTION:

GATCATCCTG CAAGTGCTCT NGTGCCTAGG ATTCATCTTT CTTTTCACCG TAGGCCCTGA 60  
CTGGCATTNT ATTAGCAAAC TCATCACTAG TCGTNGTNCT NN 102

10

SEQ ID NO:5550

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS06600

SEQUENCE DESCRIPTION:

GATCAAAACG ACGAAGAAAN GNCNCANAGA CTCAAATAAG GACAGAGTGA TTTCCAATAA 60  
TGTTCAATAG ATTTAGGAGC AGAAATGCAA GGGGCTGCAT GACCTACCAG GACAGANCTT 120  
TCCCCAATTA CAGGGTGACT CACAGCCGCA TTGGTGACTC ACNNNN 166

20

SEQ ID NO:5551

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25

CLONE:HUMGS06601

SEQUENCE DESCRIPTION:

GATCTCAGTT TCAAATCTCC CCAAGCTGCC TAAATTGAAA AAGCTTGAAC TCAGTGAAAA 60  
TAGATTCTTT GGAGGTCTGG ACATGTTAGC TGAAAAACTT CCAAATCTCN NACATCTAAN 120  
CTTAAGTGA AATAANCTGA AAGATATCAG CACCTTGAA CTTTGAAAA AGTTAGANTG 180  
TCTGANAAGC CTGGNCCTCT TTANNTGTGA GGTNCCAN 219

30

SEQ ID NO:5552

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35

CLONE:HUMGS06602

SEQUENCE DESCRIPTION:

GATCTCTTNG CGACAGTACC AAGCACGGTT CTCTACACAG GTGACTNAAG TTGCCTCTGT 60  
GTTGGCTGGC ATCCCTGAGT CCCCTNCGGG CTCCTATGGA NCNN 104

40

SEQ ID NO:5553

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45

CLONE:HUMGS06603

SEQUENCE DESCRIPTION:

GATCATCTGA GCCTCAGGAG GTTGAGGCTG NAGTGAGCTG TGACTIONGCC ACTGNACTCC 60

50

55

AGTCTGGGAC AACAGAGCAA GACCCNGTCT TAAA

94

SEQ ID NO:5554

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06604

SEQUENCE DESCRIPTION:

GATCTCCAGC TGCACAGGCC ACCGNCCCAG GGCCTGGCCG CTGTTACAGA AACAATAAAC 60  
CCTGATGGGC ATGGCAA 78

SEQ ID NO:5555

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06605

SEQUENCE DESCRIPTION:

GATCGTAACA ATGCCAAGAA GACACAAGAA TATGAGAAAG GAATTCCTAG AAAAAAGGCA 60  
AAGGTTTCAA TGAATAAGCT AATTTTNCCT AAGTCTACTG ATAACATACT CCCTACCCCA 120  
TCCTCCATTA ATAAAAGANT GGTGTTGTA TTGTATTATG AGGGAATTAA AAGTGTGATA 180  
NGANANNNNN N 191

SEQ ID NO:5556

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06606

SEQUENCE DESCRIPTION:

GATCGGAGAA TTGTGTAGGC GAATAGGAAA TATCATTTCGG GCTTGATGTG GGGAGGGGTG 60  
TTTAAGGGGT TGGCTAGGGT ATAATTGTCT GGGTCGCCTA AA 102

SEQ ID NO:5557

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06607

SEQUENCE DESCRIPTION:

GATCTCACTT CTGTCAGATG CTCCCATCCA CTATNAATGC ACTAGGTGGG AGGAGAGGGC 60  
GGCAATGACA CTGCACCTCT CCTTTCCAC CGCATTCCCT GGAGCTCCCT AAATAAAACT 120  
TTTTTTAACG TGA 135

SEQ ID NO:5558

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06608

SEQUENCE DESCRIPTION:

GATCAAGTAA AAATGCAAAT CAATGATGCA AAGAAAACAG AAAAGAAAAA GAAGAAAAGA 60  
 CAGGATATTT CTGTTTCATAA ATTAAAGCTG TAATATATTT NNANTATAAT GTAAATATTA 120  
 ATGTGTAAGC TTATATTGTG TCATTGTNCT GTTTATAAT AAAATNCTTG AGAACCTTCA 180  
 AA 182

SEQ ID NO:5559

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06609

SEQUENCE DESCRIPTION:

GATCTTGACC TCACGGTGTA AGAAGGGAGA GGATGGTTTC TCTTCTGCCC TCTCCCATGG 60  
 TGCCCGTGCC TCTNTGCTGT GTATGTGAAC CACCCACGTG AGGGAATAAA CCTGGCACTA 120  
 GGAAA 125

SEQ ID NO:5560

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06610

SEQUENCE DESCRIPTION:

GATCTTTTGA GATACAATCC TTATTTAAAA AGGAGAAGAT AACTGAGGAT TTAAAAAAGA 60  
 AGCCATGGAA AAATTCCTA GTAAGCATCT ACTTCAGGCC AACAAGGTTA TATGAATATA 120  
 TAGTGATAG AAGCGATTGA AGTTACAATG TTTTATGGCC TAAATTATT AAATAAAATG 180  
 CACAAAACCT TGAAA 195

SEQ ID NO:5561

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06611

SEQUENCE DESCRIPTION:

GATCTTGTGC TCAACATGAT NCNTTAATAG AAGTTTTATN TTTCNGTGCA CTCTGCTAAT 60  
 CATGTGGGTG AGCCAGTGGA ACAGCGGGAG ACCTGTGCTA GTTTTACAGA TTTCCTCCTA 120  
 AATNNCGCGG N 131

SEQ ID NO:5562

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06612

SEQUENCE DESCRIPTION:

GATCTAATAG CTGAACTGAT TCAAACGTGA ATAAGCTCAT CAATTCANT TCTATGAAAA 60

TGTGCTCTGT TGTCACAGGA TGTTTCTGTT GGTTCCTTTC ATTCCTGGG AATTGGTAAA 120  
CATCATGTTT CNGATGATAA CCCAGTAGCA AAANCATTG TNCTGTGTGG TACAAGCCTT 180  
NGGGACTGNN AAANAN 196

SEQ ID NO:5563  
SEQUENCE LENGTH:307  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06613

SEQUENCE DESCRIPTION:  
GATCCCATAA TATAATCAT ATCCTTTATA TTNAGAATA TCTCAAATGT ATTCCTTTTT 60  
TGTATGGTGG GTTTGCCTAG GGACGTGTAA CTACAGGCTT TACTAAGCC AAGGAAAAAG 120  
AGAATTTTNC TTTTCATCTT ACAAATTCCA GATATCTACA AANGNTGTGA AAGCACTAAA 180  
AGNGNNGNTT TTAAGCAGTA CTTTACCTGT TTTTCCTTTA GCAAACCAGG TTATGTGGTG 240  
TAAAGGTTTG TNATACGTGC CACAATATAG CATATAAATG TTATGCCATC ATTCCTTCTC 300  
TTGTTAN 307

SEQ ID NO:5564  
SEQUENCE LENGTH:188  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06614

SEQUENCE DESCRIPTION:  
GATCTATACA TGAACAGCAG AATGTATAAG CTAGCATTTA CTAGCATGTC TCTNATACTT 60  
TTGTNCATTT CTGTTAATCG TCATTTCTGT CCCCTCTGCA TGGAATTTNA TACTTGTCTA 120  
GGGTAAGAGT TTGTAGACTC TTTTCAGCAGA ACAGATTTTA ATAACCAATT TATNTGTTTT 180  
ATTTTAAA 188

SEQ ID NO:5565  
SEQUENCE LENGTH:178  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06615

SEQUENCE DESCRIPTION:  
GATCAGCACA TCCAAAAACA CCAAGACAAA CATCCATGTG GAGCAGAACC TNTCCTGCCT 60  
CGGGAGTTCT GACCAGGTTT CCCAGCAGGG TGTTAAGCCT CTGTNTCTGG CCCTACCAGC 120  
ATNCGGGTTC CACTTTTCCT AGGAGAGNGT GGAGATGGGN NGACAGGGAA AGGNNGGN 178

SEQ ID NO:5566  
SEQUENCE LENGTH:104  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06616

SEQUENCE DESCRIPTION:  
GATCTATCAT TTTAATTGAT TCTGAAGCTT GTATTAAAAA CTAGGCAATA NCATCATGGG 60

ATACATAGGA GANGGCACAT TTTACAATCA TNCATTNTGG CCNN

104

SEQ ID NO:5567

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06617

SEQUENCE DESCRIPTION:

GATCTGCTGA CAAAACCTGG GAATTTGGGT TGTGTATGCG AATNTTTCAG TGCCTCAAAC 60  
AAATNTGTAT TTAACCTATG TAAAAGATAA GTCTGGAAAT AAATGTCTGT TTATTTTGT 120  
ACTATTTAAA 130

SEQ ID NO:5568

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06618

SEQUENCE DESCRIPTION:

GATCATTTAA CATTCTGTGT ATGTAACAAA ATATCACATG CATAAATATT ATGTATCAAT 60  
AAAATTTTTT AATGGGCAAA 80

SEQ ID NO:5569

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06619

SEQUENCE DESCRIPTION:

GATCCGGTCA CTGCACTCCA GCCTNGGAGA CTACAGCAAG ACTCTNTCTC CAGTTAAA 58

SEQ ID NO:5570

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06620

SEQUENCE DESCRIPTION:

GATCTGAGGG GTGGTGCCTA CTTCCACTGT AAGAAAGAAT CTNGGTGGAT TTGTGTNTCA 60  
AATCANGATA AGAGAAGCCT GTTTAAAGGA GCAGATGCCA TCTNCTGNCT TCCTCAAGGA 120  
GCCAGTTAAA AAACCAGAGC ATTCCTTTN ATTGAAAAAT AAAATTAGTT TGTTATCAAA 180  
ANNNGGTN 188

SEQ ID NO:5571

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06621

## SEQUENCE DESCRIPTION:

GATCATAAAC CGTTGCGGGA CAGAAGTTAG ATATGTGATT GATTATNATG ATGGTGGTGA 60  
AGTCAACAAG GACTACCACT TCACCATCCT GGACGTCCGT CCTGCCTTAG ATTCACITTC 120  
GGCAGTATGG GACAGAATGA AAGTCGCTTG GTGGCGTTGG ACCTCGTAAA GCACTGTTTC 180  
AGATGGAAAA NTATAANCTA TTTTNTCTG AGCGATACAT TAAACTATTT TCCCAGAAAA 240

SEQ ID NO:5572

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06623

## SEQUENCE DESCRIPTION:

GATCCTCATC TTCCCCAAAT ACTCGTTCCC AAAATTGACG AGCCTGACAA TGTGCATGCC 60  
AGGCAAGGCT CTTGGGGTTC CCCTAAAACA CTCCTCTTT TAAGCCTACC ACTCACTCAT 120  
CATGAATATA GTCCATTGTC CCAGGGTGTA AAACCCTCTA TAGTGTTAAA TAAAAGANTG 180  
ATTGGGGAAC ATTGAAA 197

SEQ ID NO:5573

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06624

## SEQUENCE DESCRIPTION:

GATCTGGCTC AGTCTACTAT GGGCAGGGCC CCCACCAAG CTGAGCCGAA TGGAGACAGC 60  
TGAGCTGAGG CCTGACTTTT TCAATAAAAC ATTGTGTAGT TCTGGGAAA 109

SEQ ID NO:5574

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06625

## SEQUENCE DESCRIPTION:

GATCTGAGCT GATGACTTGT GAGAGAAAAA GGGAACAGAG TAAAGCCATG GAAGCCATGA 60  
ACAGTAAGAG ACTGCCGCCT GGCATGGTTT CTTCTTCTGC AGAAGATGAA ACTGAGGAGA 120  
AACAAGACAA CATCCTTCAT ACCAGGAATG GTCAAGATAA TGCAAGAAGA GNGNAGCTTT 180  
CAAACAANTC AGNAGGCAGT CAACAAACAG NAAGGGGGNC ATTCCTTCCC TGGCAGTTAC 240  
TCATANCTGA AATTGCTTAT TGTGTACACC GGGGCTTGTA CTTGGGGNAT TTAATANNAT 300  
TGCTCATTNC CAAGCTCCNA ANNNAANTTA TTN 333

SEQ ID NO:5575

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06626

## SEQUENCE DESCRIPTION:

GATCGATTGC AGTCAGAGCC TGAAAGTATC CGTAAATGGA GAGAAGAACA AATGGAACGC 60  
 TTGGAAGCCC TTGATGCCAA TNNTNGGAAG CAAGANGCAG AGTGGAAAGA AAAGGCAATA 120  
 NNGGAGCTAG AN 132

SEQ ID NO:5576  
 SEQUENCE LENGTH:272  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06627

SEQUENCE DESCRIPTION:  
 GATCTTGGCT TCTNACAGTT CTNCCTGTCC AAACCTCCATC CTGTCCCTCA GGAACGGGGG 60  
 GAAAATTCTC CGAATGTTTT TGGTTTTTTG GCTGCTTGA ATTTACTTCT GCCACCTGCT 120  
 GGTCATCACT GTCCTCACTA AGTGGATTCT GGCTCCCCCG TACCTNATGG CTCAAACTAC 180  
 CACTCCTAAG TCGCTATATT AAGGCTTATA TTTTGNTGGA TTACTGCTAA ATACAAAAAT 240  
 NTTTGANAGG GANNGGNGNG TGNGGNGTGT NN 272

SEQ ID NO:5577  
 SEQUENCE LENGTH:133  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06628

SEQUENCE DESCRIPTION:  
 GATCATCCTG TCTGGCTGCA GTGAGAGACC AACCCCTAAC AAGGGCTGGG CCACAGCAGG 60  
 GAGTGCAGCC CTACCTTCTT CCCTTGGCAG CTGGAGAAAT CTGGTTTCAA TATAACTCAT 120  
 TTAATAATTT AAA 133

SEQ ID NO:5578  
 SEQUENCE LENGTH:186  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06630

SEQUENCE DESCRIPTION:  
 GATCCACAAA CTNCCTGACA CTACTNNCAT ATTTCCACTA AAGGAGATTC AGCTACAAAA 60  
 GGAGGCCAGC CNTCGGTCTT CGTCGATGCC TGAATCAGGC ANGCCAGCTT TCCGCGTGGT 120  
 GGACACCGAG TTCTAAGCCA CAGACCGAGG CCCCAGCAGN CAGCGGCTGG AGGGNTGCCA 180  
 CANN 186

SEQ ID NO:5579  
 SEQUENCE LENGTH:136  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06631

SEQUENCE DESCRIPTION:  
 GATCCACTGC CTCGGCCTCC GAAAACTGG AATNATAGAT GTGAGCCACT GCGCCAGGCC 60  
 TGTAATTTTA TGTATCTTTA TGTGATTATT TGAATGTCCC TCTCTGACTA GATTATAAAT 120

TCTAAGGATA GTGAAA

136

SEQ ID NO:5580

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06632

SEQUENCE DESCRIPTION:

GATCCCCGTT CTAAGTGTC NCNGGGAACA TAAACNGAGA TAACATGAAA AAACCTTGACA 60  
CAGAAA 66

SEQ ID NO:5581

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06633

SEQUENCE DESCRIPTION:

GATCCTTNAA GGCAGCTGCC TTATCTTATT CCTTNTTGTA TTTCCATACC TAGCCTAATA 60  
CCTAGCTTAT ATAAGGGAAC AGAATAAATA AACAATAAAG AAAAGTCTTT ACAGCCTCTA 120  
AA 122

SEQ ID NO:5582

SEQUENCE LENGTH:262

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06634

SEQUENCE DESCRIPTION:

GATCCAGGGC CGTTCATGAA CCACTGGGCT GGATTNGACT GTTGAGTGTG GCAGTTAATG 60  
CCCCTCAANA AATCAAAGGA TGTCTTATAA GTGTCTTCCA AAAAAAGCA AATGCTGAAA 120  
TCCTATTGGC AAAGTAACT GAAATTGGCT GCTATATTTN ATATAATCAT TTCTGCAANT 180  
CCCANTTNTT GNATACTNAT GTNGGACATG GTTANTTCTT ATTAATTGTG TGGAAATTGTT 240  
TATTGTTAGN AGTGCANATN GN 262

SEQ ID NO:5583

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06635

SEQUENCE DESCRIPTION:

GATCCTGGCC AGTACAAAGT CGTTGCTCTT GTTTTATCTT CTCTTACAGA GTCTCCCTCC 60  
CTTTATAGAA TGTCAACCAA AGAGTGCCCT CCTCCCCTCT CAGCCTCCTN TNNAGCTAGC 120  
CTCCCCATCT CATCACAACG CATGTCTGTG ACCTTTGGTA ATCATTTACA GTGCCACACG 180  
GAACCCGTGTA TTTTGACAC AGCAAAACAA ACAATGTTTA GCTTTATTTA TGGTATTTGA 240  
TGCTGTAAAT GGAAATAAAT ATTGTTCTTT ATAAA 275



SEQ ID NO:5584

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06636

SEQUENCE DESCRIPTION:

GATCTCTCTC GCCACGGCAC CGTCAGCTCC TTTGTGGCCA AGCTTTTCAT CTTTGTGTCT 60  
GCAGAGCTCT GAGCACTCGC TTCGCGTCGC GGGGTCTCCC TCCTGTGCT TTCCTAACCC 120  
TGCCCTCCGG GGCCTTAATA AAGTCTTAGC AAGCGTCCA CACAGTGAAA 170

SEQ ID NO:5585

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06637

SEQUENCE DESCRIPTION:

GATCAGCTTT NAGAGTGGTC CTAAGCAGTA AACTGGATGA TGTTGCATTA GAAAAACATC 60  
AATACTTCAT ATTTAAGTNT NAGTAGTTAC TACTGATTNG ATAATCACTT AANTN 115

SEQ ID NO:5586

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06638

SEQUENCE DESCRIPTION:

GATCCTTG TG GACTGCCACT GCTGGCTGCC TCCTCTCCAA CTCATCAGAA GAGCATTTTG 60  
ACAAAGACAG AGGACTTGGA CCAGGGCATG CCCTGTTGGG GATGTTTCTG TCAGCAAGGA 120  
CATGGCATGG AATCAAGTGG GCTGATGTGT TGTTATTTAA ACAGTACCAA AGTGCATTCT 180  
TCAATGTATG TTTGCCTGCT TGAAGCAAGG CCCAAGTTGA GAATACAGTA AAGGNAACTC 240  
ATGAAAGTGA GAAA 254

SEQ ID NO:5587

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06639

SEQUENCE DESCRIPTION:

GATCCCGCCC TGACCCAGAG GAAGCCTCTA TTTATTTATT AGCTTTTGTT TACACCGTGG 60  
AATTGACCCC TTCCTCCAGG GGTCTTGGGT GGGGGAGCCC AGGGCCCCTG TGACCCCTCC 120  
TTTCTTCCTC CAATCCCAG TTTGTATTTA GCTGCCAAAT AAGATTCCCA TTGGNTCCCT 180  
GTGTTCTCTT GGGGGGTCAG GGTGCTGTCC CCTNCNNTCT GTTTACATCT CCCCTNTACC 240  
CCGCTGTATC GCATATTGNN GAGTTTNTA TTTTGCAA ATAAAGTGAT GGAAACTCAA 300  
A 301

SEQ ID NO:5588

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06640

SEQUENCE DESCRIPTION:

GATCAGAGAA AATACGGTAC ATGTCCCAT GGAGGATATG GCTTGGNCTT GGAACGATTC 60  
TTAACGTGGA TTCTGAATAG GTATCACATC CGANACGTGT GCTTATACCC TCGATTTGTC 120  
CAGCGTTGCA CGCCATAACC ATTTTCTCCA GAAGCGTGGA GGAAAGATTA TNNAAGGANC 180  
AGGCTCTTCA AAAAAANNAN GNNAAN 206

SEQ ID NO:5589

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06641

SEQUENCE DESCRIPTION:

GATCTTCTTC ACACCAAGCT CATGGTTACA TNCCGTGAGG TGTCATGAAG AAAGTNCTGT 60  
TCAATAAGGT TTTGTAATGT TAAA 84

SEQ ID NO:5590

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06642

SEQUENCE DESCRIPTION:

GATCTGTGGC TGGAATNGAG GGAGCGCCTG CTTCTTCTCC AGCTTGAAA AACAATAGGA 60  
GAAGGGTCAG CTCGCGCGG GCATCATCCC TACCAGATTG AGTGTTTTGC ACGCACTTCA 120  
ATCACAAAAT AAAACAGTGA GAAAGTCAAA 150

SEQ ID NO:5591

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06643

SEQUENCE DESCRIPTION:

GATCATCATA TCAAGATGAT ACCAAAAGTA TGTA AAAAAGA AACCTGCATT ATTTTGTAAT 60  
NATTTCTTAT AGATATTTCA TGGTAAGATT AGCAGTCAAT AAAGTTACTT TTTTNCCTTT 120  
AAA 123

SEQ ID NO:5592

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06645

SEQUENCE DESCRIPTION:

GATCCTGCAA ATATCTTCTT TCCAGTTTGN TATTGTCATT TGNCTTTTGA CTTTGTTCTG 60  
GTATTTTTTG NTATGTAGAA ATNTTTATTT TCATGTAAGC AAATTTATGA ATCTTTGNAC 120  
ACCATAAGTA TATACAATTA TGATTTGTCA ATTAATAATA TTAGTACAAA 170

SEQ ID NO:5593  
SEQUENCE LENGTH:101  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06646  
SEQUENCE DESCRIPTION:

GATCATCCGG TGAAAGAACC AGTCCCTGNG CCCCAAGGAT GCCGGGGAAA CAGGACCNTC 60  
TCCTTTCCTG GAGCTGGTTT AGCTGGATAT NGGNGGNTTT N 101

SEQ ID NO:5594  
SEQUENCE LENGTH:104  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06647  
SEQUENCE DESCRIPTION:

GATCTCCGTG GGAACATTTT CGTTGCTGTC GGTGCTGGCA GGAGCCTGTT TCTTCCTGGT 60  
CCTGAAATAT AGAGGCCTGA TTAAATACTG GTTTCACACT CAAA 104

SEQ ID NO:5595  
SEQUENCE LENGTH:91  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06649  
SEQUENCE DESCRIPTION:

GATCGTGCTG CACAACCGGA GAAGACAGAA TTACCTCTGC TCTTTTAATA TATAATGATG 60  
GCTTTAAATA AANTTAGGAG AAAATGTCAA A 91

SEQ ID NO:5596  
SEQUENCE LENGTH:126  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06650  
SEQUENCE DESCRIPTION:

GATCCAGAGA GTGGGGGTGA GGGGTGGGCC CTGAAGACTT TTTGTCTGTA GCTCTTGCAT 60  
ATTGAGTGTA TAAACCCGGC TTCTGGACCA ACCCAAGATG AATAAACTGG GGCAGAAAAAT 120  
TACAAA 126

SEQ ID NO:5597  
SEQUENCE LENGTH:393  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS06651

SEQUENCE DESCRIPTION:

5 GATCCTGGTG GCCACCAATN TGTTTGGCCG GGGGATGGAC ATTGAGCGAG TCAACATCGT 60  
 CTTTAACTAC GACATGCCTG AGGACTCGGA CACCTACCTG CACCNNGTGG CCCGTGCGGG 120  
 TCGCTTTGGC ACCAAAGGCC TAGCCATCAC TTTTGTGTCT GACGNGAATA ATGCCAAAAT 180  
 CCTCAATAAC GNCCAGGACC GGTTTGAAGT TAATGTGGCA GAACTTCCAG AGGAAATNGA 240  
 CATNTCCACA TACATCGAGC AGAGCCGGTA ANCACCACGT GCCAGAGCCG GNCCANCCTG 300  
 10 AGNCGACCGT ATTGTAGCTT TTAACNCCC TTNCCAGGC GACCATTTT TGNGAAAGTT 360  
 NGAGGTTTGT TTTNNTGGNT TTAACTTTN TTN 393

SEQ ID NO:5598

SEQUENCE LENGTH:69

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06652

SEQUENCE DESCRIPTION:

20 GATCAGAAGG CTCTGGNCAA GAGAATGAAA ATNAGGATGA GGAATAATAA ACTCTTTTTG 60  
 GCAAGCAAA 69

SEQ ID NO:5599

SEQUENCE LENGTH:85

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06653

SEQUENCE DESCRIPTION:

30 GATCTCTTTG TCCCTGAGGT GTCAGCTGCC AACAAGAAGC ATTAGAACAA ACCATGCTGG 60  
 GTTAATAAAT TGCCTCATTC GTAAA 85

SEQ ID NO:5600

SEQUENCE LENGTH:149

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06654

SEQUENCE DESCRIPTION:

40 GATCTTGGAG TCGTGGAAGT GCTGCCCCAC CGGGTCCTGC GCCGTCAGCA CAAGCCACGC 60  
 TTCACCACCA AGAGGCCCAA CACCTTCTTC TAGGTGCAGG GCCCTCGTCC GGGTGTGCCC 120  
 CAAATAAACT CAGGAACGCC CCGGTGAAA 149

SEQ ID NO:5601

SEQUENCE LENGTH:120

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06656

SEQUENCE DESCRIPTION:

50 GATCGATGTG CTCAGCCAAA TNCCTGTTT GAAATATCAT GTTAAATTAG AATGAATTAA- 60

TCTTTACCAA AAACCATGTT GCGTTCAAAG AGGTGAACAT TAAATATAG AGACAGGAAA 120

SEQ ID NO:5602

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06659

SEQUENCE DESCRIPTION:

GATCAAAACC AAAAAAATG NACCAAAGGC TTGGGTGGTG AGGGTGCTTA TCCTTTCTGT 60  
TATTTTGTAG ATGAAAAAAC TTTCTGGGGA CCTCTTGAAT TACATGCTGT AACATATGAA 120  
GTGATGTGGT TTCTATTAAA AAAATAACAC ATCCATCGGA AA 162

SEQ ID NO:5603

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06660

SEQUENCE DESCRIPTION:

GATCCTGTTC TGTAATAAAC ATATTTTGCC TTGAGTAAAT TTGTTGTAAG CTAAAA 56

SEQ ID NO:5604

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06661

SEQUENCE DESCRIPTION:

GATCCTTCTT GTATCTTGAA GTTTTGTACT TGGGATTCTT GGA CTGATAA ATGAATCATC 60  
ACATTCTTCT GGTAATATT TTCTTGAAA 90

SEQ ID NO:5605

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06662

SEQUENCE DESCRIPTION:

GATCTGAAGA AGATGATGAA GTTGTGGCAA TNATTAAGGA ATTGTAGAT ACTAGAATAC 60  
GGCCAACTGT GCAGGAAGAT GGAGGGGATG TAATCTACAA AGGCTTTGAA GATGGCATT 120  
TACAGCTGNA ACTCCAGGGT TCTTGACCA GCTGCCCTAG TTCANTCATT ACTCTGAAAA 180  
ATGGGAATNC NGNGCATGCT GCAGTNTTAT ATNCCGNNN 219

SEQ ID NO:5606

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06664

## SEQUENCE DESCRIPTION:

GATCAACTGA ACCAGTATGC CAAAACCAGG CATCCAATTT GTAAACCAAT TATGATAAAG 60  
 GACAAAATAA GCTGTTTGCC ACCTCAAAAC TTTATGAACT TCACCACCAC TAGTGTCTGT 120  
 CCATGGAGTT AGAGGGGACA TCACTTAGAA GTTCTTATAG AAAGGACACA AGTTTGTTTC 180  
 CTGGCTTTAC CTTGGGAAAA TGCTAGCAAC ATTATAGAAA TTTTGCCTTG TTGCCTTATC 240  
 TTCTTCCAAA TGTACTGTTA AATAAAAAATA AAGGGTTACC CCATGCAAA 289

SEQ ID NO:5607

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06666

## SEQUENCE DESCRIPTION:

GATCTGGAGC ATTTGAANCA AGTTTATAGA AGANCATGCC AAAAACTAA GCAGGACCAA 60  
 GGAAGAGCTT TNAAGGCCTG AGGTCTGCGG AAGGTGGGAG GAGGCAGACG CCCTGCNTGG 120  
 CCCATGGTCG GGGCGTCCAC GGCGAGGCCG GCAACAAACG GCAGTATCTN GNATTCCTTT 180  
 TTTNTTTTTT NAAATTTTTA ATNCTTTGGT NTTTCN 216

SEQ ID NO:5608

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06667

## SEQUENCE DESCRIPTION:

GATCAGAATT ATAACCATGG AGAATTTTTT CTTCTGAGCA TTTTAATATA CTTGAAAACA 60  
 ACATTGACTT GAAAAATTTT AGAACATTTT TCAGTACCTA GTTTTATTAA ATATTACACT 120  
 TGAGAGACAC TTTTAAAAA TGTGTTAATG TCAATATGAT GAGATTTTAG CCTTTCTCCA 180  
 GAACTAAGGC ATTAAGAAA ATAGCAAATA TTAATAAATA AAAGTGTAC TTTTTCCTT 240  
 CTTTCTTTT ACCTTTAGGT TAATATCCAG TATTATGTGT TATCCCNTTG GATAAGTATG 300  
 CTTTATTTTA CCTCNGTTAA AAATTAATAA AAATGATTTT TATTCATAAA 350

SEQ ID NO:5609

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06668

## SEQUENCE DESCRIPTION:

GATCCTNAAG AGAGCTGTCC CAGCACTCTG GCCACCAGGA GGGCCANATT CCCCANAAAC 60  
 TACCTNTTGC CCAAAGAACA TNCTCAGTAT TTGGGGCATT TCCTN 105

SEQ ID NO:5610

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06669

## SEQUENCE DESCRIPTION:

GATCCCAGTG TCTGAGTGAA CTAACAGTCC TGCTTTCAGC CACCATTGTG ACAAGACACC 60  
 CAGCACTGAA AGTCCCGCTG CCAGGAGCAA GGGATTCTTT GGAAGCACCC GCCCTTTGTG 120  
 CCTTGTTGGG GGAAACCGGT GACGCAGTAG TGAGTGTGGA TACACCAGAG TTTGCATTGG 180  
 AAGGAATGAG TGTCACGTGG GGAGGGAAGG GGCCAGTGA CTTTTGTAA GCTTTCCTACT 240  
 CAATAAAATG AACCTGTATG GCAAA 265

SEQ ID NO:5611

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06670

## SEQUENCE DESCRIPTION:

GATCCATGTT GAACAATACA TGTAGGTTCT TTTTCCACGC AATGTAAGAN CATGATATAC 60  
 TGTACGTTGG AAAGCATTTA CCTTATTAT ATACCTGAAT GTTCCTACTA CACAAATAAA 120  
 CATATATTAA ATTCTAAA 138

SEQ ID NO:5612

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06672

## SEQUENCE DESCRIPTION:

GATCTGTCAT GCCCCACCGC CCCCCCTACT CCCTTCAACC CTCCCTCTTT CTGCCCATT 60  
 CCTCCCACCC CCTCACTCCC ATTTCTTAGC AAAATCAGAA GATTGTGAAG AGGCCGGCTT 120  
 CAACAAAATN GGATAAANAN ATAATTTTTT AAAACTTAAA 160

SEQ ID NO:5613

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06673

## SEQUENCE DESCRIPTION:

GATCCTATGT NCTGCTTGCA CAGAGGCCTT TGGATTTTAA CCCAGGAGNT TCGNGAGNTG 60  
 AGAGCTGCCC TGTCTTTNAT TGAGCCTTAG CATTTCCCTC TCAGGCTTCC TCTCAAGCTC 120  
 AAGGAACTCA CCCCCAGATA AGAAGCTGGT GCCTCTTGTC TCTCTNATTT CAGAAACGGA 180  
 CTTTCTNATC ATGCTTTCCT ATGGTGGGTA TGNGNNN 217

SEQ ID NO:5614

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06674

## SEQUENCE DESCRIPTION:

GATCCAGAA TTCAACCTGT ATTTATAGAT GGATAATGTA NTTAGCTAAT TTTTGGTTTA 60

AATGANCTTN TTGGGTTAGC TTNCGTAAAT GNTATAATTT TTACTGTTN

109

SEQ ID NO:5615

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06675

SEQUENCE DESCRIPTION:

GATCCCCAGC TGGACTCCCC ACCCCCTGGC TTCCCCACCT CTCCAGGNGT CAAAGGTGAA 60  
CCGAGTCCAG TATTAGCTGA ATGTCATTTC GTACACCACA GCTCAGTCAG CCCATGGGCT 120  
TCGTGAACTT TGCTCCAACA CACTGATGTG TGGGCTTCCC ACAGCAGGAC TGACTTCCCC 180  
CTTTCTGTTG TTTGCACATN CCCCTCTTAC TGTACTGTCA ATAGATATTT TTGAGATTTA 240  
TTTTTAAATA AATATTCAAC TTGCAAA 267

SEQ ID NO:5616

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06676

SEQUENCE DESCRIPTION:

GATCAATAAT ATATAAATN TGAGTGTGGG TTTGTATCTA ATAAAGTATG CCAACACCAA 60  
A 61

SEQ ID NO:5617

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06677

SEQUENCE DESCRIPTION:

GATCTTGAGG CCCAACATGC TTGACTCTGC CCAAAAGTCT CCTTCCTCAG CAGGATGCAG 60  
CCTATTACAC TCAGCACAGN ATCTGGCACT CTTAGGTTCC CGGTCCATTT CAAACCTCCT 120  
GCAACCAACA AAAGGATAGT TCCTTAATAA TTTGTCAAGC CTACCTAGGG CACTGCTAGT 180  
AGTCTTACCA TTATTCACAA ATAGGGCTGA AACATCTAAA ATTACCCAC TTAGTATTTT 240  
ATATCCCTTC AACGTTCTAT CCTAAAGCTA ATGTTTCTTA GTGCTAATTA NAATCGTCAG 300  
TCTATTGACA NTNTGACAAA GGGTAAGAAA 330

SEQ ID NO:5618

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06678

SEQUENCE DESCRIPTION:

GATCCAGGN TTCTGCGGAC CGACGATACG TTTAAATGTT GTTCTAGTAA ATATTCTTGA 60  
ATGTATTAAA ATGGCTGAAA CAAA 84



SEQ ID NO:5619

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS06679

SEQUENCE DESCRIPTION:

10 GATCGTGTTC TTAGATGAA ACCATCAAGA ACCCCCGCTC GACTGTGGAT GCTCCCACAG 60  
CAGCAGGCCG GGGCCGTGGT CGTGGCCGCC CCCACTGAGA GGCACCCAC CCATCACATG 120  
GCTGGCTGGC TGCTGGGTGC ACTTACCCTC CTTGGCTTGG TTA CTTCATT TTACAAGGAA 180  
GGGGTAGTAA TTGGCCCACT CTNTTCTTAC TGGAGGCTAT TTAATAAAA TGTAAGACTT 240  
CAAA 244

15 SEQ ID NO:5620

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20 CLONE:HUMGS06680

SEQUENCE DESCRIPTION:

GATCTTCATT AGTCAAGNTT TAGTTATTN GTTGGCTTTT CCATGTAGAT TTCCAAGTGA 60  
CATTACATA CTTNATTAA AGAAAATTG GAGACTGTN NN 102

25 SEQ ID NO:5621

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS06681

SEQUENCE DESCRIPTION:

GATCGGGCCC CATGTCTGTG CTGTCTAGTT TGTGTTCAAA ATGTCAGAAT AAACACAGAA 60  
TAAATGTAA A 71

35 SEQ ID NO:5622

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS06682

SEQUENCE DESCRIPTION:

45 GATCTTTTAA AAAAGTTAAA GGACATCCTA GAGCCTTAAT AGTTAAGAAG NGTTAAATTA 60  
TCAAGCCTAT TTGTGCATTT CCTTTTNTG AAAAAGGTAA GTTGCTGATT AAGTCTAATT 120  
GGAATTGATA ATTCCATAGT CTTAGATTAN NNTGAGGATA TTTCTCCTA GATTTCCTCA 180  
TGTNATGCCA TGCATTTATA TATCTNACCA TTAATTTTAC ACTAAGGATG CTTCAACATA 240  
TAATAANNNGG TGCANGNTGG AAGCAANN 269

50 SEQ ID NO:5623

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS06683

SEQUENCE DESCRIPTION:

5 GATCTCCTTT TCCAGTGCTG CACACTCCTG GTTTGGAAC TTAATGGCGT TGCAACGGAA 60  
 TCCTATATNC AGTTTCCTGT AATTTAATTG AAGAAAAATG CATCCAAATN AAGACTTTAT 120  
 TATTAACNGA CCAGATNGCA TCAGAAATCA TGTGTCTGTT ATNATTATCA GAATATGTCT 180  
 TAACTTTTNN GGGCAAAGTT AACACTGAAA GTTCTAGCTT AAGTGTGAN ACTTTTGTGG 240  
 10 GGNAAAAAAN TCACTTTTGA AACTCAGACT TCAGNGTATA CCCANTAATT TAANGTTCNT 300  
 GTGAAATGGT TTAAATGTGT NGGACTCGTA ATGACTGTTT TANTGGTTCC AGTTTCTNCA 360  
 NGTGGGTAN TTGGN 375

SEQ ID NO:5624

15 SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06684

SEQUENCE DESCRIPTION:

20 GATCTGATAA CTTGAATTCA GAATATTAAG AAAATGAAGT AACTNATTTT CAAA 54

SEQ ID NO:5625

SEQUENCE LENGTH:182

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06685

SEQUENCE DESCRIPTION:

30 GATCTGTTTT TATAAAGTGC TCCATGATTC TCTGAAAACA GTATACTATG TATCTAATTT 60  
 TTGGATACAG GATGGACATA CGTACTCAAA CTGTGTTTTT CAATTTGTAC TGTATTTGTT 120  
 TCTCTCGACC TGACTIONG ATAGAGGTAT ATAAAGTNT TCCACTAGCA TGGTAGATTA 180  
 AA 182

35 SEQ ID NO:5626

SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06686

40 SEQUENCE DESCRIPTION:

GATCCTATGG NTTTTCCCGG CTGGTTGCCA CTACTGTACA ACATTCAGTG CCCACATCCA 60  
 TCTNTGCCAT TAAGCTTTTT TGAGACATGA GAGATGCCTC TNCCCTGCTG TATGACATGC 120  
 ATTTGGGAAG TTGGAAAGAA ATGACAAANT CAGGGAGAAA ACATCCAAGC TTCTTACCTG 180  
 45 TAGATAGANT CAGCCCTCAN TTGGTGCTTA TNACCAGTTA TTCANGACA ATAACANCAA 240  
 CAAANTTAGT AGACATCCAA GAGGCACATA TTAGGGCCAA AGATAGCATC ANCTGTNTTT 300  
 GAGGGANCTG TAGTTTTGCG CATTTTNTAT NCATTTTAT AAAGGTACTG TNATTNTTTC 360  
 ATTGANN 367

50 SEQ ID NO:5627

55

SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06687

SEQUENCE DESCRIPTION:

GATCTAGTTT GACTTTCTAG TTAGTGGTGT TTTGAAGAGG GTATTTTATT GTTTTTTAAA 60  
AAAAGGTTCT TAAACATTAT TTGAAATAGT TAATATAAAT NCATAATTNC NTTTCCCCTG 120  
TTTATTGTAA TGTATTCTAA ATTAATGCAG AACCATATGG AAAATTTTCAT TAAAATCTAT 180  
CCCCAAATGT NCTTTCTGTA TCCTNCCTTC TACCTATNAT CCTGATTTTC AAAAATGCAG 240  
TTAATGTACC ATTTNANNTG CTTGATGAAG GGAGCTCTAT TGCCNTTANC AGNAATTGTN 300  
GCTAAGGTAA TTCCNAATAG AAAGCTGCTT ATTNNN 336

SEQ ID NO:5628

SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06688

SEQUENCE DESCRIPTION:

GATCTTCTTG ACCTTCTCCA TCATCGCCAT CCTTTCCCAA AGGCCAAGGA AGTGACCTGC 60  
CTGTGGCAT TGGCCAGACC ACAGCAGCAC CTCCTCCATG CAGGCCTTAA CTTTCCCCTG 120  
GTCAATGCAG TTTTATCAG CCTTGCTTTG GATAGGACCT CCAAGGACTA AGGCCTCCAG 180  
CCCCATGTNT GACCTTGTN ATCTCTCTGC CCCACATAAT TCTGTACTT TGCTATGTGC 240  
TCCTAATGTA TCTAGTGTGT CCTGTGACAA CACTCATCAN ACTTCAGTGN AAATCACTTG 300  
GTTTTAATTG ACTGTNTNT CCTATAGACT GTAAGGNTCC ATGAGGGCAG GGCACATGTT 360  
GGTN 364

SEQ ID NO:5629

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06689

SEQUENCE DESCRIPTION:

GATCCCGTGT GCCACCAGGA GGGAGTGGCA GCTATAGTCT GGCACCAAAG TCCAGGACAC 60  
CCAGTGGGGT GGAGTCGGAG CCACTGGTCC TGCTGCTGGC TGCCTCTCTG CTCCACCTTG 120  
TGACCCAGGG TGGGGACAGG GGCTGGCCCA GGGCTGCAAT GCAGCATGTT GCCCTGGCAC 180  
CTGTGGCCAG TACTCGGGAC AGACTAAGGG CGCTTGTCCT ATCCTGGACT TTTCTCTCA 240  
TGTCTTTGCT GCAGAACTGA AGAGACTAGG CGCTGGGGCT CAGTTTCCCT CTAAAGCTAA 300  
GACTGATGTC AGAGGCCCCA TGGCGAGGCC CCTTTGGGCC ACTTACN 347

SEQ ID NO:5630

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06690

SEQUENCE DESCRIPTION:

GATCAAGGTG TGAATAACTG AAGAAAATAA CTTGCTGGCT ATATAGGAAA ATGCTGTGGA 60  
 AATGAACTGT GTATATACTT CTGGGAGGAA CAAATTTAAT CATTTCCTCT GTTAAGCACT 120  
 AATCAGTATA GTGCAACTCC TGGTCTGTN CTGTATTNA TATGCAACAT ATATGCTTTA 180  
 ATATTNNNT GTTTGTNCAT TAATATTNC AATTGTGTTA ACCACTTGC TGCTAAGATT 240  
 TTNCCGTCCC ATCCCATTT NTCCCTTTAC AATNNTAAAC ANGTTTCTTC ATTAAANNCT 300  
 ATGGTGATGA AAAANAAN 318

SEQ ID NO:5631  
 SEQUENCE LENGTH:185  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06691

SEQUENCE DESCRIPTION:  
 GATCTGTGGG TGTTTTAA AAAACTCAAC CTATCTGGTG TTTTATTTA ATGGATAAAA 60  
 ATGTAATTTT CCTAAGGTAG CAACTTATTT CCAAATTAAT ATAGATGANA AATAGATNCC 120  
 ANTNGACTA AATTGAAAGC TTTNNTCCT ATATTNCAAT AGCCTTTGAG AATATTGNTN 180  
 AGTGN 185

SEQ ID NO:5632  
 SEQUENCE LENGTH:130  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06692

SEQUENCE DESCRIPTION:  
 GATCAAATAA ACTCANTTTT TTATGGTTAC TGTA AAAAGA CTGTNTAAGN CAGCTCAGCA 60  
 CCATGCTTCT NGTAAAGCA GCTTCANTTA TCCACTGGGG TTATCTTTTG ACAACTTGCC 120  
 ATTATCTGNN 130

SEQ ID NO:5633  
 SEQUENCE LENGTH:123  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06693

SEQUENCE DESCRIPTION:  
 GATCTTAACA AGCTTAAAAA AGAATTTTAT GACCAGAATC CAACAAGAGC TCTATTTTGG 60  
 AATTGTGCC AAGTTGGTGA TGTTTACTCT AAAATTAATA ATAAACTAC TTGTAAGCAC 120  
 AAA 123

SEQ ID NO:5634  
 SEQUENCE LENGTH:235  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06694

SEQUENCE DESCRIPTION:  
 GATCTGAACT GCCTCCTCCT TTCTCTGGCC-TCTNCCCCT TCCCTCTTCT CTTAGCTAG 60

GCTAGCTGGT TTGGAGTAGA ATGGCAACTA ATTCTAATTT TAATTTATTA AATATTTGGG 120  
 GTTTTGGTTT TAAAGCCAGA ATTACGGCTA GCACCTAGCA TTTCAGCAGA GGGACCATTT 180  
 TAGACCAAAA TGTACTGTTA ATGGGTTTTT TTTTAAAATT AAAAGATTAA ATAAA 235

5  
 SEQ ID NO:5635  
 SEQUENCE LENGTH:250  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 10 CLONE:HUMGS06696

SEQUENCE DESCRIPTION:  
 GATCAGCTA CTGCACTCCA GTCTGGGCAA CAGAGCAAAA TCCTATCTCA AAAAATATAT 60  
 ATATATTATC CAGCCCCAAA TGTTTATGGG GTTGTATTG ATGAACCCTG CATTAAACAA 120  
 15 TCCCACAGTC GGTGCTGCGG TGAGCCGTGA TGGGTACCAC TNCATTCCAG CCTGGGTGAC 180  
 AGANTGAGAC CCTGTCTNNA AAAAAAANGT NNAANTTGT TTCCCNATAT TTTGGNNGGA 240  
 TTNGTGGGGN 250

20  
 SEQ ID NO:5636  
 SEQUENCE LENGTH:131  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06697

25  
 SEQUENCE DESCRIPTION:  
 GATCTTGTGT ATTTTGTCC ATATCCAATG TTATATGAAC TAATTGTATT GTTTATACT 60  
 GTGACCACAA ATATTATGCA ATGCACCATT TGTTTTTTAT TTCATTAAAG GAAGTTTAAT 120  
 TTAAATTGAA A 131

30  
 SEQ ID NO:5637  
 SEQUENCE LENGTH:58  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 35 CLONE:HUMGS06698

SEQUENCE DESCRIPTION:  
 GATCTTAATG GGCAGGGTTA AGAAAGTTAT TTAAAATAAA GTTACCTATT CTAATAAA 58

40  
 SEQ ID NO:5638  
 SEQUENCE LENGTH:250  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06699

45  
 SEQUENCE DESCRIPTION:  
 GATCAGAGTG ATGTGTTATG CAGAGAATTA AAGGGTGATG TGATAAAGTG ATTGGGTCGT 60  
 GCTTTATGTT GGCAAAAAAA ATCTGGAGTA TAAGAAAGTTG CTGACTTGGG TGATTTGGAA 120  
 GAGATTGGGA GACTGGGGGG ATTCAGANCT GAAGGANCAG GCTATAGGCT GTAAGGCAAA 180  
 ANTATACTTG CNATGTTCAA ATTACTNAGA GGNTTNTACC NNCNTGCTTT TCTTTAAAN 240  
 50 ATAAACNTTN 250

SEQ ID NO:5639

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06700

SEQUENCE DESCRIPTION:

GATCTTGTTA TTGATTAACC ATTTTCTTAT GCCTTGCTAT TGACATATTC ATGCTCTTTC 60  
TACGTCTAGT GGCTGAAAAT NTTTGCATTT GTTCATTTGA CTAATGGTGT GATTTTNGTT 120  
TCTATATTAT NAGACCTGTA ATGTTTTAAA ATGTATTNA TTAAATTTGG ACTGGATGTA 180  
TGTCTCTAGC AATACGAGGT ACTTCTAAA CTATTAAGGG AGGGGTTGTA TCCTCATGTT 240  
GAGATAAGAT GATGGTCGTT TAANTTTNGC AATTTTTTTT GGCTGCAGG GATATTTTGT 300  
GTTTATGTGT CCAAAANNGG ANTAANTTGG CATTCTTGTG CCAAANGTTG TTNN 354

SEQ ID NO:5640

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06701

SEQUENCE DESCRIPTION:

GATCTGCATT CTGTAAAAGA GGTACTTTCC CATGATGTAG GCATGAAGTG GTGCCAGTAA 60  
GCGTAGAGCG GAAATNTTGA CTTTAGTTAA CATTGGGTNT AGCATTTCCTA GTGCAGCATT 120  
ATCAGTGGGC CTTTAAAAAT ACTTCGTAAG TACATTAGCT TTCACCTTGT NGTNAAATTA 180  
TAGCAGACTC ATTATAGAGA ACAAGTTTGC CTTGATTNN TTTAAATGA CTTCTGCTAA 240  
GCACCCAGAA GATAAANTTG ACATATTTT NTAATNTAAG CATACTTTT TNGTACATNG 300  
TGTNCATTCT TGANTAANAT GNGGTTCTGT GTTGGCTTGT NN 342

SEQ ID NO:5641

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06702

SEQUENCE DESCRIPTION:

GATCCAGTAT AATTNCAGAT TCTNGTGTCC CATCGAAGTT TCTAGCAAGA GGAAGTTGT 60  
CACATTTCTT TCTTGACTC ATTACTGGTC ACTGAAAACC AGAAGAAGTT GGTGAACCAT 120  
CTAAAGAAGA GAAGGCTGTG GNCAAGTATC TNCGATTCAA CTNTCCAACA AAGTCCACCA 180  
ATATGATGGG GTCACCGGNT TGATTATTTT TTTGCTTCAA AAGCAGTGGN CTGINTTTNG 240  
GGATTCAAAG NGGGNAAAGT CCANGTANTG GN 272

SEQ ID NO:5642

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06703

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCGCAATG AATTTNTAAA ATTACTATTT AANATATTGT TGAGATTCCA TTACCTCCAA 60  
 TCAGTCTTGG GACATTAGAA CAGTGGTATA ATTAAGACTG TATGTTTAAA TTGAGAAATT 120  
 TTGCACAAC TTAACAAGTA GCAGANCTAA TTGTNCACTG ATGGCTTTAA AGATGAAATA 180  
 NTTCTGTGAA TNCATGANAC TGTGAGGGNC TCTNCGTGGT TGTCTAGGTT TATTTATATG 240  
 CATNCTCATT AATNAAAGTN NTTN 264

10 SEQ ID NO:5643  
 SEQUENCE LENGTH:247  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06704  
 SEQUENCE DESCRIPTION:  
 15 GATCTTTTTT ATTTTATAC ACATGACAAG ATTTTACATC AAGAATAGTC AGTTAAATAG 60  
 TACAAATTTA CATTTCATGAG GAATGTTAAA AAAAATTCAA CTAAAAAACC CACTTTTTTC 120  
 TGTGACCCAT AATCCCAT TTTACAGTGC AGGGGAGAAG GGGATTAGGG GGCATNCAAA 180  
 ACAAGTCTCT CCCAAAAAGA AAAATGCAGG CATGCAGGGN CGGCGTAATC ANTNCCNGN 240  
 NNNNNNN 247

25 SEQ ID NO:5644  
 SEQUENCE LENGTH:318  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06705  
 SEQUENCE DESCRIPTION:  
 30 GATCCATACA GGTGTGTGT CATCTGTCCT CTTGAGGTC AGGAGATTCT AAATTGAATA 60  
 TTCCACGGTT TGGGACAGCA TNCGGAAGTT TTCCCTATNA CTTTATATTT TGTATTATGT 120  
 CAAATGTTAT GGCAGGGCCC AAATAGCATA GCCACAAGTT TGGTTTATGT GGGCATAAAA 180  
 TTCTAACCAA ACCCAGACA TAGGGAGTCA TTTGGAGAAA GCCTGTATGT GGTGTTTTAA 240  
 CCTAATAAAG TTGATGAGAG AGAAGGGGAG AGGAAGCGAA CATAAAGCGG GTCAAGTGTA 300  
 GTGCATCTTT TGTATTGN 318

35 SEQ ID NO:5645  
 SEQUENCE LENGTH:197  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 40 CLONE:HUMGS06706  
 SEQUENCE DESCRIPTION:  
 GATCTTTTGA CATACTCACT TTGAGTGGCA TATGCCAGG AAAATATTTA AAAGAAAGAA 60  
 AAGCTATTTT TACAAAGTTT TCTAGCAGTT CCACTCAGAT AACTTTAAGG GGGAAAAAAG 120  
 45 CCCAACGNTT GGNNATGGTT AAGTAAATTT NGGTGTATTG CTAGTGCTAT CNCNGANTGT 180  
 GTATGATGGC CNTNCAN 197

50 SEQ ID NO:5646  
 SEQUENCE LENGTH:210  
 SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS06707

SEQUENCE DESCRIPTION:

5 GATCCCCCGA ATAAC TTTT TCAATCAAGT TGAAAAACCA AACAGCTATG TAAAGTCCCC 60  
AGGAGAGCTC TTTTCCCTT ATTNCTCAT TTNTTTTGTT ATAACTGTT TAAATAGTTC 120  
AAATGGTTGT NCATGCCTAG GGGATGAAAC CTATGTAATA GAAATGTACT GTTTTATGAA 180  
TAAGGAGTAA AATTNTTTTA AAAAATTAAA 210

10

SEQ ID NO:5647

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS06709

SEQUENCE DESCRIPTION:

20 GATCTGAAAC AGAAACCACC CTCCGGAACC GCCCAAGAAA GGNETGCTCC ANANACTCTT 60  
CAAGCGGCAG CATCAGAACA ATTCCAAGAG TTCGCCCAGC TCCAAGACCA GTTTTAACCA 120  
CCACATAAAC TCAAACCATG TCAGCTCGAA CTCCACCGGA AGCAGCTAGT TTCGGCTCTG 180  
GCCTCCAAGT CCACAGTGGG ACCAGCCCAG ACCCTTCTCC TTAGAAGTGG AAGTAGTGGA 240  
GCCCTGCTC TGGTGGGGCT GCCAGGGGAG ACCCGGGGAG CCGGGGAAGG AAGGCCGTCC 300  
ATCCCGTCGA CGTAGAACCT CGNGGTTTTT TCAAAGNAAT TTCCACTNNG GTCTGTTTTT 360  
NCGAGGGGGG NN 372

25

SEQ ID NO:5648

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS06710

SEQUENCE DESCRIPTION:

35 GATCCTTGGT ACCCCTAAAA AGATTGCCAA TTTTTTTCAT CTTTGCCATA TGGAGGACTG 60  
TGACAGACTT TGGACAGTGG CCTCTTGAGT TCCTCTGCAG TTTTGACATT TAGGATTTTG 120  
TGCTTTTAA ACTGAAAAAT CTTCTAGCAT GTTGGGTTGT TACAGAGTAT ATTTTGTCT 180  
GCAGCTGTTT GTTGCCCAT TCCTAAGAGG AGTTTATCCA TCCNGAAA 228

SEQ ID NO:5649

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS06711

SEQUENCE DESCRIPTION:

45 GATCAAAACA AGATTTTCCC AGTAAGAATA TACTGGGACA TAACAAATGA AAATATTTAT 60  
ACCAAAATAC CAAAAGTNAT TCACCTCTTT AAAATATCCT ACTATAGTCT AATTAGTAGC 120  
TTGTNCAAGA CCAAGTAACC ATTTTNNCT GCNCTTTTGA NTGATGATTA GAAATCAAA 180  
CAANGTATTT NNN 193

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SEQ ID NO:5650

55



SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06712

SEQUENCE DESCRIPTION:

GATCCAAGTG CGGAANTCAC AGAAGGAACG GATTACAATT CTCCTNCAGN TAGGGAACCC 60  
CTAAGNCCAC AGAAGATAAG GAGGAAACAA TACAGAAACT AGAGACCCTG GAGAAGAAGG 120  
AAGAAGAAGT AACTTCAGAG GAGGATGAGG AGAAAGAAGA AGAAGNAGAG ANGNNN 176

SEQ ID NO:5651

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06713

SEQUENCE DESCRIPTION:

GATCAAGTTT TAAAAATTGT NCTNTTATTG TTTTAAATTA AGAACTTTTT GAACTAAAC 60  
CAGAACTCT GCCATAGTTC ATTGATTTTA ACATGAAACA TTTATTTACA AGATGATATC 120  
AAGATTACTT TTCACAAAAT AGGCACATTA TATCANCACT TTGCNCTGCT TTGTAAATTT 180  
NCCATCCAGG ATTTTGGGGT GGTATTCATG TGAAATTAAG GCAGATTCTC TAGCAGTTTC 240  
CTATAGCTAC AGTTTTNNNN NTNCCCTGG NTN 273

SEQ ID NO:5652

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06714

SEQUENCE DESCRIPTION:

GATCCTGTGT GGAGAGGGAA TGTGAAATTA ACATCATTTT TTTTGGGAG AGACTTGTTT 60  
TGGATGCCCC CTAATCCCCT TCTCCCCTGC ACTGTAAAT GTGGGATTAT GGGTCACAGG 120  
AAAAAGTGGG TTTTAAAGT GAATTTTTTT TAACATTCCT CATGAATGTA AATTGTNCT 180  
ATTTAACTGA CTATNCTTGA TGTAAANCT TGTCATGTGT ATAAAAATAA A 231

SEQ ID NO:5653

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06715

SEQUENCE DESCRIPTION:

GATCAACATG GTGGAACAAA ATGATAAAGA NCAGAAAACA TTTCAATATA TTACTAATAA 60  
CTTTTCCAA TATAAATCCT AAAATTCCTA TAACATAGTA TTTTACAGTT TTATGAAGCT 120  
TTCTATTGTG ACTTTTATGG AATTAAGAGA TGAAGAAGAT GAGATATTTT AGCATTTATA 180  
TTTTTCAAAA TTATATGTAT ACTTAANANT AANGTANCTT TATGCAAA 228

SEQ ID NO:5654

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06716

SEQUENCE DESCRIPTION:

GATCACAAC GTGAAAAAA ACTGCACACG CAAAAGACTA CAGGGAAATA TGTAATTNAT 60  
TATNTTGTTT TCTCTCAGTG ATAAGATGGG GTGGTTTCTT CTTTGTACTT TTGTATTAAT 120  
TTCTTACGGT GTTTGTATTA CTTTATAAT CAAGAAC TTTTAAAAA ATAAATCAGA 180  
AA 182

SEQ ID NO:5655

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06717

SEQUENCE DESCRIPTION:

GATCGTAGCT AGTTTGTATT GTCTTGTCAG TGTACAGAC TTTTAAAAA AAACAACCAC 60  
CAGTGAAATG TGTGTGTATA CAATAAACTG AAA 93

SEQ ID NO:5656

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06718

SEQUENCE DESCRIPTION:

GATCAACATT TATGACCTAA GTCAGGTAAT ATACCTGGTT TACTTCTTTA GCATTTTNAT 60  
GCAGACAGTC TGTTATGCAC TGTGGTTTCA GATGTGCAAT AATTTGTACA ATGGTTTATT 120  
CCCAAGTATG CCTTAAGCAG AACAAATGTG TTTTNCATA TAGTTCCTTG CCTTAATAAA 180  
TATGTAATAT AAATTTAAGC AAACGTCTAT TTTGTATATT TGTAAGTAC AAAGTAAAT 240  
GANCATTTTG TGGAGTTTGT ATTTNGCATA CTCAAGGTGA GANTTAAGTN TTANNTAAAC 300  
CTATAATATT TNNNCTGANA CNCNNGNACC N 331

SEQ ID NO:5657

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06719

SEQUENCE DESCRIPTION:

GATCAAGCCA AAAAATCCAC CAGGAANTCC TACTGACTCT CTTTNTAAAA TATAGTCATT 60  
TAACNGTCAA AAGAGTCCCC AATAATGTCA GTNCTAAGAT TNCCCCTATT TTTTAAAAA 120  
ACAAAGTAAA TGAAGACTCA AAGAGCAAGT AACTAGTCTA AATTAGATAG TCACAGGTGG 180  
TAAAGCCAGA AATCTGTCTG GNCAGTCTAA CTCTATACAN CCCAGGCTTT TAANTATTAG 240  
AAAGCNNNNN 250

SEQ ID NO:5658

SEQUENCE LENGTH:409

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06720

5

SEQUENCE DESCRIPTION:

GATCTCAGTA TCATACTGAG ACACCTCCCC TGAGCCTTAC CTA CT TAAAT TGGTAACCGT 60  
 CCTACCAAAA TTTGTCAATT TNAATCAAGT GAGGCAAGTT GCAAGGGAGC CAGAGATACG 120  
 TGAAAAAAGA AAAGCAGAAA TACTGATACT TTCTAAGAAA GAAGTTGTAA TAATTNCTTT 180  
 10 GGCACATTGA CTTACTGATA TCTTTTGAAA TGCATAGATG ACTCTTGTGA ACCAANGAGA 240  
 GCAGTNGTGG TTNTTCCCCG GCGCAATAAA AATGCCTTTG TGTATCACTT GCGGTTGCCA 300  
 GTCATTTCTG GTGCCAGTTG CTTTTNNTNN CCAGAGGTTT GGCCTTNATT CTTCCGAAAN 360  
 NAGGGTGATG ATTNTTGAA GNTGGGGTTT TCCTNACCAN ATTATTNTN 409

15

SEQ ID NO:5659

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS06721

SEQUENCE DESCRIPTION:

GATCTGGAAG AGTCAAGAGA AGAGAGCAGA AAGCAGGCTC TTGCTGCTAA AAGAAA 56

25

SEQ ID NO:5660

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06724

SEQUENCE DESCRIPTION:

30

GATCTAAAGA TGATGGAAAA CATCAGCTAC ATTAAATACT CATAAGCAAA ATAAAGGCTG 60  
 GCCTGTAAA 69

35

SEQ ID NO:5661

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06725

SEQUENCE DESCRIPTION:

40

GATCCAAAGG GAAGGGACTA TGCAAGGGCA TTTATAAACG NTGGACAAGG GTTCATTATA 60  
 GAACACCANT GTNATGGACT ATCCCAAGCA TGTACCACTG TGTCTCATGC ATGGTAAAGG 120  
 TCCCATAAAT GTTATTGCTC TCTTGCACTA TAGTAGTAAT AGTAGTGGTA GCTGNNTTAG 180  
 GAGTAAAAAC AGCNAAAAAAN AGANNNNN 208

45

SEQ ID NO:5662

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06726

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## SEQUENCE DESCRIPTION:

GATCTGAAAA AAAAGTTTCA CCGTTTGTTC TCTTACCTCA TTTTAAGAAG CATGTGAAAA 60  
TGGGATACTA TAGACTACTG AGAATTTTCAG AAATTGAGAA CAATTTTCATA ATAAAACGGC 120  
TATATTTGAA GAGAGANTAC ATTTTATATA ANCAGGAAAA TACATTTGAC ACTTTATGGA 180  
ATTTNATGAG ACTTTTTGTG GGAACAGAAG GTCTTCAAAT TGTAAGATGT AAAGNTTGCN 240  
CTNTTTNTTA NGTCTTTAAC AGGGGTGTNT TTCATTGTNT GTTTTGGGTA TGGCTTTGGN 300  
ATAANTCATT NTATATNTNA NTTGAN 326

SEQ ID NO:5663

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06727

## SEQUENCE DESCRIPTION:

GATCTGCACA GTTTGGTTTT TGCACAAAAG TCATTAAAA AAATCTGAGT AATTGTCAAA 60  
TATTAAGAGA AAGNTATTCT TCCTGGTAAG GAATACAGTT TTNAGTCAAA GTGGCCATTA 120  
CATCCNCTTT TNAATTTACA TAATACAGNT ACTTGTGAAA GTTGTGTGGG TGTGTATGTC 180  
CAAGNNAATN CTTTTTTATT GGTGCCTATA TTGTCACANT TNTNTTN 227

SEQ ID NO:5664

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06728

## SEQUENCE DESCRIPTION:

GATCCACCCT CCTCGGCCTC CCAAAGTGCT GAGGATTACA GGCATGAGCC ACCACAGCTG 60  
GCCCCCTTCT NTTTTATGNT TGGTTTTTNA GAAGGAATGA AGTNGGAACC AAATNAGGTA 120  
ATTTGGGTA ATCTGTCTCT AAAATNTTAG CTAAAAACAA AGCTCTATGT AAAGTAATAA 180  
AGTATANTTN CCATATAAAT TTCAAAATTC AACTGGCTTT TATGCAAAGA AACAGGTTAG 240  
GGACATCTAG GTTCCAATTC ATTCACATTC TTTGGTTCCN GGTAATAATCN GGNGGNNTAT 300  
ANCAATTTCT ANTTGGGGTT TNCN 324

SEQ ID NO:5665

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06730

## SEQUENCE DESCRIPTION:

GATCCTTCCA CCTTGGCCTC CCAAAGCATT GGGATTACAG GCGAGAGCAC TTGGTTGGCT 60  
AAAAATTTTA TATTTACCTG NCATNATTTG TTGATTTGGG GGCTAGGGAG TTCTTAAAC 120  
AACAATAAAA AATCTTCTGT GGCTGCAAA 149

SEQ ID NO:5666

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06731

SEQUENCE DESCRIPTION:

5 GATCACAGTC TTGAGGTCCT CTAGCAGGGG TGAGGGGAGAG CAGCGACTTC AGCTGAGTCC 60  
 CTGCCAGTGG TTAAGCAAAC AATGGTTTCA AAATTCAAGG TCCCCAAATG GCAGCATTTC 120  
 ATGTTCTGAC CTGTTTGTGT TATATAGTGG TGTTTTNNNN CCNCTTTGGA NCTCTTGNGT 180  
 TGTTAATAAA ATGAAATGAT TACTTTTNA A TAAANTGAA AAANGTAAAA AANAAN 236

10

SEQ ID NO:5667

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS06732

SEQUENCE DESCRIPTION:

GATCGCGCCA CTGCACTCCA ACCTGGGTGA CAGACTCTGT CTCCAGAACA AAACAAACAA 60  
 ACAAAAAGAT TTTATTAAAG ATATTTTGTT AACTCAGTAA A 101

20

SEQ ID NO:5668

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25

CLONE:HUMGS06733

SEQUENCE DESCRIPTION:

25 GATCCATGGA CCATCTGGGT CATGGCGCCT GGTTCAGAC AACCTGAATC AAATCTTAGG 60  
 GGTGGGGCTT TGGGATGTCA TTGTTCAATA GGCACCTCAG GAGATTCTGA GCACACCNNT 120  
 GTTTGAGAAC CACTAAAATN AGGAGTGGA AAAAAAAAAAT AGGTGTTTTG TTAATTTAGA 180  
 30 GCTGAGCTGN GANGNTAATA TATTTNNTT GTCANTGCCA TTACCAGNTA TGCACTGNTT 240  
 CTTTATACC TACANTTTN 259

35

SEQ ID NO:5669

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06734

SEQUENCE DESCRIPTION:

40 GATCCTGAAG CTTACTATGC AGCCTACAAA CAGCCTTAGT AATTAAAACA TTTTATACCA 60  
 ATAAAAATTT CAAATATTGC TAACTAATGT AGCATTAAC AACGATTGGA AACTACATNN 120  
 ACAACTTCAA AGCTGTTTTA TACATAGAAA TCAATTACAG CTTTAATTGA AAACATAAAC 180  
 CATTGTGATA ATGCAACANT AAAGCATCTT CAGCCAAA 218

45

SEQ ID NO:5670

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06735

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## SEQUENCE DESCRIPTION:

5 GATCAGATTG AGGTTATGCA TTTTGGCAA GAAAACCACG GCAATGATAT GCCCGTCTCG 60  
GTGCATTINA TCAGGAGATA CTTGATGTCG ATGTGTCATA TTAAGTGGTGA TGTAAACCTT 120  
GGTTAAGGTT AGTAGCTTTC AGGTTTCTCC ATTGTAAAGT TGCTATTACT TCTTAATATA 180  
ATAGGCTAGG TTGTACTGCT ATAACAAATA TACCTTAGTA AA 222

SEQ ID NO:5671

10 SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06736

## SEQUENCE DESCRIPTION:

15 GATCCTTGAA TGAAAAGGAA CCCTCACCAT GGGGCTTACT GTTATAATGT TTCTTCATT 60  
ACTGTTATTA AAAGATTAT GAGAAA 86

SEQ ID NO:5672

20 SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06737

## SEQUENCE DESCRIPTION:

25 GATCAGAAGC TGCCAGGAAC AAGGAGAAGA CGCTCCCCTT CCTCACCTTC CCACCCCCAC 60  
ATGGCTTCTC ANTCGGGGAA AAGATACAAC TTAACTTAA ACCAAGTNTT AAGTTTGTAT 120  
TATNACATGG GATTAGATGC ACCAAAAACA ATTTCAAGTG ACTGTGGGGC ATTCTATTGC 180  
CTGAGAATGT TCAAGAGTCC TGATATGACC TGTTGTNTT ATCCTAAACA GTGAAAAATT 240  
CATCCACCAA ATATATAGGA ATAGAGGGTG ACAGNAAGAT GCTTTCTGAA AGGTATCCNA 300  
30 TATTTGGGGG TTTTGGGTTA CATATNNCTN ATGTNGGNTT TTAANCTATA GCTCTTCANT 360  
TANNNTTACT CNATCCATTN CTTGAAAGGA N 391

SEQ ID NO:5673

35 SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06739

## SEQUENCE DESCRIPTION:

40 GATCCTNTGT ACATGAAATG AAAGGTGCAT CANCTTGGGG GCTGGGAAAC CTGCAGTATG 60  
GNTTACTNC GTCCCTATCA CTGGTGTGGC TGTGGGCAA CCACTTATTG CCTGACCTAC 120  
CTCACAGGGA TGTGTGAGG GTTTGATGAG AGAATGAATG TTAATAGGAA TTGAAAAATT 180  
CAAAGCATT AACAATGTA AACAGGTAAA 210

SEQ ID NO:5674

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS06740

## SEQUENCE DESCRIPTION:

GATCTCAAGA AAAAGCAGGA ATTAAATAAG ACAAGGNNCA GATTAANATA CCTTCCCAG 60  
CAGGGGAAAC AGCAAACTTA AAGGTTCTAA GGCACANGAG AGCATGGCAT ATATGACGAC 120  
CCAAAAGAGT GGCCAGATAT CCAGACATCT AGAAGGTCTA GCTAAGTNCT TAGGAAAGTAG 180  
TATAANCAGA NAAGANAAAN TTGTGGCCTC TTTTNNAAA ANN 223

SEQ ID NO:5675

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06742

## SEQUENCE DESCRIPTION:

GATCATGCAC TGTTGACCAC TGAGCAATCT GTGTNACACT AGAGTTCACA GGGCATTTTA 60  
AGTGTAGACG TGAGTCCTTA AACATATTTN GNTTCTCTC TCAGGTTTAA AATGTTTCAA 120  
ATGTAATTNT TGCTCATCAG TGCAGTTATC AATGCAATTT NATATTCCTT GAGGGGAGAA 180  
AGNGGGGTCT TATTGTACAT GTCCAAGGGG GGTGATAAGA GTATTANCTG TTTAATTTAA 240  
TTGGANCAAN CCATTGTCTT AACGCAGCCA TGGTTTGANT TTGTCATCTT NGGGCTGACC 300  
GGTGCATGTA AATACAGTAT GCNCTTTGGA TGTAATCCTT NGAAATGNCA GTGTGNATG 360  
GTAGGTTATC CTTNNGTNAA CCCTTNTCTC N 391

SEQ ID NO:5676

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06743

## SEQUENCE DESCRIPTION:

GATCCCTATA ACTCAAAATA ACTTGTTTGT AAAAGAAAAT TTGTTTACTT ACCCATTAGT 60  
AAGTTCCTGC ATATTCATTA TAAGATGGCA AATCAAACTT TTCTAGGATG AAGACAGCTT 120  
ATNTTNAAGT TGTATAGTCT TAGTTGGTTT AGGGTCTCAA TTTTAATTAA TAAAATNCTT 180  
GGTTTTAATT TGCTTGTCTT TTTGAATTCC NGTTTTAATA ATTNTNNNAG NGNGCAAAGN 240  
GATGTTGAAG TTCAGATTAA NCTCTNCTGA N 271

SEQ ID NO:5677

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06744

## SEQUENCE DESCRIPTION:

GATCCTGGAA GTAATCCGGG CACACTTACA TTTGTTGTCA ACAAGAACAA TCCTTTCATC 60  
TTCTTGGGCT TTCACATGAA CAGCCTTAAT AAAAACC GCC AGGACTCCCC AGAAAAGCAA 120  
ATGGTTCCTC ATCTTGACTT CACTTCTTCT GAAAACTGG AGCAAA 166

SEQ ID NO:5678

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06745

SEQUENCE DESCRIPTION:

5 GATCACAAAT TAATGTTGGG GAAAATAAAG ATTTAATATT TCTTTAAATA GAAAAAGAAT 60  
TTGGTTTTCC TCGTTTAAGA GCAATGAGAA AATNATGGAA TGTTGACTGT NTTTGGCACA 120  
CAGGACACGN ACCTTCATGG AAGTCCTTGC TCTGCGTGGC ATCTGTCAGC TTTNCACCTT 180  
TCATTCTTAT TCTTCACTTT TGCTGCTGAG CCTAGCTGTA CAAACTTNGC ACTTTCATTT 240  
10 GCTAATATAA ATTCAGTTTT ATTNTACCAT TTTAGAGACT ACTAATGGTT AANTGTAGAA 300  
GGNGNGGGGT GNACATGTTT TTATGTNGNG TGTTNAAAG GATATGTTTT NTNACCCNT 360  
GTNATGGTGG CAGCTTTNTN TTTTNN 386

SEQ ID NO:5679

15 SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06746

SEQUENCE DESCRIPTION:

20 GATCCAGGAA GCGGCTGGAG ACATTCCTGA GCCTCCTGGT CCAAAACCTG GCACCTGCAG 60  
AGACGCATAC CTAGAGGAAC TCTAACCCCG GTGTACCTGT ATAACTGAA CTGTGAAACT 120  
GTTTCGGTTA TCTCTGTCTT TTGAGGATGG CTTTGTCTCG TTGCTGGTTA ACATTCACCT 180  
TCCTCTTTTG AGGAGTATTT TTCCATTATG TATTCATAAT AATGTTAATT TCAATAAATG 240  
25 ACATTCATGC AGCAATTAAT 260

SEQ ID NO:5680

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS06747

SEQUENCE DESCRIPTION:

35 GATCAACATT CCAGGGTTGG TAATGTTGGA TGATGAAACA TTCATTTTTC CCTTGTGGAT 60  
GCTAGTGCTG TAGAGTTCAC TGTTGTACAC AGTCTGTTTT CTATTTGTGA AGAAAAGNTA 120  
CAGCATCATT GCATAATTCT TGATGGTAAT AAATTTGAAT AATCAGATTT CTTACAAACC 180  
AAA 183

SEQ ID NO:5681

40 SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06749

SEQUENCE DESCRIPTION:

45 GATCTCACTA TAGAGGCATC ACTAATTGGG GAAAGACAGA CTAGGTAATA GTCAGATGTN 60  
ATATAGTATG TTAAANCTAT AGGATGGCAG GTNCATGANT NTTGGTTGTA TTATCCTTTA 120  
TNTN 124

50 SEQ ID NO:5682



SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06750

SEQUENCE DESCRIPTION:

GATCTGAAGT TGCAGGTAA GCTTGTNTGG TCAACATTCC AGTGTGGAAA AATAATTTAA 60  
ACAATCTTAT TCTCTTAATT CTTTGGCAA CAAAACTAT TAGTAATAGC TATTGGGAC 120  
CAGACAAAAT CAGCTTTCAT CTATAATTCA TTGGGGATAA TGGGAGATT AGATAATGTA 180  
TCCNGATTTA AACCTACCAG TTGTCCTAC CCCTTANGCG TTAAANATAA ANTATGCANC 240  
AAATTTGGNG GNANGNNGTG TGNNGTN 268

SEQ ID NO:5683

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06751

SEQUENCE DESCRIPTION:

GATCAATGCA AAAATTGTTA TATATGAACA TATAACTGGA GTCGTCAAAA AGCAAATTAA 60  
GAAAGATTG GACGTTAGAA GTTGTCATTT AAAGCAGCCT TCTAATAAAG TTNTTTCAAA 120  
GCTGAAA 127

SEQ ID NO:5684

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06752

SEQUENCE DESCRIPTION:

GATCTTTACA ATTACAGTGT AGTAGACAAT TCGGAATTAA TTTGAAACAC ATCACAACAT 60  
AACTTGAGAA AATTCCTAN TGTATATGTA GTGGAATAA ATGTTTAAAG GCTGCAAGGA 120  
TTGCATTATA AANNCTGTTT GTNGGCTTTC TAAGTCTTTN ATNCCTGTAT TGGGANTAAN 180  
CAGATTTNAG AAAATGGATA TAAGCTGANA TGTATATTTN N 221

SEQ ID NO:5685

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06753

SEQUENCE DESCRIPTION:

GATCATAAAT TTTTCTCAGT GTCCTTTTGG TGTGTAACAC ATATATCTGA AACCTGTATT 60  
TAACCAGATA TTTCTACTCA ACTGAATATA CAAGTGTAAG TTTGATTGGA AAATTGTATA 120  
TTATAAATGA AAATACAATA ATCAAA 146

SEQ ID NO:5686

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06754

SEQUENCE DESCRIPTION:

5 GATCCACCCA CCTCGACCTC CCAAAGTGCT GGGATTACAG ATGTAAGCCA CCGTGCCTGG 60  
 CCAAAGTTT CTAATACCTG TTTATAATCC CCTTCTTTGT CCTCAGGTAA CACTATCTAC 120  
 TACGTGTCTC TNCAGATTAG CTTGCATTTC CTAGAATCTA ACTTATATAA TTAAAATAAT 180  
 ATAGTATATA CCCTTCTTTT GGCTTTCTTT ATTCAGCTAT GTTGTGAGAT TCATTCATGT 240  
 10 TGTITAGAGT ATCAGTTACT AAGTAGTATT CCATTTTNGG CTATATCAA NNTNGTTTGN 300  
 CCATTTACCT ATTAANGGGC ATTTNGCACT GGNTCCAGNN TGAN 344

SEQ ID NO:5687

SEQUENCE LENGTH:132

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06755

SEQUENCE DESCRIPTION:

20 GATCTCTGTT TTGACTAAAC TAGAGGAAAA ATNATTGGAT GTGTTTATTC TTTTCTAAGC 60  
 AGAATGGTTT AACTTTGTAC TCTTTGAAAA ATAATGCTGA TTTATAAATC TCTGCCTATA 120  
 NCAGAATGGA AA 132

SEQ ID NO:5688

25 SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06756

SEQUENCE DESCRIPTION:

30 GATCCTGCTG TGGCACGGGG CCTATGTGTC TCTGTCGCGT CTGCTGTGAA GACATGATGC 60  
 TCTATTTATT GTAGAGAGTG ACTTTATTTG CTTTCTAGAA TTGTTTATAA CAGATGGTAT 120  
 AAGAGAGGTA ATAAACAGAG AAAAATCTAT GCTTGTAAG AATACAAAAG TTAATTTTAC 180  
 CTACTATAAT ATGGCTGGCT GAANCTTATT TCCTCTCTNN GNAATAAATG TTCTANTGGG 240  
 35 CAAA 244

SEQ ID NO:5689

SEQUENCE LENGTH:143

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06757

SEQUENCE DESCRIPTION:

45 GATCTTNTCT ATACCATTTA ATGTAGAAAA ACTAATTTTC TATAATTNTN TCTATTAAAG 60  
 GTGACATTAA TGCTGATAGA AAAATATTCC CACATATATC TNACTTGGAA AACTTATAAA 120  
 AATTGTGCTG TCTTTAAAT AAA 143

SEQ ID NO:5690

SEQUENCE LENGTH:219

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06758

SEQUENCE DESCRIPTION:

5 GATCGCAAAG GGATTGTTCT TATAAAAGTG GCATAAATAA ATGCATCATT TTTAGGAGTA 60  
TAGACAGATA TATCTTATTG TGGGGAGGGG AAAGAAATCC ATCTGCTCAT GAAGCACTTC 120  
TGAAAATATA GGTGATTGCC TGAATGTCGA AGNTCTACTT TTGTCTATAA AACACTATAT 180  
AAATGANTTT TAATAAATTT TTGCTTCAGC ACTTGGAAA 219

10

SEQ ID NO:5691

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS06759

SEQUENCE DESCRIPTION:

20 GATCTAGATG AGATTACCCA TAGCAGGGAA AATAATTCAT CACCTACCAA AGACTGTACG 60  
GAAAGGTGTG TTATTTTCAA AATTGCATTT TAGTTTGAC ACATGTAAAT NATTATCCTA 120  
TGTTAATCTA ATTGACAATT CANTTAGCTC CGCATCCTAA GACTTAAAC TAGCAATTCC 180  
TATGCAAATC ATCTGCTTAA CTGANCTACA AACGTTTTTC ATTAATTCAT TCTTTGATGA 240  
CATATTCCAT GTTATATANT ANTNCANAAT AAAGTTAATA TACTACCCCA AA 292

25

SEQ ID NO:5692

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06760

SEQUENCE DESCRIPTION:

30 GATCCTCTCG CTGTTCCT GGGGCATGTA CAGTGGGCAC GGGAAGCTGG AATTCGTATG 60  
ACGGAGCTTA TCTGAAC TACTACTGAA CAGCTTGAAG GCCTTTTGAG TTCTGCTGGA 120  
CAGGAGCACT TTATCTGAAG ACAAATCAT TTAATCATCT TTGAGAGACA AAATGACCTC 180  
TGCAAACAGA ATCTTGGATA TTTCTTCTGA AGGATTATTT GCACAGACTT AAATACAGTT 240  
AAATGTGTGA TTTGCTTTTA AAATTATAAA AAGCANAGAG AAGNCTTTGT ACACACTGTC 300  
35 ACCAGGGTTA TTTGCATCCA AGGGAGCTTN 330

40

SEQ ID NO:5693

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06762

SEQUENCE DESCRIPTION:

45 GATCANAGGT CTGAGGTCT TTACATCTTG ACATATACAC TGAACAAAAAN GGGGGTTGTA 60  
TGTATNAATG TGCTACCCAA ACCTNTGGCC GCCACTTTTA AATTCTCAGA TTGCCCTGAA 120  
TTTTGNCACT TTNAATAAT GNN 143

50

SEQ ID NO:5694

SEQUENCE LENGTH:273

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06763

SEQUENCE DESCRIPTION:

GATCTTAATG CTTCTCCTGC TCTGTAAGCC TCTNAAGAGC AATATCTAAT TAATTATTAC 60  
 TGTAATTTTT TAAAAGGCTT TAAAGTGCCT CAGGGGTCCC CTGAAACTAA TTCCTATTT 120  
 CTGGGATTCC CTGGATTCAT TATATGNNAT GGTGACATGA TTAGAGGAAT TCNTTTTAAG 180  
 TATGAAANTT GTCCCTTTCC TNCTTCAGTA CTTGCCTCCT NGCTGGCATT GANTTAACAC 240  
 AGGGACAAAA TTTGGTTAAT TNNTNATTNC NAN 273

SEQ ID NO:5695

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06764

SEQUENCE DESCRIPTION:

GATCTGTAAT ACAGGAACCA AATGTCATGC GTCATACATG TGGGTATAAA GTACATAAAA 60  
 TATATCTAAC TATTCATAAT GTGGGGTGGG TAATACTGTC TGTGAAATAA TGTAAGANGC 120  
 TTTTCACTTA AAAAAAATGC ATTACTTTCA CTTANCACTA GACACCAGGT CGAAAAATTTT 180  
 CAAGGTTATA GTACTTATTT CAGCANTTCT TAGAGATGCT AGCTAGTGTT GAAGCTAAAA 240  
 NTAGCTTTAT TTATGCTGGG NTGGTGATTT NTTTATGNCA AAATTTTNT AGNGCGAANC 300  
 ATGTGGTGGN TAGCTTGGNN ATGAANGAAT TNTGNCN 337

SEQ ID NO:5696

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06765

SEQUENCE DESCRIPTION:

GATCTAGAAG TTGCAACATT CGTTTGATAG GAATTCAGCA AAAGNAGAGT TATGAGAATA 60  
 GGGCAGAGGA CATAATTAAG GAAATAATTG ATGAAANCTT TGCAGAACTA AAGAAAGGTT 120  
 CAAGTCNCGA GATTGTCAGT GCTTGTGCGAG TACCTAGTAA AATNGNATGA AAAGAGGCTG 180  
 GCTCCTAGGC ACATCTTGGT GAAATTTTGG AATTCCTAGT GATAAAGGGG AAATNATAAG 240  
 GGCTNCTAGN GGGNGANGGG AATTNCNTGC CAGGGANCAG GNTCAGTTGN 290

SEQ ID NO:5697

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06766

SEQUENCE DESCRIPTION:

GATCATTCCT GTATTAAACT TTCATATGCC AAAAGGGTTT GTCCCGTTTN ATCTGCCATC 60  
 AGTGTGTTGAC CTGTTTAGGG CAGAGGCAAT AAGTCAGAAG TCTTGAAGTT GAAATAGTTA 120  
 TATGTGTGTC ATTGGACTGG ATTATAAACA GCTGTCTTGG ACTTTCCTC TCTTAACACT 180  
 GACTGGTNAT CAGTATCATT AGTGAAAAAG NAAGCAAATT GTTTGTNATC ATCTCTTTAG 240

NCAGGTAAGC TGGAATGGGT GGGGCTTTAA ATAATANAAN CATGCGCATN GTTGGCTTGT 300  
GTATGGGCCT NCTCTGGGA TTCCTNGTNG TNATGGGCTT GGTATTTTGG GTNCNTGATT 360  
TTGTCCANNG GCANTNCCAG GTGGGTGCCA NCN 393

SEQ ID NO:5698

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06767

SEQUENCE DESCRIPTION:

GATCCANGNT AAGAGGCNCC CCCCCGACCA GCAGAGGCTC ATCTTTGCAG GCAAGCAGCT 60  
GGAAGATGGC CGCACTCTTT CTGACTACAA CATCCAGAAA GAGTCGACCC TCAACCTGGT 120  
CCTGCGCCTA NGGGTTGCTG TAAATCTTCA ATCAATGCAA TNNCNATGCC CATNAN 176

SEQ ID NO:5699

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06768

SEQUENCE DESCRIPTION:

GATCTACTCA GACAGGACCT TCGCACCTTT GCCAGAGTTT GAGCAGGAAG AGGATGATGG 60  
TGAGGTAACT GAGGACTCTG ATGAAGACTT TATACAGCCC CGNAGAAAAC GCCTAAAGTC 120  
AGATGAGAGA CCAGTACATA TAAAGTAAAA TNACATGGAT TTAAATCAAT TGTTTAAA 178

SEQ ID NO:5700

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06769

SEQUENCE DESCRIPTION:

GATCGTTTCT TTAGAAAAGT GGCATTGGCT TTTGAATATG AAATCTTCTC ATAGCTGCCT 60  
AAAAAAGACT AGAATGTATA TGGATATCAG AAACCTTTAA TAATACATAA TTTATGCAAA 120  
GATAAGATAA AGCAACATAA CACTAATTAT AAAACTATTT TTAAATCCCC ATTTTAAATG 180  
ATAANTATAC ATTTNTATTT AATTTCTTTT GANTAAAACA NTTGTAAAGT AAA 233

SEQ ID NO:5701

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06770

SEQUENCE DESCRIPTION:

GATCTTCATC TGACTATGAC ATAAAAACAA CTTTATACCC AGAAAGTTAT TGATAAGTTC 60  
ATACATTGTA CGAAGAGTAT TTTTGACAGA NTATGTTTCA AACTTTGGAA CAAGATGGTT 120  
CTAGCATGGC ATATTTTCA CATATCTAGT ATGAAATTAT ATAAGTNTTC TAAATTTTAT 180  
ATCTNGTAGC TTTATCAAAG GGTGNNANTT ATTTNNTTCA TACATATTTT NGTAGCACTG 240

ACAGATTTC ATCCTNGTCA CTACCTTCAT GCATAGGTTT NGCAGTATAG TGGCGCCACT 300  
GTTTTGAATC TNATAATTNA TACAGGTCAT ATTANTNTAT NGCCCTTAAA AAANATCAGT 360  
TGTTCCAGNG GAAN 374

SEQ ID NO:5702  
SEQUENCE LENGTH:452  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06771

SEQUENCE DESCRIPTION:  
GATCCTCCTG CCTCAGCCTC CTGAGTAGAC GGATTATAGG CACCTTGCCC AGCTTCTATA 60  
GCAGCATTTT TTTCTAACAC CTAATAAATG GAAACAAGCC AAATGCTCAT CCACTGGTAA 120  
ATGGATAAAC AAAGTGTAGT CTTTCTATAC ACTGGAATAT TTGGCTATAA AANAGANTGA 180  
NATATTGATA CATGCTACAA CATTGATGAN CTTCAAAAAC ATGCTAAGAG AAAGCCAGTC 240  
ACAGAANAAT ACATNGTATT CTATAAGAAT GTCTAGGGAN CGTNAATCTA TATNGGCAGA 300  
AGGTAGGTTN GTGGTTGCCT AGGGCCCGGG GGGAAAGGGT TAGGGGGCCT NGGGGGTGNC 360  
AGCTTATGGG GCTGCTAATN GGGCCTNCCG NTTCTCTTN GGGGGTTGGT ACCCTGCTAA 420  
ATTGNCCTNN TTGGCNTGGT TTTNNCCCG GN 452

SEQ ID NO:5703  
SEQUENCE LENGTH:257  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06772

SEQUENCE DESCRIPTION:  
GATCTGTCTG TGCACATGCC TCTGTAGAGA GCAGCATTCC CAGGGACCTT GGAAACAGTT 60  
GACACTGTAA GGTGCTTGCT CCCCAGACA CATCCTAAAA GGTGTTGTAA TGGTGAAAAC 120  
GTCTTCCTTC TTTATTGCC CTTCTTATTT ATGTGAACAA CTGTTTGTCT TTTTTGTAT 180  
CTTTTTTAAA CTGTAAAGTT CAATTGTGAA AATGAATATC ATGCAAATAA ATTATGCAAT 240  
TTTTTTTTCA AAGTAAA 257

SEQ ID NO:5704  
SEQUENCE LENGTH:77  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06773

SEQUENCE DESCRIPTION:  
GATCANGAAG CTATTTTCNA TTCTGGGGAA CGATTATAAC TTAAATNATT GTTTTAATAA 60  
AAATTCTAAG CTGGAAG 77

SEQ ID NO:5705  
SEQUENCE LENGTH:278  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06774

## SEQUENCE DESCRIPTION:

GATCCAATTT CTTTGTGGTA CCTGCAGTTT ACAAATAAT TTGACTTCAG TGAGCATATT 60  
 GGTATCTGGA TGTTCCAATT TAGAACTAAA CCATATTTNT TACAAAAAGA TATTAATCCC 120  
 TCTACTCCCA GGTTCCCTTT ATATGTTAAG ATATAATGGC TTTGAGGGGG GAAAAATAA 180  
 ACCTAGGGGA GAGGGGAGTT TCCTGTAGTG CTGTTTCATT AGAGGATTC AGTAAATTAA 240  
 ATTCCACAGC TAATTGAATA AATAATGGNA CCTTTAAA 278

SEQ ID NO:5706

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06775

## SEQUENCE DESCRIPTION:

GATCTGCATA TNATGTATTA GGTTAGGTCA CAAAGGTTTT ATCTGAGGTG ATTTAAATAA 60  
 CTTCTGATT GGAGTGTGTA AGCTGACCNA TTTCTAATAA AATTTTAGTT GTACACTTTT 120  
 AGTNGTCATA GTGAAGCAGG TCTAGAAAAT AAGCCTTTGG CAGGGAAAAA GGGCAATGTT 180  
 GATTAACTC AGTATTAANC CACATTANTC TGTATCCCAT TGTCTGGCTT TTGTAATNC 240  
 ATCCAGGNCA AGNCTAAGTA TGTGGTTAA TAGGNATCCT TTTTTTTTTT TTNAANGCCT 300  
 AANNNGGN 308

SEQ ID NO:5707

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06776

## SEQUENCE DESCRIPTION:

GATCGTAACC CCTTGTTGAC TAATCTNGCC GTGGTTTTGT NTAGGTCTGC AGGAAGGAAG 60  
 NCTNAAAAAG CGGACGAAGA TTTTNACTTA AGTGGGACTT TGTN 104

SEQ ID NO:5708

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06777

## SEQUENCE DESCRIPTION:

GATCCTAGTA AGTCANTNGT AGTTTACTGG TGANGTGAGC ATTNTAGATT CCCCCNTTAT 60  
 CACTAATCAC ACAACAATTT TAAGAAGTAG GCTATAAAC AAAAAAAGGT TGCTGTTTTT 120  
 TATTTTAAA TAAACNN 137

SEQ ID NO:5709

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06778

## SEQUENCE DESCRIPTION:

GATCTCATTT GCTGGAATGA TTGATTTAAG AGTAAAATTA GCCACTGCGT NTGTNTNGTG 60  
 TATAGTAACC GGTITTNTTG CACTTGTCTG TGGCTGAAAC ACTTACCTGC AGTGGAAAGC 120  
 CGTGCAAGGA GGAGGTAAAC ATTGGAGATG TTTGTNAAAA TATTACTCTT GCTGTGAGGT 180  
 TTTAGTTTGT TTTGAATGAG AAAAGACTAA GTAACTTAAT CCATCTCAAT GTAGTGTTTT 240  
 AATANNNGG GNNCCTAATA TTTGANATGG GTCTCAGACA TGTCTACAAA TATGGGTACT 300  
 ATTTTNTTGC CCGTGTATTT TCACATTNA NAN 333

SEQ ID NO:5710  
 SEQUENCE LENGTH:126  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06780

SEQUENCE DESCRIPTION:  
 GATCCTTATA AATNAGAAAC ATGCAAGCTT CAGCTGCTCG AGTTCTATAG TGTCACCTAA 60  
 ATCGTATGTG TATGATACAT AAGGTTATGT ATTAATTGTA GCCCGGTGNN CNTCGNGGGN 120  
 ACCTTN 126

SEQ ID NO:5711  
 SEQUENCE LENGTH:133  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06781

SEQUENCE DESCRIPTION:  
 GATCCGGCAA ACAAAACCACC GCTGGTAGCG CGTTTGTNTT TGTTTGCAAG CTTCAGCTGC 60  
 TCGANTTCTA TANNGCCACC TAAATCGTAT GTGTATGATA CATAAGGTTA TGTATTAATT 120  
 GTAGNCGTTN GCN 133

SEQ ID NO:5712  
 SEQUENCE LENGTH:116  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06783

SEQUENCE DESCRIPTION:  
 GATCCTTTTA AATNAAAAAT AAAGTTTAA AAAAAACAT GCAAGCTTCA GCTGCTCGAG 60  
 TTCTATAGTG TCACCTAAAT CGTATGTGTA TGATACATAA GGTTATGTAT NCNNNN 116

SEQ ID NO:5713  
 SEQUENCE LENGTH:268  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06784

SEQUENCE DESCRIPTION:  
 GATCTTCTCA ATGGGTGGNC TCCTGGTATT CGTGGGACCA CCTGTGGGCA CAGGAGCCAA 60  
 TGTGGTTCAG ACAGCTGGGC AGAGGGAGCT GCTAGTCAGC TGTTTGCCCA CACTCTGCCT 120  
 GTCATGGTGA TTTGNACCCT ACCCCCTGG TCCCAGNGNC CTGGGGCTCA CTTGATACCG 180



TTGAAAGTAA GCACAGNCTG CATGTNCTCA GGNAGGNCCT GGGGCTCAGG GCACTCGAAG 240  
NCATCAATGN TGGGNACANT GTTNTTGN 268

5 SEQ ID NO:5714  
SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06785

10 SEQUENCE DESCRIPTION:  
GATCTCAGAA TACAAATTTA AATAAATTAA TTTAATTCTC AAAACACCCT TGATTGGAAC 60  
TTACAGCTGG CCCTCTGTAT TCGTGGGTTT AACCAATCAC TAATTAAAAA TATTGGAAAC 120  
AANNNNNNN 129

15 SEQ ID NO:5715  
SEQUENCE LENGTH:214  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06786

20 SEQUENCE DESCRIPTION:  
GATCCTGCAT TTATGGTGTA GTTCTGAGTC CTGAGACTTT TCTGCGTGAT GGCTATGCCT 60  
TGCACACAGG TGTTGGTGAT GGGGCTGTTG AGATGCCTGT TGAAGGTACA TCGTTTGCAA 120  
25 ATGTCAGTTT CCTCTCCTGT CCGTGTGTTT TTAGTACTTT TATAATGAAA AGAAACAAGA 180  
TTGTTTGGGA TTGGAAGTAA AGATTAAAC CAAA 214

30 SEQ ID NO:5716  
SEQUENCE LENGTH:253  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06787

35 SEQUENCE DESCRIPTION:  
GATCTAATCC CTTCAAGGAA GTGATAACAC TGGAGTGGTA ACAAGAGGAG CAGGAAGCAA 60  
GGCCAGCCCT GGTTCTCCAT CCCCATGTGT TTCAGGTGGA ACAGGAGGAA CTGGNCCAGG 120  
CCAGGCCTCA TCCTCCTGGA CCCAGCAGGG GCAGAAGGAG GAAGGGACTG GTCCAGGCAT 180  
GGGTCCCTTC CCNNTGCTCC ATGGGCANCT CTGCTGTATT GATATCACTA GTAAAGTCTG 240  
40 TCTGCACTGC AAA 253

45 SEQ ID NO:5717  
SEQUENCE LENGTH:332  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06788

50 SEQUENCE DESCRIPTION:  
GATCATGTCT TTCAGAATCC ATGTACATAT AGGCTGTNCT AGCCACAGTG GTAGATTTAT 60  
GATTACATC CGAAAGTGTG CCTTAGTTAT CAATTTAACA TTTCTCTAGT ATTCATATCC 120  
55 CTTTCCTTAC CATATACCTC AGTGTATCCT TCCTGTGTCA AGCCTTATAA ATCATGTAAT 180

TTAGTGCCAC TCATGTAAAT CAGTAAAATC ACAAAGGTCT ATTTAATGAA AACGATTAC 240  
 CAATGTTGTT TTTTTTTAAC AGGANAAGNA NTAGNAGCAC NTTGTCATTT TTNAGANGGN 300  
 GGNNTTGTTG GGNNGTGGGG GGGNNGNTTG GN 332

SEQ ID NO:5718  
 SEQUENCE LENGTH:284  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06789

SEQUENCE DESCRIPTION:  
 GATCATGCCA CTGCACTCCA GCCTGGGCAA CCAGGTGAGA CCCTGCCTCA AAAATAATAC 60  
 AATAAAAAGT AAAAGCAGCC CTGGGGAAAT GGAGACAGTG GACAAAGCAG GCTGGGGCAC 120  
 CAGGTGTGCA TGTGGGTGTG AGTCTGTCAT GAGAGCTGTC CTGANTGCCC TTAACGCCAC 180  
 TGAAGTGTAT GCTGGAAAAC AGTGACAACA GTGGATTTTG TTATATAGAC AATTANANN 240  
 GTATANCACC CAGAAANANT GTGTGNNTGT TGGGNGTGG TGNN 284

SEQ ID NO:5719  
 SEQUENCE LENGTH:253  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06790

SEQUENCE DESCRIPTION:  
 GATCTTTAAC TCCTCCTGGC TGCACCTGGG TAGGGATGGT GGCATCGATG CCCCTCTGTC 60  
 TGCTGAAGGA CCTGTTGCTG CTTCTGTCTT TTCACCCCTC CTTGGCTGAT GACCCAGAGC 120  
 CCTCTGATGA TGGCATTCTC CTGGCAAGAG AAAAAGACTT AACTAGACTT CTGAACTGA 180  
 ACAGTTTCAG GTTATATTTT AATTTNNNT TTTTGTGAC NGGTNCNGAT NCTAATACAT 240  
 TNCACCNNGC AAA 253

SEQ ID NO:5720  
 SEQUENCE LENGTH:389  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06791

SEQUENCE DESCRIPTION:  
 GATCCACCCA CCTCGGCCCC ACAAAGTGCT AGGATTACAG GTGTGAGCCA CCATGCCCGG 60  
 CCCAGAATAC TTTTAAAAG AAGAGCAGGT TAGAGGAAAG AAAAAATTG ATGCTGAATG 120  
 TGGTGATGAA AGCATGTTTC TAAAATGGGA AGCAGATGCT TAANGAGGAA AGACTAATCT 180  
 GGGATTTTGC CCCATTTCTC TGGNTTTTCA CTCCTATATT TNATTCTCAC AATCGTGTG 240  
 TCACATAGTG CANAANACAN ATTTCTTGTA AAGTCCCAG GGGTTTATGC TTGGGTGAAA 300  
 GTTTTAGCCT GAGTATTTT CTTNCTCTAA AAANAGGTGG GGANTGNGNC ATTTGAGGNT 360  
 NTTNACCTTT TAATTGTNCT GCTATNGGN 389

SEQ ID NO:5721  
 SEQUENCE LENGTH:174  
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06792

SEQUENCE DESCRIPTION:

5 GATCTGGTTG GGGTTTGGG TTTTGTGTTG TTGTTGTTTA TTTGTTATTT TAAAGGTAAA 60  
 TTGCACTTTT AAAAAAATAA TTGGTTGACT TAATATATTN NCTTTTTTNC TCACCTGCAC 120  
 TTAGAGGAAA TTTGAACAAG TTGGAAAAAA ACANNNTTNG TTTCAATTCT ANGN 174

SEQ ID NO:5722

10 SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06794

15 SEQUENCE DESCRIPTION:

GATCCTATGT TGCTGGAAC TGCCAAACAG GATGTTGTGC TCAATNACCC CATGTGAGTG 60  
 CGTGGACTCC TGGGAGCTCC TGCTCCNTAC AGTGGGCTGC AACTCCTGTA CTTGAAGCTG 120  
 AGACCTCATA TGACGTGGCC TTCGTGTTGT CAGAGAGTGT CTGGAAGCTG CTGTTGCCAT 180  
 CTTGAACAAC TCACCAACCT CCAACCCAGA GCCCCAGTGA GAGAGGAGCA TTTGGCCTCC 240  
 20 TGCTTCCTTC TGTGGCCTCT GCCGGGCTCC ATTNCCAAGG AAAAGAGAGG AGCTTGGGCT 300  
 CACAGAAAGA GAAGGGGATG AAACCCCAAG NGGCCCTATC TTTTGGGATT TACATGGGAT 360  
 TTTTATN 367

SEQ ID NO:5723

25 SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06795

30 SEQUENCE DESCRIPTION:

GATCCTGAGT AATCCTTTTA GAGCCCGAAG AGTCAAAACC CTCAATGTTT CCTCCTGCTC 60  
 TCCTGCCCCA TGTCACAAA TTTCAGGCTA AGGATGCCCC AGACCCAGGG CTCTAACCTT 120  
 GTATGCGGGC AGGCCAGGG AGCAGGCAGC AGTGTCTTTC CCCTCAGAGT GACTTGGGGA 180  
 35 GGGAGAAATA GGAGGAGACG TCCAGCTCTG TCCTCTCTNN NNNCTCCTNC CTTCAGTGTC 240  
 CTGAGGAACA GGACTTTCTC CACATTGTTT TGTNTTGCAA CATTTTGCAT TAAAAGGAAA 300  
 ATCCACTGAA A 311

SEQ ID NO:5724

40 SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06796

45 SEQUENCE DESCRIPTION:

GATCCTCCGG CCTCAGCTGG TCTACAGGCG GGTAATCAAG GGAAGGGAC TACAGGCGCG 60  
 CCCTGCCGCG CCGGGACAAG TTTTGTATTT TTAGTAGAGA CAGACTCTCC CTGTGTTGCC 120  
 CAGGCTGGTC TCCAACTCCT GGGCCTCCCA AAGTGTGGG ATTACAGGCG TGAGTCACCC 180  
 CTGCAGGCCA CAGCTTTGCT TTTTAAAGC ATTTCTGCAT AACTAAAAAG ACAGGAAATT 240  
 50 ACGAGCATAC GGNAACTGAT TTCTGCTTTC CTGAATTTTC TAAATGTATT TAATGGGCAT 300

55

GGTTCTTTTG CAATGAAAAA GTAATANATT NGGGTNTCAT CN

342

SEQ ID NO:5725

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06797

SEQUENCE DESCRIPTION:

GATCCGCCGA CCTCGGCCTC CCAAAGTGCT GGAATTACAG GCGTGAGCAC GTGCGCCTGG 60  
 CCAAGAATGG ACATTTTSTA AAAAAACATC AGTACTTCCT ACCACTGCTG CATGAGTATA 120  
 ATGCTCCGGA ATTATCAGAA AGCATAATGC AGAAATACGA ATTAGTGGA CTTAATCATG 180  
 TGCCATATAA GCTTACCTAA CAAACAGTTA TATCCCTATT CCTCAACTGA ATGTCTTTTA 240  
 ATAAATNAGA NTTTATCATT TNNNGTANGG GTGNGTGTGN GGNTGGNNGG GGGGGGGGNG 300  
 GGGNNGGGGN GN 312

SEQ ID NO:5726

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06798

SEQUENCE DESCRIPTION:

GATCCTAGGC TCCCTCCATC CCTGGTATGT GGTCTCATT TTCATATAGA CCAAGAGCTA 60  
 GAGCTCCAGT TACCATTCTT TAAAGTATAT TTTAATGCCA AATAGTGAAT AAAGGTGGCC 120  
 AGAAAAATTCA AA 132

SEQ ID NO:5727

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06800

SEQUENCE DESCRIPTION:

GATCANCTAA GGTCAGNAGT TNGAGACCAG CCTGACCAAC ATNGTGAAAC CCTGTCTTTA 60  
 CTAAAAATAC AAAAATTAC CAGGCACCTA TAATNCCAGC TACTTCAAAG GCTGAAGCAG 120  
 GAGAATCACT TGANN 135

SEQ ID NO:5728

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06801

SEQUENCE DESCRIPTION:

GATCAGTGGG CCTCCAAGGA GGGNCTGTAA AATGGAGGCC ATTGTGTGAG CCTATCAGAG 60  
 TTGTGCAAA CCTGACCCCT GCTCAGTAAA GCACTTGCAA CCGTCTGTNA TGCTGTGACA 120  
 CATGGCCCCT CCCCCTGCCA GGAGCTTTGG ACCTAATCCA AGCANNCTCTT TGCCCAGAAA 180  
 GAAGATGGGG GAGGAGGCAG TAATAAAAAG ATTGANGTAT TTTGCTGGAA TANGTTCNGA 240

TTCNTCTGAA CTCAAACTGA GGAATTTAC CTGTNANCCT GNGTCGTACA GANAGCTGCC 300  
TGGTNTATCC AAAANGCTTT TTNTTCCTCC TGTN 334

5 SEQ ID NO:5729  
SEQUENCE LENGTH:158  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS06802

SEQUENCE DESCRIPTION:  
GATCCTGTAA GCAGACTTGG GCAGTCTCCT TTAGAAATAG GTTGTCTGTA CATGTTCTAN 60  
GGTNTTGTAG ACACGTGTGA CTGTNTANGT GTATTGATGT GAATANTATT AAATATCCTA 120  
ATTATNTAAT TCATTGTATT GTTCTGNGA AGTTGGGN 158

15 SEQ ID NO:5730  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS06803

SEQUENCE DESCRIPTION:  
GATCCATANA AGAGCTCCTA AAGAAGAACC CACATGAAAA ACTATCAGAA TCATGTTTAA 60  
GCTAAACCCA TATNCAAAGA CCAANCNACG NACCACCATT CTTCGN 106

25 SEQ ID NO:5731  
SEQUENCE LENGTH:105  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
30 CLONE:HUMGS06804

SEQUENCE DESCRIPTION:  
GATCCTGGTG TGTGTATTAT ATAAAGAGAC CCCTCCCCTT ATTTGTGTT TTCCATCCCT 60  
CTCCCTTAAC AGGATTGAAA TAAAACATGC TTCTGTTTTT GTAAA 105

35 SEQ ID NO:5732  
SEQUENCE LENGTH:243  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
40 CLONE:HUMGS06805

SEQUENCE DESCRIPTION:  
GATCANCAAA ATCCAATTTT ACATGTGGCA CTAGGAAAAT GGAATGCTAT AAAATTAATC 60  
CCCATACCC AAGTAGGGAT GCTGGTGCTT TTATACTGAG TCTTTACTGC CAATAAGTGA 120  
TGCTGGCTGC AAAGGANCAG CTCTACAGAA AGTTTTTGGG TTAGTGTTC CTTAGCTTAT 180  
TNCTGCANTG GGGAAAGCCA GTTTCATACC AAAAANGANA ATGNAGGTGN TTATANTGNN 240  
NNN 243

50 SEQ ID NO:5733  
SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06806

SEQUENCE DESCRIPTION:

GATCTCGGTC ACGTGTCCCG GCGGCTGAGG GGAAAGGAAG CGGGCATGAT TGTAGACAAT 60  
GAGGGGGTTC TCTTGATGTA ATGAAATGCA ATTTTATGGT TTGGTGCAAA AACTCCTATT 120  
TTCCAGTAAA TTAACTTTAT TTCTAAAGCA TATTTTGATT TGCCATCAAG AGCAATAAAG 180  
CATTAAATCT TAAA 194

SEQ ID NO:5734

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06807

SEQUENCE DESCRIPTION:

GATCTGGGCC CTGAAGTATA TAAGTAGGAA TTTGCAAGAT GGATGAGGTA GAAAAANNCTA 60  
TTTCATATTG TGGAATAAAC AGAGGGAAGA GCCATTGTC TTATCCCCAA CTCCAGAACT 120  
CTACTACTCA TGGAGTCTGA CACAAACAAT GTTAATAATC TGTTTNAGTT CTCATNATAG 180  
GGCACTGGAN TTGGCTGTAA ANTNC AAA NC ACNTNN 216

SEQ ID NO:5735

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06808

SEQUENCE DESCRIPTION:

GATCTTCTAG TTNCTGTGTT GTTTAGACTC AAAGAATCAC AAATNTGTCA GTAACATGTA 60  
GTTGTTTAGT TATAATTCAG AGTGACAGA ATGGTAAAA TNCCAATCAG TCAAAAGAGG 120  
TCAATGANTT ANN 133

SEQ ID NO:5736

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06809

SEQUENCE DESCRIPTION:

GATCTTAGCA CCCAACTCTG CTGCCCTTNC TGCTGGGCAG TGCCTNTCCT AAGAGGGGAC 60  
TCCCTAAAGG CCAGAGAGAG GGTGCTCATC TCCAGGACCT AGGCCACCTG TCAGCACAAA 120  
CAGAACTTAT TCCAGACATA AACATGAGTC TTCTTATTC AAACACTGGA GCAACTGNTC 180  
AAATATCACT CTCCTACTTA CAGGNCTCAN CATACTNGTC ACAGCCCTTT ACTCCCNCTA 240  
CATATTTNCC ACANCACANT GGGGCTCANT NNCCN 275

SEQ ID NO:5737

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06810

SEQUENCE DESCRIPTION:

5 GATCATGCTA GTNACTTCCT GCCCCCAGGC ACCGTGCCAA ANACTGGATG CCCCCTACTC 60  
 CTCAGGGGAC TGTCCAGGGC GCCCAGTGGT AGTGAGGGAG AGTGTCTCTG TTCTTTTGCT 120  
 CAGCCTGCTG GGCCCTTTGT GTTTGAGGAT GCTTAATGAT TCCAGCCTCT CACTGTGCCT 180  
 TATGCATTAA AATTNCTTTG TTACGAGCAA A 211

10

SEQ ID NO:5738

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS06811

SEQUENCE DESCRIPTION:

GATCTNCTTT ATAGCCANCT CTCCTCACTT AACAGGTACT TTCTCCAAAA ACCTAAGAAC 60  
 CAAAGTCTTC CGCTTGCAAC TTGGGATGGT GATATGGCTG TGTCCCCACC CAAATCTCAT 120  
 CTNCACCTGN NNN 133

20

SEQ ID NO:5739

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS06812

SEQUENCE DESCRIPTION:

GATCATCGCA AGGAAGNAGG CAGACAAGAG TAAGGCACAC CTGACTCTTA GGACTAGCAG 60  
 TCAGAACAG GAGGAAAGNT TTTATTGCTA TGCGGGTAGG TAAGAACAGA TTTTACTTAC 120  
 ATCCATATAG TTACTIONAAG TCCAGTTTTC TGTAAACNN NNTTCTNNN 169

30

SEQ ID NO:5740

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS06813

SEQUENCE DESCRIPTION:

GATCTCTTGT CCACTAAGTA TCTTGTTAAA TGCCAGTATC TCAGTCTTTC TGAAGCCCTG 60  
 AAATGGTAAT TGTAGCATTT CAGAAAATNT CTTTCATTTT AATCAATAAA AAGCTTTTGT 120  
 AAATAAA 127

40

SEQ ID NO:5741

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

45

TOPOLOGY:linear

CLONE:HUMGS06815

SEQUENCE DESCRIPTION:

50 GATCTTCCAG ATTAGGCTAA ATGTAATGAA AACCTCTTAG GATTATCTGT GGAGCATCAG 60

55

TTTGGGAAGA ATTATTGAAT TATCTTGCAA GAAAAAAGT ATGTCTCACT TTTTGTTAAT 120  
 GTTGCTGCCT CATTGACCTG GGNAAAATGN AACAAACAN TAAGGCAANT GGTAGGAAA 179

5

SEQ ID NO:5742  
 SEQUENCE LENGTH:196  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06816

10

SEQUENCE DESCRIPTION:  
 GATCAGCCCT NCCCTTCAGC ATCCTCAGNT CCTGNAGCAG AGCCTGGAAG ACACCCTAAT 60  
 GTGGCAGCTG TCTCAAACCT CCAAAGCCC TGAGTTTCAA GTATCCTTGN TAACACGGNC 120  
 ATGACCACTT NCCCCGTGGG CCATGGCAAT TTNACACAA GCCTGAAAAG ATGTTGTNTC 180  
 TTNTGTTTTT TTCTTN 196

15

SEQ ID NO:5743  
 SEQUENCE LENGTH:326  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06817  
 SEQUENCE DESCRIPTION:

20

GATCCGCAGT CCTAACAGGG TGAGAAAGCA CAAGAGGGGC CAGCTCGGCT GAGGCCTGAG 60  
 GAGAAATAAT GAGAAGTTTT GTTTCGTCT TGGGCTGGGG CATCTCAGGA ACAGTGAGGG 120  
 CAACAAGCTG TCCCTCAGGG ACCCTCACCT GCCCTCCCAT GTGACCAGGC CCTTCCCAGG 180  
 TGGGGACTGG GGCTTGCTTT ATTAAGTGAG CTCTTGGGCT TTTGAAGTAG GACAGAGGGC 240  
 CCTGGTTTGG CAGAGAGGAG GCAAGGGAGG GCTTTAGAAC ATCTGAGAAA TGTTAATAAA 300  
 ATANTTCAGA AANTAGGAAA AAAATN 326

30

SEQ ID NO:5744  
 SEQUENCE LENGTH:105  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06818

35

SEQUENCE DESCRIPTION:  
 GATCTCGAAC CCTGTCTAGA AGGAATNTAT TTGTTGCTAA ATGTTCACTT TTTATAGTNA 60  
 TGTCCTGTAT TCTAAACAGT AAAGGGGNTT TATTNCTATC AAAAA 105

40

SEQ ID NO:5745  
 SEQUENCE LENGTH:167  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06819

45

SEQUENCE DESCRIPTION:  
 GATCTCAGAA GTTTTAAAA ATAGCAAAGA AGACTGNATT TGGAAANCAT GGTCTACAAT 60  
 TGGNTGTAA ATNCTGAAGC TATGAAGAAT AAATATTTCA ACTTTGGATT ATGAAACCCC 120  
 ATTTATGATT TTTTAAATAC ACTTGAAATA AAAATGATTA AACTAAA 167

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55



SEQ ID NO:5746  
SEQUENCE LENGTH:258  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06820  
SEQUENCE DESCRIPTION:  
GATCTNTAGA ATTNTTATTG TAATTTTCCT ACTTCTTTGA TAAAAGAAAA ATAAGTCAGA 60  
TTGTTAACTC CAAGATTGAA AAAAAAACT CTTGAAAGAN GATTATNAGT TGTAACNAAT 120  
TTGGGGGGTC TGGGCACAGA CATCTAACCT GGTATTGTAA GGCAGAGGCT CCCATTGGAN 180  
TGGTAGTGGT CCGGGTCAGT TGTTTCATGGT GTAAGCTTTG CACNGTGTAT TGAACATTNG 240  
NAGGNTCTGN CTNGAAAN 258

SEQ ID NO:5747  
SEQUENCE LENGTH:350  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06821  
SEQUENCE DESCRIPTION:  
GATCCCTGCC CTTNTCAAGA CTTTAGCTNT TCCTTCCATC CGGTGGCCTA TTCCAGGAAT 60  
TCCTCTTTTG CTTAAATCAG TTGGAGTTG TNTCTGTTGC TTGTAATCAA GCCTTTATGG 120  
CTGCTGGGCT GAGTGACACA AGCACTTTAA TGGCCTGGAG GGACTTTTAA TCAGTGAAGA 180  
TGCAATCAGA CAAGTGTTTT NGAAAGAGCA CCCTCGNGAA GGGTGGATGA CAGGGCAGGG 240  
CAGGAAGGNC AGGNAGATGG CAGAACGGTG GTGGCTGCAG CCGGGGGTNC AACCAGGANA 300  
CTGGTTGGCA AGCTNNGGGC TAGGGGGTAA GGNNTTTTNA GGGGTNGAAN 350

SEQ ID NO:5748  
SEQUENCE LENGTH:331  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06823  
SEQUENCE DESCRIPTION:  
GATCTTCCAT GTTTTGACGT TTGCAGTCAC ACACAACACC TTAGTTCCTC TAGGGGCTGT 60  
ACAGTATTGT GGCATCAGAT AATGCCACCA AAGGAGACAT ATCACTGCTG CTGGGACTTG 120  
AACAAAGACA TTTATATGGG TTTATTTTCA TTCTGCCAAA GTAAANCANT ACATCAACAN 180  
GAGGAAACTC AGNTTTAACC TGTTATTTCT ATGANNNTGG GATGATTGCT TTGTTTATGC 240  
ACTTTTTCCT GNCTGTGCAT CCGCCTGTNA GTGTTTGGCC CTNTAGTCCC TCACTAGCCA 300  
TGCTTNTGTG NTGGGTATC ANGGGNGTNN N 331

SEQ ID NO:5749  
SEQUENCE LENGTH:236  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06824  
SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCGAGGAT ATTTTAAAG AGGTTCAAGC TTGTGACTGT TAGTAGTGCA AGGATTTGTA 60  
 TGGGCTCAGT GATTACAAAC AAAGACATGC AAANTACAAC TGTTTAAACA TTTCAAGGT 120  
 ATTTTAAAG GTTTTGTATT GAAACANTGT TTATATTTNC TGAGCTCCTA AAAATGGTAG 180  
 ANTACACATG ANANCTTTTG TTTAGGAAAN GTTANCTTGT TAANTNCTNT TGATTN 236

SEQ ID NO:5750

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06825

SEQUENCE DESCRIPTION:

GATCCACCT TTGCTCCTGA CAACACTCAT TACACTAAAC ACCTCTTGGA TTTGGTGAAA 60

SEQ ID NO:5751

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06826

SEQUENCE DESCRIPTION:

GATCACTGGA TGGATAGCTC AGCCTGGGGC ATTTAGTGTT TTCCCTGGTG ATAAATCCCC 60

AAGGCAGCTG GATTTGGAGC TGGTGGCAAG TTGAAATNAT TAAAAATTGA TTTGTGTGGG 120

ACTGTCAAA 129

SEQ ID NO:5752

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06827

SEQUENCE DESCRIPTION:

GATCTTTGGA CTGAGAATGT TTGGTAACAT AGTCAAGCAT TTGTTAAGCC AAGTGTGGAA 60

ATGTTCACTT TTAACTTTA CAGTTTTTTT AATGAGCAAT TCTACATTC TAAGAAAAAA 120

GATACTTCAT TTTTATATAA GGTTACAAC TCTTTATAAA NCTGTATTCA CAATGTCAAA 180

SEQ ID NO:5753

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06828

SEQUENCE DESCRIPTION:

GATCTGGCCT TTTCTTAACA AAATCNGTGC AAAANATGCA GGTGGATGTC CCTAGGTCTG 60

TTTCAAAGA ACTTTTCCA AGTNCTTGTT TTATTATTA AGTGTCTACC NNGTAAATN 119

SEQ ID NO:5754

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06829

SEQUENCE DESCRIPTION:

5 GATCTCCATA AATNACTTAG TCTTCTATGT ATAGCTATCA AGGAAATAAA ACCAATTTTG 60  
CCACAAA 67

SEQ ID NO:5755

SEQUENCE LENGTH:323

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06830

SEQUENCE DESCRIPTION:

15 GATCAGAACA AAAACACCAC TCTTTAATGG GTCTTTTCT TGGCTAGAAG TCTTTCCTCA 60  
GTTTTTGTG ACTATCATAC GCTGATTTGT GGGTNATGGA AGGGGGCTAG AGATAACGTT 120  
TCTCTGTACT TTGGTAAAGN ATGAAGGAGT CAGAGAGGGA ACAGAAAAAG TGAGAGAGTG 180  
GCCTGCTGAA ATAATAGCCT GCCTCTAAAA GTTGTGACCA GAAAGTATGA TTCATTTGGG 240  
20 CCCAGNGGGN GTAANNTATG TTTTNCATN TACCTCCCAT AGNACANGGT GTTNGGAGGG 300  
NNGGAGTGAG TGTNNTAGAN GGN 323

SEQ ID NO:5756

SEQUENCE LENGTH:274

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06831

SEQUENCE DESCRIPTION:

30 GATCAGGTGT CTATAACATT TTTAATTCTC TCTGGAACA GACTCAGGTT TCTTTGGACC 60  
AAATCCAAAA GAACACATAG CTGTAACACA GCTGTAGTTG ACTAGAATGC TCTGTATACT 120  
TTATATTAATA AANTGCTTTG CATTTCTNCC AGTGCAATGA ANTCATATG GTGTCCCACC 180  
TTATTTAATG ATGGTACANT TTAATACTT AGTCAACTGC TGTNGAAAGT TTTCTCTATG 240  
ANAGTNANGC TGTTGAAGA ATTNANGNGN TTNN 274

SEQ ID NO:5757

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS06832

SEQUENCE DESCRIPTION:

45 GATCCGCCCA CCTCGGCCTC CCAAAGTGCT GGGATTACAG GTGTGAGCCA CTGAGCCCAG 60  
NCTGTATCCA TGTNTTCTGC ATGTTGATTC AACCAGCTAC ACATGGACAT TGTAGTTAGG 120  
CCTATGATGA TTGTGTCTGT TCTGAAGATG TACATACCTT TTCTTCTATC ATTATTCCCT 180  
AAACANTAGA GTATAACAAC TATTTACACA GCATTTACAT TGTATTGGGT NTTNTANGTA 240  
ATCTAAAGAT GGTTTAAAGN ATNCAAGAGG GTATGCATAG GNTATATGCG AATACCACCT 300  
CATTTTANAT NGNTGACTTG NGCNTCGANN ATGAGGGGAT NTGN 344

SEQ ID NO:5758

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06833

SEQUENCE DESCRIPTION:

GATCATGATA CAATTATTTT ATTAAGTCAT GGTAAATAAC AAATGAATCC AGACTTGTCT 60  
AACAGATTTT CCATCAACAA ATATTGTTAT GTGCAAAAGT ATTGCCTATG TTGTTTTACA 120  
CACCCTGCA TTAAC TAGAA CTGCTGAGAG GACTGTATAT ATGATTTTAA ACCTAAGTTG 180  
ATTTTTTTC TCACTCTTGA AAGGAGTACT TCTTTGTGAA AGCAGTTCTT ACAGCTTTGT 240  
TTTCAACCAG CTAAAAATGT TTTGTATATN ACTCTAACCT GTTGCTCTCC ACATTCTGTT 300  
GGTNCTGATT GNTGCTGTNT NCTGGTTTN 329

SEQ ID NO:5759

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06834

SEQUENCE DESCRIPTION:

GATCTATCCC TCGGCCCTCC ACACCTGAAC TTGCCTAACT AACTGGCAGG GGAGACAGGA 60  
GCCTAGCGGA NCCAGCCTGG GAGCCCAGAG GGTGGCAAGA ACAGTGGGCG TTGGGAGCCT 120  
AGCTNCTGCC ACATGGAGCC CCCTCTGNCG GTCGGGCAGC CAGCAGAGGG TNNGTAGCCA 180  
AGNTGNTTGT NCTGGGGGCT GNCNTGTGT ATCACCACC AGGTAAATTA GACCATTNN 239

SEQ ID NO:5760

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06835

SEQUENCE DESCRIPTION:

GATCAACTTT CCTTCTGTGT GTGGCTCAGN AGTTCTTCTG CAGAGATGGC GCTATCTTTC 60  
CTCCTCCTGT GATGTCTGTC TCCCAACCAT TTGTACTCTT CATTACAAAA GAAATAAAAA 120  
TATTAACGTT CACTATGCTG AAA 143

SEQ ID NO:5761

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06836

SEQUENCE DESCRIPTION:

GATCGCATCC CACAATGCGA GAATAATAAA ATAAAATTGG ATATTTGAGA AA 52

SEQ ID NO:5762

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06837

SEQUENCE DESCRIPTION:

GATCCTCCCG TNTCAGCCTC CTGAGTAGCT GGGATTACAG GCGCACACCA CCAATGCCCA 60  
 GCTAGTTTTT GTNTTTTNNNA TAGAGACGGG GTCTCGCCAT GTCATTACAGG TTGGTCTTGA 120  
 ACTCCTGGGC TCAAGCAGTC TGCCTGCCTT GGNTTCCCAG TGCTGGGATT ACAGGCGTGA 180  
 GCACCGTGCC CGGCTAAAAA GTATTTTNA GTTCTGCATA TNGCTTATTT CACTTAACAC 240  
 TATATTAGAG NTTGTTTTAT ANCANTACAT ATAGATATGC TTATCCTTGN TTGACAGTNG 300  
 CATAATTNTT CCANTAAAAAT TTGGTTGTAT CNAGGGGCAN TTAACCCAGT TACTTAGNN 359

SEQ ID NO:5763

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06838

SEQUENCE DESCRIPTION:

GATCATNAAG GACATTCCGA ATCTGGAGGA CATCAGGAAG ACCTTACCAT CTGGCTGCTT 60  
 CAACACCCCG TCCATTGAAA AGCCCTAGTC TCTTTAGGGC TGGAAGGCAG CATCCCTCTG 120  
 ACAGGGGGGC AGTTGTGAGG CCACAGAGTG CTTTGACACA AAGATTACAT TTTTCAGACC 180  
 CCCACTCCTC TGCTGCTGTC CATCACTGTC CTTTTTNAAC CAGGAAAAGT CACAGAGTTT 240  
 AAAGAGANGC AAATTAANCA TCCTGANTCG GGNACANAGG GTTTTATCTA ANANNNGGTN 300  
 GNNNGTGN 308

SEQ ID NO:5764

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06839

SEQUENCE DESCRIPTION:

GATCATAAAT ATTAATAATN AAACTGAGA AACTATTAC AATGCATTCC TTATAAATAA 60  
 ATGCTACATT TAGTAACTCA TTTACCCAA A 91

SEQ ID NO:5765

SEQUENCE LENGTH:320

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06840

SEQUENCE DESCRIPTION:

GATCAGCACA AGTAACAGAA AATNAGCCTG ACGGTGGCTT AAGCAATGGG AATGTTTATC 60  
 TCACATAGCA AAAAGTCTGT AAATAGATGG TTCTAGAGTT GGGTGGAAGC CAAAATGTCA 120  
 TCAGGATTC CTTGGAACCG TCTGCTTTC CATCCTCAGT ATTGCAGAAT GGCTGCTCCT 180  
 GCGCCAAGCA TCATTCTGCA AATNATGGTG TCCACAGCCA GAGTGGACAG TAGTACAGGN 240  
 GCCTTCTCAT TCTGCCCTTA TCCGGGANTA ACCGTCAGCN GCTCCAGCAA CCTNCCCCT 300  
 GTCTNTTAT AGNGTGGGNN 320

SEQ ID NO:5766

SEQUENCE LENGTH:320

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06841

SEQUENCE DESCRIPTION:

GATCCCACTC TGATTGCATC CATTTCTCTG AAAGACTTGT TTGTNCTGCT TCTCTTCATA 60  
TAACTGAGCT GGCCTTATCC TTGGCATCCC CCTAAACAAA CAAGAGGTGA CCACCTTATT 120  
GTGAGGTTCC ATCCAGCCAA GTTTATGTGG CCTATTGTCT CAGGACTCTC ATCACTCAGA 180  
AGNCTGCCCTC TGATTTACCC TACAGCTTCA GGCCCAGCTG CCCCCAGTC TTTGGGTGGT 240  
GCTGTTCTTT TCTGGTGGAT TTAATGCTGA CTCACTGGTA CAAACAGCTG TTGANGCTCA 300  
GAGCTGGAGG TGAGCTTCNN 320

SEQ ID NO:5767

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06842

SEQUENCE DESCRIPTION:

GATCCAGTGA CAATNTGCCC CCTGCCAGCC TGNGTGTCGT CACTCATCAT TCATTCATCC 60  
ATNCTAGAGC CAGGTCTCTG CNTCCCAGAC GCGGCGGGNG CAATGCTCCT N 111

SEQ ID NO:5768

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06843

SEQUENCE DESCRIPTION:

GATCATTCTC TCTGAGGGCA GNTGNGGCGC AGGNAAATAG TCTTGNAAT GTTAAATATG 60  
ATGGGTAAAT TAAAAGTTTT ACAACATTCT ACCTAATATT TTNCTTTTAA CATACTTTTT 120  
CTGTTCTATT GTATTATGGT GTCCGAAAGC TAAATAACGN CTAGGNAAAA TTTTTTTAAA 180  
AAAAGNAAAA TCAGTTTAAT GTGGGNAGTA CTTAAGTGGT ATTATATTN NCATTTTCAC 240  
GTATAGTGCA TANAGN 256

SEQ ID NO:5769

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06844

SEQUENCE DESCRIPTION:

GATCGTGTTC ACAGAGGACT TCTTTAAAGT GTCACATTTT TAAAATGTAA ACATATTTTT 60  
AATGCATACT TAAGTAATAT TTAAGAAACT AAACAAAATA ATGATACANT TGCAGTGTTC 120  
TGCTTGTTGT CAATGACAAA AATAAAACCA TTTTGGTGGT AAA 163

SEQ ID NO:5770

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06845

SEQUENCE DESCRIPTION:

GATCTCCAAG AAGTGACTCT AGCAGAAGAT TTTATGGTGA TAAGCATNCC AATCANGAAA 60  
TGAAACCAAGT GTTCCTGAGT GCACACTGAC ATGTCTGTGA ATATGTTACT GAACCTATAG 120  
TCCAGTTTTT TNATNTCTTG TTTTAGTCTG AAATNATTTG GGCCCTAATA ATCCTAAAAAN 180  
GAATGGAGCT GCATTGATGA ATTGGCTCAG TATTTAANGG GAGCAAACCT NTNGATAATA 240  
NNTCTTTTNA GGN 253

SEQ ID NO:5771

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06846

SEQUENCE DESCRIPTION:

GATCTGAAAT ACTGACAGNG TTCCCCAAAG TTAGATATTA ACACAGCTTT TNACNTCTCT 60  
TATGAGAACT TTAAGTAAA TATACCTTTA TCATAGAAAT GAGATATCCA ATACCTNATG 120  
GNGACTACAA AAAGGNN 137

SEQ ID NO:5772

SEQUENCE LENGTH:371

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06848

SEQUENCE DESCRIPTION:

GATCCCAGAG TTCAGCCAGC CTGGGGTCCA GAACTCAAGA GTCCGCCTGC TTGGAGCTGG 60  
ACCCAGCGGC CCANAGTCTA GCCAGCTTGG CTCCAATAGG AGCTCAGTGG CCCTAAGNAG 120  
ATGGGCCTGG GGTGGGGGCT TATNAGTTGG TGCTAGAGCC AGGGCCATCT GGACTATGCT 180  
CCATCCCAAG GGCCAAGGGT CAGGGGGCCGG GTCCACTCTT TCCCTAGGCT GAGCACCTCT 240  
AGGCCCTCTA GGTGGGGGAA GNAACTGGA ACCCATGGCA ATAATAGGAG GGTGTCCAGG 300  
CTTGGGNCCC TNCCTGGTN CTCCNAGTGT TTTGNTNGGG TAATAANTTG GANCTATGGG 360  
CTCTNAATTG N 371

SEQ ID NO:5773

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06850

SEQUENCE DESCRIPTION:

GATCGCACAC TACGCTCCAG CCTAGGTGAC AGAGTGAGAC TCCATCTCAA CAACAACAAC 60  
AACAAAAAAC CACAAAAACT ATATTTTAA TCATGTTTGG TAGCTTGAAA ANTAAATNCT 120  
TTCTGCCTAA A 131

SEQ ID NO:5774

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06851

SEQUENCE DESCRIPTION:

GATCTGAAA ANCTGCTGAC AGAGTGGCCA GACACAATAC CACTGTCTTT GGCTCTGGGG 60  
 NCAGTTGGCA TGCCAGGCCT GACTGCCTAC TTTGGCCTAC TTNAATCTG TGGTGTNAAG 120  
 GGTGGAGAAA CAGTGATGGT TAATGCAGCA GCTGGAGCTG TGGGCTCAGT CGTGGGGCAG 180  
 ATTGCAAAGC TCAAGGNCTG CAAAGTTNTT GGNGCAGTAG GGTCTNNTGN AAAGGNTGCC 240  
 TACCTTNAAG AGGN 254

SEQ ID NO:5775

SEQUENCE LENGTH:346

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06852

SEQUENCE DESCRIPTION:

GATCCTGGTG CTATGGTTTG AATGTCCCCA CAAAACTCA TGTGAAATT GAATTGCCAT 60  
 TGTTTAACAG TATAAGGGGT GACTGGGCCA TGTGAGCTCT GCTCTCATGA ATGGATTAAT 120  
 GCCATTGTCA TGGAGTAGGT TAGTTTTCTC TGGCGTGGGC TCCTGGCAA AGGATGAGTT 180  
 CTGCTGCCAT GCTGTCTGTN TCATGCACTT GCTCACCATG TGAGCCTTCT GCNTCACACA 240  
 GGATGACCCT CACCAGATAC TTGCACCATG CTCTNGGGAC TTTCCCAAGT NTCCAGAGCN 300  
 GTGAGCCAAA TNAACTNGCT NTNCTTTATA AAANANAAAN ANAGTN 346

SEQ ID NO:5776

SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06854

SEQUENCE DESCRIPTION:

GATCCAGGGT GNCTAAAGAA TAGAAGTAGA GTTCCACCCA GGGCCAGAGG GAACAATCTG 60  
 GGATTCAGAC ACAGCAGTGG TGCCAACGTG AATCTACCTC GTNCTAGAGT CTGAGTAGCC 120  
 TAGTCTATCA CCCAACACAG ATAAGACTGG ACAGGGGCTC CCAGGAACCA ACATCTAAGN 180  
 GGGGAGTTTG GAGAGGGGCT AAAAGAAAGC AGGTTAAGCC CCAANTGTAA CTGATTGATG 240  
 ACCAGGGATA ACTATTTACT AGTGCTTTTN TGGNTTTATT GTAACCTCTGT NACTTTCCCA 300  
 GTATTTGTNA ATTNTTNNNC TTCTGNNTCT CCTGTN 336

SEQ ID NO:5777

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06855

SEQUENCE DESCRIPTION:

GATCTATTTA GGTGGAAATA GTTGTGGATG TACTAAGAGT AATGAAATAA AATTATAGCT 60  
 TCAAA 65



SEQ ID NO:5778

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06856

SEQUENCE DESCRIPTION:

GATCTTGNGA CGAACTGAGC CACGAGCGTG GCTTTAAGGG CCGTCCGAAC GCTGCAGGCC 60  
GGCCAGGTCC CTGGGCGTCC AGGCCTGGCC TACGCACCAC TTTNTCCCTT AGCGTTTAAA 120  
GGNNNNN 127

SEQ ID NO:5779

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06857

SEQUENCE DESCRIPTION:

GATCCTATGT GAAAAGAAAA GTGAAGCAAC TGAATCTTCA GCATGTNCTC ATCGGCGGAC 60  
CTTCTTGTT AATGTAACT GTGCCATGTT ATTAAAAAT GTGAACTAAG CTTCCAAA 118

SEQ ID NO:5780

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06858

SEQUENCE DESCRIPTION:

GATCTAGTAT AAACCTCACT TTACTCTTTT GGAATAAAGT GATTGGNTAG GACCCCATG 60  
CCAGGAATAA GANTCAATAT GCTGCTGAGA AGGAACCCAT GGTGTTGANG ATGTTGAAAA 120  
GACANACAG TCAGTAACGT GGAGAAATGG CCTGGNTTCA ANTCTGGCT CTGACACTTG 180  
GTAGGTATGA GACCTTGGAG ANGTTTCTGN NCCTCTCCAT GCTTCATTTT TNTGANGGTT 240  
TATTGTGTGG TTAAANTTN 259

SEQ ID NO:5781

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06859

SEQUENCE DESCRIPTION:

GATCCTNAGC GGAGGTAAAG ATATTAAGTN ATTTCCCAT TGAATCAGAA TTATATTGAT 60  
TCTGTGCAAT CAAAACAAAA GGCAGANTAG AATGCTGAGA TTGGTTAAGT TTGCAATNAC 120  
CATCTTGAAC CACAGATTTC TNCTATGTGT CATCAAACA TCTAGTNNG N 171

SEQ ID NO:5782

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06863

SEQUENCE DESCRIPTION:

5 GATCCTCAGA CCCTGCACAG CCCTGANTGG CTTACATCT NTTGGTCAGT GTCTTCATTC 60  
TCCCCAGTCA GGGACCTNGG ATGTTTGTTA CTNCCAGAAG CCCTTNTCTCA CCCN 114

SEQ ID NO:5783

SEQUENCE LENGTH:55

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06864

SEQUENCE DESCRIPTION:

15 GATCACACTG TGAAGATACA CAGAGTCAAT AAATGTGCAC TGTAATGGAC TTAAA 55

SEQ ID NO:5784

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS06865

SEQUENCE DESCRIPTION:

25 GATCCTGGAG AGCTCCCAGA CTTTGCTCAG CGTTCTCANG AGGNAAGCTG GGAACCTGAC 60  
CAAGGCTACA GCCCCAGACC AGAAAAGTAG CGGCGGCAGG GACAGCTGAC CAGACCACGG 120  
GCAGGGCCTG CNTCCNTNTG CCCCTCAGCT CAGCCCCAGC AAGTGTGTGC TCAGAGCATC 180  
TTTGTCTTTC ACGGTAGCAG CTACCTTCCC TCACTGTCTC AGGTGCCGAG AGGGGCAGGT 240  
GCCAGCCTNC ACTGGCATCA NTGACAAGNC CANGGCANGN NCCACCNGNG GGGTCCTN 298

SEQ ID NO:5785

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS06866

SEQUENCE DESCRIPTION:

GATCAATTGA TTGTTTAACA ATGGAATTTT GAGAAATATT TGGGTAGAAA AAAAAGTAGT 60  
TTTAAAAGAN GAGAATCCAA CCATTAAAC ATCAAAANNT GANATTNTTT GTAAATN 117

SEQ ID NO:5786

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS06869

SEQUENCE DESCRIPTION:

50 GATCAGCATG TGGACTGCAC TGTTTACTTT TGGTTGGACT GGGACAATTT GGGGAATATC 60  
TACTATGTTT ATTCTTCAAG AACCCATCAT CCCATTAGAT GGAGAAACCT GGAGTTATCT 120  
CATTGCTATA TGTGTCTGTC CTAAGTGCAGC ATTCTTAGGA GTTTATTATG CCTTGGNCAA 180  
ATTCCATCCA GCTTTGGTTA GCACAGTACA ACATTTGGAG ATTGTGGTAG CTATGGTCTT 240

GCAGCTTCTN GTGCTGCACA TATTCCTAG CATCTATGAT GTTTTGGAG GGGTAATCAT 300  
TATGATTAGT GTTTTNTCC TTGCTGGCTA TAACTTTAC TGGAGGAATT TAAGAAGN 358

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SEQ ID NO:5787  
SEQUENCE LENGTH:128  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS06870

SEQUENCE DESCRIPTION:

GATCTATGGG TAATTTTAAA TNTTGCCTGT CAAGCTTAAN AGGGACTTGA CAACAGCTAG 60  
GATNGAAATN ATTTCAACAC TTAAATATGC TACTTTGTG CCGGACGCTG TTCTAAGNCT 120  
TTNACAAN 128

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SEQ ID NO:5788  
SEQUENCE LENGTH:339  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06871

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SEQUENCE DESCRIPTION:

GATCCACCTA CCTTGGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCAC AGTGCCCGGC 60  
CTGTATTTGG TGATATTTTA AAAAATTCTA CTTTGACCTT AAGTGCTTCA AGAATTGTGT 120  
TCAGTTAGTA GTCCTNTTGG TAAGACTAAC TTTCATATGC TATCTTTGCT CCATGAGCTA 180  
TCATAGTGCT GTTTTCTTTC ATTACCCGTA AGAGTGGCTC TATCACAGCA TTTACTGTTA 240  
AGGGCTACAG TTAGACCTCT TGTTAACTCT ACTTTNATTT GTGATGGCTG TGTTCACAC 300  
TACCTTGATT TATAAATGTA NGTAATGTNG TTAAATNGN 339

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SEQ ID NO:5789  
SEQUENCE LENGTH:343  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06872

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SEQUENCE DESCRIPTION:

GATCCTNTGT ATAACATCGG GGCCTTGCTC AGGGGCTGTT GCGTGGTTGC CCTGCATTGC 60  
CTCCGNCGCA CCGCCTTCCG TATCAAAACC TAAATAGAAG TTGTTGTTAC CGTGTGCCAA 120  
TGTGTCCCAT GTGGGTTGTG CCAGGTAGAG AAACAGGAAG TCAATCATCT GTNACAGTCT 180  
CTATTCTGTC GTTTGTCTCC TTGGTATTN ATTTGCACTA TATTNAGGTG AAGCCTGTTC 240  
ACTGTTTAAA NCCGGAGTNT TCTTCAAANG GCATGGNGAC CTGGTTCAG TAAATGTCCC 300  
ANCAGTGGGG GTTTTAGAAN GCATNNTTCA NTGACCNTNG NAN 343

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SEQ ID NO:5790  
SEQUENCE LENGTH:330  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS06873  
SEQUENCE DESCRIPTION:

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# EP 0 679 716 A1

GATCATTATG TAGTTTCTGG ATTAAAAAAA TTTGTGTGTG AAGTTGCTTT GTAAAGTGCA 60  
 TGTGGAATTA ATGGGACAGT GTGCCCTTTG TGTTAGATGT TAGAGCAAAA GAAAGGGCTT 120  
 ATAGTGTTAG TATTGGAGCA CTTTGAAGAT AGATATTTNC AGAAAAGATG TAGGATTTAA 180  
 NAGTTAAATT TTAANTTTTA GAANANGATA TGATGGCAAT TGGNAATAGT CACAATGNNG 240  
 TTCTTCATCC AGTNGGTGTT TAACCAGTGT TNATTTTGCC NCTGGTAATG TGGTNACCTG 300  
 TGNGTGNTTT CCANTAGATG NGTTATGGGN 330

SEQ ID NO:5791  
 SEQUENCE LENGTH:265  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06874

SEQUENCE DESCRIPTION:  
 GATCACCACA AAGTCTGGCT CAGTGACTAT GGCTTTGCAA AACTAAACA TTCCTGTCTC 60  
 AAGTCCTGTA GATGGCTTGA AATAGTATAC ATAAGCATGC CTTATAAACA TCTTCAGTCT 120  
 TTATCAACTC TTTGGAGATT CAGCCATTCT TTTTGTACT TTAGGGAATT AAATCANNNN 180  
 ATAATGTATA AATCTGAGCA TGGCCGATGG CAGAAGANAT TTTGTCATAC GTTTTTAAAG 240  
 ANNTAAGANT GTATTATGTT TAAA 265

SEQ ID NO:5792  
 SEQUENCE LENGTH:191  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06875

SEQUENCE DESCRIPTION:  
 GATCAGAAAC CCTCATTTAA TATAGATTAT TTTGGAAATN AAAAAATTG TAACAAGGTG 60  
 GCTTTCTTAC CCACCCTAAA ATGTAAATAA AACATGCAAG CTTCAGCTGC TCGAGTTCTA 120  
 TAGTGTACCC TAAATCGTAT GTGTATGATA CATAAGGTTA TGTATGCCCT GTAGCCGTTN 180  
 NNNNNNTNTNT N 191

SEQ ID NO:5793  
 SEQUENCE LENGTH:204  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS06876

SEQUENCE DESCRIPTION:  
 GATCTTGTCT TTATCTACTT TCTTCAGTAA ACTCTGGAAG AAAAAAATT CCTGGAAGTT 60  
 TGGGCAATCA TTTGCCATTA TTTNCCTTTC CTGGAATTC TTGATATCAT GAATACTGCT 120  
 GTAGTATGGG ACATTATGTA TTTNGGTAAG CAGACTTCTC TNCTGTATTT GTNTTTNGTT 180  
 AAACAGAATG ACAAGTTCCT TAAA 204

SEQ ID NO:5794  
 SEQUENCE LENGTH:237  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS06878

SEQUENCE DESCRIPTION:

GATCCCACCC CAGGCCTTGC CCCTGCCCTC CCACGAATGG TTAATATATA TGTAGATATA 60  
 TATTTNAGCA GTGACATTCC CAGAGAGCCC CAGAGCTCTC AAGCTCCTTN NTGTCAGGNT 120  
 GGGGGGTTCA GCCTGTCCTG TCACCTCTNA GGTGCCTGCT GGCATNCTCT CCCNCATGCT 180  
 TACTAATACA TNCCCTTCCC CATAGCCATC AAAACTGGAC CAACTGGNCN NTTCTN 237

SEQ ID NO:5795

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06879

SEQUENCE DESCRIPTION:

GATCAAAAGC CAAGCTCTGT CCCCGTCAGC ACGTCACCCT CCCTCACTGT AATCCCTGAC 60  
 TGTTTTCTCT AAATGAAGAA TTATTTAGAG AATATAANTT AGAAGGGCCG CCACGTCAGA 120  
 TTTGCCTGAN TGGGAGCAGT CTTTCCAGCC TCGAAAAATG TTTAANCAAT ATGCAGATGA 180  
 CCTAGCACAA ATAANGANTG CTAGCAACCG CAAA 214

SEQ ID NO:5796

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06880

SEQUENCE DESCRIPTION:

GATCAAGTGA TACTAGGAAT ATAGGTACAA GTAAGACTGT CATTTNCATT GTTTTCTCTT 60  
 TGGACTGATT CTTTNCATTA TAACAGCGTT GTGAAGTAGA GGTGGGATTA GGAACCNTCT 120  
 GCTGTAATCA ACTCCCTNGC TGCCCAAACA CCAGCCTNAT ACACAACACC ANCAGGTCCN 180  
 GCNTNGN 187

SEQ ID NO:5797

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06882

SEQUENCE DESCRIPTION:

GATCTTTNAG TGCTTTGGGG ATGGGGTGGG CTGGGGTGGG TGGATGGGCA ACAGTGA CTT 60  
 TAATTACCTT TGCTGCTCTG CATTTNCCAG TTTATNCTTT TGTTCCTTTT ATCTGACTGA 120  
 CTCTGTCAAA CAAGTGTCAA AGTTGTGTGT TAAAAAATGT TTAACAAAAA ANNTGTTGTA 180  
 ATGACACAAA GCCTTATGAN ANTNTTATG GAGTTCAATA AAAGANGTAA GAGGTCAANC 240  
 CNNAGGN 247

SEQ ID NO:5798

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06883

SEQUENCE DESCRIPTION:

GATCTTCCCA ATATGAACAA ATATACTATG TATATNGTGT GTATTTCTAG AAATCAATGG 60  
CAGCTGCTGA TGGNGTTGTA ATTAGAANTC TATATAGNNT ATAGAN 106

SEQ ID NO:5799

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06884

SEQUENCE DESCRIPTION:

GATCAGGACC TACGTTAAGG TGGATTTTNA ATTATTTAAA ATTCTGATTT TGTTTTATTT 60  
TTAATTAATC TTTGGGGGAA GGATGGGAGG GGGGTGAGGG TTGAAGAAGT AAACATTGTA 120  
CCTATTGGAT ACAATGTTA ATATTTGTGT GATGGGCACA CTGGAAGCCC AAACCTCACT 180  
ATTACACAGT ACATTCATGT AACAAGCCTG CAAA 214

SEQ ID NO:5800

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06885

SEQUENCE DESCRIPTION:

GATCCTTAAT GGTGGCCAGA GCTACCATGC AGTGCAAAAA TAAATTAAGT GAAAAATGTAT 60  
TATTGAGATT AACAGTGCAA GGCCAATACA TTTTATAAAT CTGTCAGTAT CTTTTTAAA 119

SEQ ID NO:5801

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06886

SEQUENCE DESCRIPTION:

GATCCTCAGT GAAGTGCATT CGGAATGAGG ATGGAACCTG GTTAACACCA AATGAATTTG 60  
AAGTCGAAGG AAAAGGAAGG AACGCAAAGA ACTGGAAACG GAATATACGT TGTGAAGGAA 120  
CGACCCTAGG AGAGCTGCTN AAGAGTGGAC TTTTGCTCTG TCCTCCAAGA NTAANTCTCA 180  
AGAGAGAGTT AAATAGCAAG TGAATTTCTA CTACCCTCTC AGTCACCATG TTGCAGACTT 240  
TCCCTGTCTG GAGGCTCACC TTAGAGCTTC TGAAGTTTCC AAGCTCTGAG GTCAACCTNC 300  
ACATTTTGGG CAATGGCATC TTCAAAAACA ATTAATTTN 339

SEQ ID NO:5802

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06888

SEQUENCE DESCRIPTION:

GATCTCCAAG CGAACTCAGC CTCCTCCCAA GCTCCCTGTG GGTCTTAGCC ACAAGCTCTC 60

CAACAATTAC TATTGCACTC GCGATGGCCG NCGGGAATCT GTGCCCCCTT GCATCATCAT 120  
GTCGTCGCAG AAGGCGCTGG TGTCAGGCAA GCCAGCAGAG AGCTCTGCTG TAGCTGCCAC 180  
TGAGAAGAAG GCGGTGACTC CAGCTCCTNC CATAAAGAGG TGGGAGCTGT CCTCGGACCA 240  
GCCTTACCTG TGACATTNCA CCNTNACGNC CACCCGNCTA CTTTGCCTN CTTTGGATTT 300  
NCTTCAGGGN GAATNTTGAC CTAATTGTAT GACAATTTAC GTAGGGGCTC AGGTATTAC 360  
TTCTGAGGTN TTACTTTTGG N 381

SEQ ID NO:5803

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06889

SEQUENCE DESCRIPTION:

GATCTACACA TGTGCTTG CATTGTGGT AATCTACACC AATGGAAACA TGTACTACAG 60  
CTATATTTGA TTATGTATGG ATATATTTGA AATAGTATAC ATTGTCTTGA TGTTTTTCCT 120  
GTAATGTAAA TAAACTATTT ATATCACAAA 150

SEQ ID NO:5804

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06890

SEQUENCE DESCRIPTION:

GATCCTAAGC AAAATCGGAG ACTTGAACAA AGTTTGTTTC TGGCTGTNTG CCCTTCCATT 60  
TTCTGTTCTC TTCTTTCTCC CTGGAGATGA NAGAACACAG AATCANATTN CCAACCTCTC 120  
TCTCCNATGN ACTCTCTCAT CCCCCAGCCC AGCCACATTT ACACATAGGG CAGACACATC 180  
TCACACAAAG GAAGTACCCC TAAAGACCTC ACATAAATAA AACTAGCAA ANTTCAAGTT 240  
GNNTCTTGGC AAANGTAGTN NTGGGTATGT NAGTCN 276

SEQ ID NO:5805

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06891

SEQUENCE DESCRIPTION:

GATCANGTTC NGGGCTCTNT CAGCCGCCAC CTCTGGGAAA GAGAAAAGNT TTGGGTCCAC 60  
TGAACATCAT GTTTGTAGAC GCTGACAGGT GGGGTCCTAA TNAGAGCCAA CACATGCTCA 120  
CTGCCAGCNC CTGCCCTGAG TACTGGGAAG TTTCTCCTGG AAGCCCTTGT GAGATGGCTC 180  
NGNNGGCTGG TATCCCGACT TGGAAGATGA GGAAACTNN 219

SEQ ID NO:5806

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06893

## SEQUENCE DESCRIPTION:

GATCAGTTTT NTGCTGAAGG CACCTACTCA GTATCTTTTC CTCCTTATCA CTCTGCATTG 60  
GTGAATTTAN TCCTCTCCTT TGTGTTCAAC TTTTGTNTGC TTTTAAATC AGCTTTATTC 120  
TAAGCAAATC TGTGTCTACT TTAAAAAACT GGAAATGGAA AAAAAATTAA ATCTNNGCCA 180  
GGTCCTTCAA A 191

SEQ ID NO:5807

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06894

## SEQUENCE DESCRIPTION:

GATCTGCAGC TTCGCGGGGA CAGAGATGTA ACCCAACTCG TTCACGGATG TNCCGCGCGC 60  
CGTGTACCG GCTGCGGGCC AGGGGTACTC GGAAGGCGCG GGCAGGAGCC TNGCGAGGAT 120  
GCACCTTCCC CTGCNTTGA AAGGTAGAAC TGGGGAGTGC GGGAGGNTGA AGGTGGCCCG 180  
GAAAAGAACA CCTNTTCGA ACCAAA 206

SEQ ID NO:5808

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06895

## SEQUENCE DESCRIPTION:

GATCTAAATA TGTATTCAT AATNTTCCA TAATAAATTA TATAAGGTGG CTAAA 55

SEQ ID NO:5809

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06896

## SEQUENCE DESCRIPTION:

GATCTGGTTT NATTCCTGTA ATTCAGCCAC CTGATTGCT TGAGGGGGNG GNATANTATG 60  
TGGGTTTTTG TACAAACATG TTTCTCAGTG TGTGTATT TTGGAAAAA TGAGGGGAGG 120  
GAGTTTTGCA AGAATGNGAG AAAATGANTG AAGAAGGCCT AATCNTCTCT CTTTTCCAG 180  
TGGATTNAAT GGGNCCN 197

SEQ ID NO:5810

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06897

## SEQUENCE DESCRIPTION:

GATCCAATGA TTAAATTTT GGGAAGAAAA ATCCAGTGAT TAAAGTCATG CAAGGAGATG 60  
GCCTGGGGCT TGCTAAAAGT CAGGTTGCAG TTTCCATTGC ATTCAAGAAA ATCAGAAAA 120  
TAAATACAAC TTTTAGAAGA AACTGAGTTT TCTCCATTCT ATGTTTAGCT ATTGGGGGGT 180



CTCATACTTC TGGACTTGCT TAGACCTATG CTATCTAATA TGGTNGCCTC TGCCCATCCA 240  
TATGTGGCCA CTTGGGAACT TGGAAATGTN ACTAGTTTTG AATTAAGGTG TGCTNGTAAC 300  
TAAATNCAC CCTGNGGTNT CAAAGGCTNN AATAAANGNA NGGN 344

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SEQ ID NO:5811

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06898

SEQUENCE DESCRIPTION:

GATCTATCTC CCTGTTAGGT GTNCTTTTTC TCCTCTTTAG AAAGNAGCCA AGGNAACCAG 60  
GGTTCTCTCA AAGTGAAAA TACTGGAACT NATGTACTGN TATCATAATG N 111

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SEQ ID NO:5812

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06899

SEQUENCE DESCRIPTION:

GATCCATTGC TTTAGACAG GACTGGGTTT TGCTGTCCAA TGATATACAN TAATAGTNCT 60  
TCTTACAGCT AAGCTGGCCC CAGCCTTGTC TTGATATTAA TACATGAANT NTTTATAATT 120  
GTCTCATTGT CTCATTTAGA AACATCCANA TTTNCTGCT GTGNCATN 169

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SEQ ID NO:5813

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06900

SEQUENCE DESCRIPTION:

GATCAGTAAC TTTATCTCTA TCCTTAATGA ACATTTGTTT TATTGGTGGC TGGAAATATT 60  
TCTATTGTAT TTCTGTGTAT ATNNTNAATA AAATAATTTT TGGCCTCTNA AA 112

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SEQ ID NO:5814

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS06901

SEQUENCE DESCRIPTION:

GATCAGCAGC TCGGAAGACT CAGATGCCGA AAACCTCGTCC TCCCGAGAGC TGGATGACAG 60  
CAGCAGTGAG TCCAGTGACC TCCANCTGGA AGGCCCCANC ACCCTCAGGG TCCTTTGACG 120  
AGAACCTTGC TGACCCCAA GCAGNAGACA GACCTCTGGT TTNNTTTGAC CTCAAGATNG 180  
ACAATGAAAG TGGGTTCTCC TGGGGCTACC NNNACCCNTT TCTAATTTAG TCTCTNGAGT 240  
CCCAAAAAGA AGTNCAGGCA GAGCCATCTN N 271

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SEQ ID NO:5815

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SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06902

SEQUENCE DESCRIPTION:

GATCATGAAA AGAAAAATNA ATGGCAGGAA AAAAGTTTGG TCCTTAATAT ACTTTGGCCT 60  
AGTNAATAAATA TGTGCCITTT TGGTGTGTTT TGTTCATCAC TACAAGATAA AAAGGAAACA 120  
TTACANCTCA AGGCTTTAAA AAGTTCATTT ATTGAAAATC ATATGTATAG CCTAGCATAC 180  
GAATGTGCAG TTTTAAACAC ATAGCTTCAA GCCATTTCTG NAAGCATNCA CCGGGNGCTC 240  
TGCTCAGNTA GAGTCAGNCT CCNNGCTCCA GNCCGACTGC GTGCGGGGGA CCAGCGGCCG 300  
CGTTNNATGG NGGGNCN 317

SEQ ID NO:5816

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06903

SEQUENCE DESCRIPTION:

GATCTAGGAG AGGCGGCTCT GAACGAGTAC CTGCGGGTCA AGACAGTGAC CTTGATTAC 60  
TGAAGAAAGG TCTTTNTGAG AAGAAAGTCC CTGCCCCTCC CTCGTGGCTG GGGTCCCCTC 120  
CCTCTTGAGC CTNGGTGCAC AGCANCTCCC ACCTGGGGGG CTAGTGGAAG CCCTCCTGCC 180  
TGCACACCAT GTCTGCATCT TGGACGNCCT CTGTCCAGTC AGAAGCAGCC CTTGGNTNNG 240  
GGTGAGNTGT GNCCCTTCCA GGGGGAATAA AGCTTCTGAA GAGAGACCGT CAAA 294

SEQ ID NO:5817

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06904

SEQUENCE DESCRIPTION:

GATCAAAATC AATGGGAAGG TGCTGCCAAG GTGTCCTAAG CTTCTAGGAT AATATTNATN 60  
CTCTCAGGGT TTTGGAAGT CTGCCCCAAG TCATAGTTCT CAGTCCTGGG TGTGAGTCAG 120  
ANTCACCTGT GGAGCCTGGC AAACCTTACA GACACCCTGG CTCCAGCCCT GGAGATTTTN 180  
ATTTANTGGA AATATCACTT AGAATTCTAT TGTAAGCAAT AAAAGTNTAT TCTCACTAAA 240  
CTTTCAAAAA NTNGNGNTGN NNN 263

SEQ ID NO:5818

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06906

SEQUENCE DESCRIPTION:

GATCTTTCCC NTTTGGATGT GCGTGTGTGT CTGCNTGTGC CATGTGCGTG GCACGCATAT 60  
GAAGTGTGTG TGCGTGTGAA CGGCTTTGGG TCCTGCTGGT TTTNCTGTGA GCTNCAAGTGT 120  
TCTGTGGGTC TGTGGTATCT NACACTGTGG NCATTAATGT ACTTCTTGGA CATTTTAATA 180

AATTTTNNAA CAGTTCAAA

199

SEQ ID NO:5819

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06909

SEQUENCE DESCRIPTION:

GATCANAAAA CCTAAANTCC ATAGGNACCC NAAATCCTCA CAGTTACAGA GACACCAAGA 60  
 AGANTCTGGA CAAATAGGAC TTGCTAAGGC CTCCACAGTT TATN 104

SEQ ID NO:5820

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06910

SEQUENCE DESCRIPTION:

GATCGAACGG ACTNTAAATC CGCTCTTTAT CGAAAGCTAA GCAAGCTGTG GCTTTTTTCC 60  
 AACTCCGTGT AACGATTCTA AGTGTAGTGT NGTAGGACCC CGACGGGTNT GGCAGCAACT 120  
 GCCCTGGAGC CCCAGCCCTT GCTTCCATCT NTNCTGTGCG CCCACAGTA GACGTGCAGA 180  
 CGTCCCTAAG AAGGTTCTTN AAGATGTTTA TTTTATATAG TCCTNTTTTA CTGGAAGACG 240  
 TACGNATACT CCATCGATGT TGTATTTGGN GGGGGGTGNG GAATTCTTGT ACGCAGTTTT 300  
 CNTTNGGCTT TACGAAGCCG GTNAANNGAC CGTTTTGAAN TAN 343

SEQ ID NO:5821

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06911

SEQUENCE DESCRIPTION:

GATCACTTGA GCCCAGGAGT TCAAGACCAG CCTGGGCAAC ATGGCTAATN AACACTAAGC 60  
 ATAGTTTTAA TGTCTTTNAT ATTAAAGACT TTCTCAAATT CTAAA 106

SEQ ID NO:5822

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06912

SEQUENCE DESCRIPTION:

GATCCATTCC AGCCACTCGG GGCTGACAGC GGCACCCCGT TCCAAAGTAA AAAGGGGTTT 60  
 GGGGACCCGT TTAGTGAAA AGACCCATTT GTCCCTCCT CTGCAGCTAA ACCTTCTAAG 120  
 GCCTCTGCCT CGGGCTTTGC AGACTTCACC TCTGTAAGTT GAGTCCTCCG NCTCCGGGCC 180  
 ACCCACTCC CTTCCGCTTG CAGCTTCCCT GGGATTTTNG TNTCCTTTTA AAGGCAAACC 240  
 TCCCAGCTTC TTTAGCCTCT TGGTACCTNA CACTCTCTGT CCNTCGCGTT ATTNATTCTA 300  
 CACTGCCACT TCTGTAAGAA AAACAGTTTN TCAATAAAAA AAANAGNTGN 350

EP 0 679 716 A1

SEQ ID NO:5823

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06913

SEQUENCE DESCRIPTION:

GATCTCGTCT CTAATAAAAA TATACAAAAG AGTATTGGGA GGGGGTATGA AGAATGTATA 60  
GGGCAATAAT TGAAATCTGT TGAAGCTGGG TACACAAAAG TNCATTATGT TGTTTCTCTA 120  
CATTTATATC TATTNTNAGT NNTTTNATAT CTATTTTNAN TTN 163

SEQ ID NO:5824

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06915

SEQUENCE DESCRIPTION:

GATCAGTGGT TTCCATTGTC AGGACTGGGC ATGGGGAAGT NTGGCTGTAC AAGAGGAGCC 60  
CAAGGGAACCT CTTGGTGGT GATGGAACCT CTCTGTATCT CAAATGTCTG TATCTTTAGA 120  
AAGAANTCTA CATATGTNAT AACACTGCAT AGAAATATAT ACATGTACAC ACAAGTGAAA 180

SEQ ID NO:5825

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06916

SEQUENCE DESCRIPTION:

GATCAGTGAA ATCCTAGGGT GCTCTATGAG ATTGTACTAG GCCTATNAAG AGTGGTAAGC 60  
CAAATAGGTC TCCATGGGAG ATACATTATG TAAATAAATA AACAATGGTT TGCTGGTTCC 120  
TGTTGGTGTC TCCACAAGTA GGTAANCATG TTTAAAGGAA CCCGGGTTCT TAGATTTTNT 180  
NAGACTTTTT AANCTCAAGG CTGNGCATAA GTNCTTGAAN ATAAANTGCT AATNCTTAAG 240  
TGTCAAA 247

SEQ ID NO:5826

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06917

SEQUENCE DESCRIPTION:

GATCAAGAAT TGCAAAAATG GAAAAAATTA ATGAAAAGGC ATCTGATAAA TGTGGACGGC 60  
TCCAAATCAT GTCCTTAGAA AATCTTTCTA TTGAAAAGGA GACTAAATTG TAATGTGATT 120  
CACAATGTAA CAATATAANN CTNNGTTTTT NTATAATTNT NTAANAGTN 169

SEQ ID NO:5827

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06919

SEQUENCE DESCRIPTION:

GATCACCTCC GGGCACAGGA TGCGAGGAAC TGTGACATT CAGGGATGTG ACCATAGAAT 60  
TCTNTCTGGA GGAGTGGGAG TTTCTNAACC CTGCTCAGCA GAGTTTGTAT AGGAAAAGTNA 120  
TGCTAGAGAA CTACAGAAAC CTGGTCTCTN TGGGTCTTAC TGTTTCTAAG CCAGAACTGA 180  
TTAGCCGTCT GGAGCAAAGA CAGGAGCCCT GGAATGTGAA GAGACATGAG ACCATAGCCT 240  
GGGCGACAGA GCGAGACTCC GTNTCAAA 268

SEQ ID NO:5828

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06920

SEQUENCE DESCRIPTION:

GATCTGTGCC CAGAGACGGG ACTGGGAGGG CCCACTTCAG GGTTCCTCCTC TCCCCTCTAA 60  
GGCCGAAGAA GGGTCCTTCC CTCTCCCCAA GACTTNGTGT CCTTTCCCTC CACTCCTTCC 120  
TGCCACCTGC TGCTGCTGCT GCTGCTAATC TTCANGGGCA CTNCTTGCTG NCTTTAAGTC 180  
GCTGAGGGAA AAATAAATGA CAAATTGCTT GNGNCCAAA 219

SEQ ID NO:5829

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06922

SEQUENCE DESCRIPTION:

GATCATAAGT NCTCTATCT GCTGAGCTTT ATTTATTNAT TTTGGACAGA AAGTTTGGTG 60  
GGAAGGTTGC AATAAAATCA GAATCTCTCT TGTNTGAATT ATGCAGTTTA ACCCTGTCCA 120  
TGGNNNGGCT GTACTCTATT CTNACTGTAT TTN 153

SEQ ID NO:5830

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06923

SEQUENCE DESCRIPTION:

GATCTTGTTT TNATTAAATA TGCCAGTTTG TATTTNCCTG CCTTGGGATT TTTTGTGTC 60  
CGCTGTACAG TATTCTAAGG GAAAAAGAAA AAGAAAGATG TGTAAGTAA CAGAGAGAGG 120  
TGGCTATGGT GTAGAGACCT CTTTCTAATA AAGAAATGAA AATATGTCTA AA 172

SEQ ID NO:5831

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06927

SEQUENCE DESCRIPTION:

GATCCCAGGG AAGACGTCTC TCTCNGCATC CCAAGCCATN CAGCCCTTAT CGCTGTACCC 60  
AGTAAACCCT CAATAAATAT CTTTNTCAGC CAGAAA 96

SEQ ID NO:5832

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06928

SEQUENCE DESCRIPTION:

GATCACTGTA TTAATTTTGG TTTATCTTGG CATATATNGT TCAGTTTGTN TTTATTTTTA 60  
ATTTTNCCTT TTTTCCGAT TAGGCTTTGG TCAGCATTTT NCATTTAAAG AAAAGTAACA 120  
CTCCCATCCA CTCATAAGCT TGGTACAAAA ACTTCTCTGG CAGTTACTTT TGAAGCTTCA 180  
CTCTGCTTTC TGTATAAAGG GCAGTCTGTG GTCACGCAAG ACTTTAAA 228

SEQ ID NO:5833

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06929

SEQUENCE DESCRIPTION:

GATCTTTCTG CTTTCGAAGG TATANTGTAT CTATTTCTGT CAGGAATNAT ATTTCCAAAT 60  
GAAATGTAA AGAACATTGG GAAATAATAA ACTTTCCTTT CAAAGTAAA 109

SEQ ID NO:5834

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06930

SEQUENCE DESCRIPTION:

GATCTGTGTT TGGAAAGAAA AGAAGGAAAC TAAGACGTGC GAGGGNAAGA AAAAGGAAAA 60  
CCTAATTAAA AAATATGTAT CCTCTATAAT NAGTTATNAC AGCCATTTGT AATGAATTTG 120  
TCGCAAAGAC GTAATAAAAT TAACTGGTAG CACGGNCAAA 160

SEQ ID NO:5835

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06931

SEQUENCE DESCRIPTION:

GATCGACCGG CACCGCTGTT GCCTCGTAAG CCATAGCGCA TGCGCGCTCT CAGAATAAAC 60  
AGGCCCTGCC TGGGAAA 77

SEQ ID NO:5836

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06932

SEQUENCE DESCRIPTION:

GATCANATAA CAGAATGCAC CAGTCATCAG CTATTCAGTT GGTAAGCTTC CAGGAAAAAG 60

GACAGGCAGA AAGAGTTTNA NACCTGAATA GCTCCCANAT TTCAGTCTTT TCCTGTTTTT 120

GTAACTTTG GGTAAA 137

SEQ ID NO:5837

SEQUENCE LENGTH:402

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06933

SEQUENCE DESCRIPTION:

GATCCAGCTT CATTCAACAT TACTACCAGT TATTTGATAA TNATAGAACC CAACTAGGCG 60

CAATTTACAT TGACGCGTCA TGCCTTACGT GGGGAAGGACA ACAGTTCCAG GGGAAAGCTG 120

CCATTGTGGA GAAGTTGTCT AGCCTTCCGT TCCAGAAAAT TCAGCACAGC ATCACC GCGC 180

AGGACCATCA GCCCACTCCA GATAGCTGCA TCATCAGCAT GGTGTGGGC CAGCTTANGG 240

CGGNTGAAGA CCCCATCATG GGNNTNCGCC AGATGTTCTT ATTAAAGAAC ATCAACGATG 300

NTTGGGTTTG CACCAATGNC ATGGTTCAGG CTCGTCCTGC NCANNTTTGG CTGNCCTNCT 360

TTGCAGNTTG GGNACTNANG NTGTTGCTT GCTGCCTTTT GN 402

SEQ ID NO:5838

SEQUENCE LENGTH:261

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06934

SEQUENCE DESCRIPTION:

GATCTTCGTA ACGGCCTCGG CACGCTCCAC ACCCCTGGAG TCTCCCGAGG CCCCCATGTG 60

CTGCTGAGTG GCCAAGATGA TGCCAGGCTG CCCTATACAC TGGGGGATTC TGCCCTGGCC 120

CATGCACACC CGTCTTTCCA TGATGGCAGA GACATCCAGT NAGGACCTGA CCCGTCTCTG 180

TCTGAGGCCG GCTCAGCAGT GCAGCCTGGT CCCTGGGGGC TGGACCCAGG CTCCTAAATA 240

AACCAGCAAC TNCCTCGNAA A 261

SEQ ID NO:5839

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06935

SEQUENCE DESCRIPTION:

GATCTCGGCT CACTGCAACC TCTGCCTCCC GAGTCCTGGT TCAAAC TATT CTCCTGCCTC 60

ANTCTCCTGA GTAGCTGGGA CTACAGNNAC GAGCCACCAC ACCCTNCCCC CGNATCCCCCT 120

GCCTCCATCC TAGTAAAGAC TCCTTGCTAT GCTGCAA 158

SEQ ID NO:5840

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06936

SEQUENCE DESCRIPTION:

GATCAGTTTT GCCAAGGGGC CAGAATTATT CCTTGTTAGA ATTGCTCCAG TTCAAGTCTG 60  
CTGCTTTCCT ACAGTTTTTC AAATTTTATA ATGTATTAAC TACAATAAAC TCTGTTTAAA 120  
AAATAAA 127

SEQ ID NO:5841

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06937

SEQUENCE DESCRIPTION:

GATCAAAGAA AATTTATCTC TTTTATAAA CTTAAGGACA GTTGCAAAAG GCTTCAAGGA 60  
ATTTATCTCA ACATTATTCT TTCTATGTCC TAACTAAATT CCTCAACTGT NATGANTTTT 120  
CCANCTACTT CTTGAACAGT GGTCTATNCT GCTACATGAN GATGAATACA AACAANNITT 180  
TTGTATAACC TACTATNCCA GTNCTCCTGT GTCAGTCTTG CCTATGGATN TN 232

SEQ ID NO:5842

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06938

SEQUENCE DESCRIPTION:

GATCTCCAGN GCGCAGTGGG TTGGAGGAAG TACTACGTGA CAGCTGGGGG AGCCTAGCCC 60  
TTGTNTGGGN ACTCACACAT CCACTCTAAC CCTTCTNACC ACAGGTCCGG CCGCCCCATT 120  
AGCTTCATNG TGGTTTTTAT CACCCCCAAC CCCCTGAGCA AGATTTCCTG GGTCAACAGG 180  
TTACATTTGG CCANAATCGG ACTCCGTGAG TATAGCCCCA GGGAGAGTGC CTNAGGGGGC 240  
AGNGGTGTGG AACGNGNAGG TTTNGGGTGA GTNNGGGTAC AGAATGTNGN 290

SEQ ID NO:5843

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06939

SEQUENCE DESCRIPTION:

GATCTTGTA CATTCCTTCT CCTGGACAAT NAGTCTCAGG AGCTCCTCAC CAAGCACCTT 60  
GTTACCCCCA CCCCTGCCCA CAAGAGAAAA CGCACGTAA CTGTAATTIN TCCACTACCT 120  
ACCCAAATCC TATAAACTG CCCACCCCCA TCTCCTTTTG CTGACTCCAG GTGATTAAAN 180  
AACTATTGCT CAGGGAAA 198

SEQ ID NO:5844



SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06941

SEQUENCE DESCRIPTION:

GATCTTTTT CTAACACATA TTTGAACTGA ATAACAGACT TAAAGAAAGC CTTTGTTTAC 60  
 ATTGCTATTT ACTNTTGTGT TTGGGGGAAA ATACGAGGGA TTGATTTTAA ATAAAAACA 120  
 TTCCNTCTTT CATTNAATAT CAGTATCAAA AGAGGNGAC AAACATCTAT CTTTCTCATC 180  
 TNTATTNAAG TNCCTTTTGT TANTGTAGTA TCAANGTTT TTAGGTGNTG CAAGGTTTTA 240  
 CAANTCATTT GTGGN 255

SEQ ID NO:5845

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06942

SEQUENCE DESCRIPTION:

GATCCCTCAG AAGACTTAAC TTGGCTGGAG TGGGAGGAAC TGAAAATACC ACTCCATGGT 60  
 ATACCCATAT ATCCAAATCG TAGAGAACGA GAAGCTATGA TTTTATCATC TTATGCTGGA 120  
 ATCTTAATGA ACAGTATCCC GATTGAGGAA GTCTTTAAAA TTTATGGGGC TGATTCTNCT 180  
 GNCGATTCTG GTACCATCAA GTTTCCCCGA GTTTCATCTN TCCGNCCTC CTNCAACCNC 240  
 TNTTGCCATG TTAGCAGNAN CNANAGCAGC AGCATACGGC CGCAAACNGG GTGTCNAGTC 300  
 AAGNANGGTT GCAGCAGN 318

SEQ ID NO:5846

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06943

SEQUENCE DESCRIPTION:

GATCGGAGGT TGGGTTCTGT ATTAACTTC ACTGTGTGTT TTCTATNTCG GAAA 54

SEQ ID NO:5847

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06945

SEQUENCE DESCRIPTION:

GATCAGAGAN TTACCACCCC TGCTTNGAAG CAGTGTGGT GTATTCCCAC TAAATAAAC 60  
 CAACTGGTAT AACATTCCCT GGAGCTTAAT AAGCACTCAA TAAATATTG TNGANTAAAN 120  
 ANAGAAN 127

SEQ ID NO:5848

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06946

SEQUENCE DESCRIPTION:

5 GATCTGCAGA TTCCAAATGG GAATAAGCTC TATCATATTC TGAACAAGA ATTAGAATGN 60  
 CTTGAGAACG GGCAAATAAC AAAGCAAACC AATATAATTA TATGGTCATT CTGACCCCAG 120  
 CTCTTATACA NNTTATACAT GTATTTTGT GTATGTTTGT GAGAGTTGTA TGTATGTGAA 180  
 TGNGTGTGAG TGTGTATTCA CATACACATA TN 212

10

SEQ ID NO:5849

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS06947

SEQUENCE DESCRIPTION:

20 GATCATAAGG TGAAGTCCCA CAATAGGCCG TCTGCAAGCT GAGAAGCAGN GNAAGCCAGT 60  
 CTGAGTCCCA AAACCCTAAC AGTAATCCTT TNCTAACGTC AGGNTGCGTA TCGACCTGTG 120  
 TGTGCACATT TGCTGTGCAG AGTGTGCACT GCTGAGGAGA ATGGTGCCCA AGAAGGGCAC 180  
 TGTTTGNCCC AAANTNTTNC AANTAANCAT TGN 213

25 SEQ ID NO:5850

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06948

SEQUENCE DESCRIPTION:

30 GATCATCTTG AATTACTGTG GGATGTANGT TTCAAAATTT TCAAATAAAG CCTTTGCAAG 60  
 ATAAA 65

35 SEQ ID NO:5851

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06949

SEQUENCE DESCRIPTION:

40 GATCACATAC TGCAGTCCAG CCTAGGCAAC GGNGCAAGAC GTCATCTCAA GGAAA 55

45 SEQ ID NO:5852

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06951

SEQUENCE DESCRIPTION:

50 GATCTCCCCA AATCCATTGN TNTCACCAGG CCCTCCCAGA ACCTCCTCAG TTCCTTCACA 60  
 GTGCAACCCT NTGTACTTGG CCCGCAACCC ANTAGTATTG TGCCTCACTT CACCTTCCAT 120  
 GGGCAACTGC CCTCCCTTCT GGACATAAAA CCTNATATNT TAAATAAAGT TGAANTATGN 180

55

NAAGAN

186

SEQ ID NO:5853

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06952

SEQUENCE DESCRIPTION:

GATCAACTGA AAAAAGCATG ACTTTTGAAG TCTCTGAATG CCTTGGTTCT NAGTATTATC 60  
 ATNCTTNATT GAATTTATTT CTNATTAAAN TATGTAGTTT TN 102

SEQ ID NO:5854

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06953

SEQUENCE DESCRIPTION:

GATCATGTGG AGTGAAAGGC AAATCTTACT GCTTAATGTA TAAACTCTCA CCACAGGAAG 60  
 CATCGCTGTT TCCAATAAAT ATTGCTGAAG ACAGAAA 97

SEQ ID NO:5855

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06954

SEQUENCE DESCRIPTION:

GATCTGTCCA GTTTGTGTAT GAAATGGATT TGATAAAGTT TTTGCTAGTT ATTACTACA 60  
 TTTTGGGATT AATAAGTGAT TTANATGCAT ATNTTCCTGT AAATCTACAG TTTTGTGTAC 120  
 AAGATATTCT ACAAGTNATG ANGCTAAGGG AAGAAAATGC CAAAGATACC TCTAGTTATG 180  
 TTGANCACAG CCAGCACAGT TTCGACAGGT CAAGGAAGAG CTGTTTCAGT AAAGANTGAN 240  
 GTGAAAACNC TTATTTNGGA AANTGTTTCT CANTANTAAN CTGTATAGTT GTTCTCTNA 300  
 NACCCCN 308

SEQ ID NO:5856

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06955

SEQUENCE DESCRIPTION:

GATCCCAAGT GTTTAGAAAA CTAAGTAAAC TTTGTTGTCA AGCAATTTGT CCATGTGGAA 60  
 AGAATTTAAA GAGAAGCTGA ACAATGGAAT AAACAAATAA AGCATGTTT TNATCTTTC 120  
 CCATTTAA 128

SEQ ID NO:5857

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06956

SEQUENCE DESCRIPTION:

GATCTTAAAA ACTGCAGTAT TCCCCCATTT TTTAATGAGA GTGTGGGGCT GGCAGGGNTT 60  
GGTTGGAGGG AGGAGAGAAG ACAGAGGAGC ACTTAAGGTG CAAAGCAGCC TATTTTTCCT 120  
TCAATAAAAA TTGTTAAGGG AAA 143

SEQ ID NO:5858

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06957

SEQUENCE DESCRIPTION:

GATCCGTGGA AATAGCCTGG CTCCTCTTA CCCAGTAATG AGGGGCAGGG AAGGGAAGT 60  
GGAGGCAGCC GTTTAGTCCT CCCTGCCCTG CCCACTGCCT GGATGGGGCG ATGCCACNNN 120  
GTCATCCTTC ACCCAGCTCT GGCCTCTGGG TCCCACCACC NAGCCCCCG TGTNAGAACA 180  
ATCTTTGCTC TGTACAATCG GGCTCTTTAC AATAAACCT TCCTGCTTNC ACAA 235

SEQ ID NO:5859

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06959

SEQUENCE DESCRIPTION:

GATCCAGTAC TATCAGAATG ACATCCCCTA CTGAGGAGGG GACCTTCGAG GGCCTCTGCC 60  
CCATGTGCCC TCAAAGCTGT CCCACAATCA TGGAGCCCTG CNACCTNCCT GCCCTGNCGN 120  
CACATGCAGT NGAGGAGAGG CCTGTGGCCA AAGAACCTGG TAGCGGCTCC TNGGGCAGCA 180  
CGTGGNTGGC GCACTTTGGT AACGCCATGG GANTGCAGCG NCCANTCGAA TGGGATNGGT 240  
GCTGTTNTAT GCACAGGN 258

SEQ ID NO:5860

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06960

SEQUENCE DESCRIPTION:

GATCAGATTA CCAGGAACAT AGGAGTGGAT TCCTGCCCCA ACCAAACCGC ATTCGTGTGG 60  
ATTTTTTAT TCAACTTAAT TGGCTATTCC AAAGATTTT TTTTCCCTAT TTTTAACGAT 120  
TGGAGCCCTT AAGATGCACG ATGGAATTGT GTTTTGCCTT TTTNGGNAAA NGGGAGCAAA 180  
GCGGGGNCCT GNGATAAAC GNTTGGAGCA ATCTCCTTNG GNAGGGATTT CAGCANGGGG 240  
TTAGNTNGGT GAAACATTTT AAAGGGGGGA AAGGGGGGGG GTTTTTTTTT NAAANTGGGN 300  
TAAATNCGN 309

SEQ ID NO:5861

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06961

SEQUENCE DESCRIPTION:

GATCATGTGG ACCAGAGCAA ANNAAAGTTC AGTTTGTGTC ACAATTCATT GCCAGACTTC 60

ATTGGAATGC TTTGTTTGAT GATGTATGTN CATTCTCAGC TTTATTTTCA GATGCTTAAC 120

TGGGCAATGA AGTCTAACTT CAGGTTGAAC TNTCTCCNGN NTAANCTCAG GCTAAATGN 179

SEQ ID NO:5862

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06963

SEQUENCE DESCRIPTION:

GATCGTGGTG GTGGGGACTG GAGACCGGAC CGAGAGGCTG CAGTCCCAGG TGCTTCAAGC 60

CATGAGGCAG CGGGGCATTG CTGTGGAAGT GCAGGACACG CCCAATGCCT GTGCCACCTT 120

CAACTTCCTG TGTCAAGAAG GCCGAGTAAC TGGAGCTGCT CTCATCCCTC CACCAGGAGG 180

GACTTCACTT ACATCTTTGG GCCAAGCTGC TCAATGAACC GNCAGGAACT GACCTGCTGA 240

CTGCACTCTG CCAGGCTTCC NAATTGCTTT CANTCTTATC TACCCTTTTG GGACTTATNT 300

NGGCTTATCA ACATAATAAT TTGATACAAC TNNTTCCCAA A 341

SEQ ID NO:5863

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06964

SEQUENCE DESCRIPTION:

GATCTGGTGA AAATAGGATT ACATTGGAGC CAATTGAATA AATTTATTCT TTCAATCAAA 60

SEQ ID NO:5864

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06965

SEQUENCE DESCRIPTION:

GATCTGGGAG GTGGAAGCCA GGCCAGAGGA CTTGGGGAAA ATAAGATGGA GGAAGGAAAA 60

AGGGAGAAGC TGAGCCACAG CTAACTCCT ACAGAGTGAA ATNAAAACGG GCTGAAAAATA 120

CCACCCAGG AGAGGACCTC GCCCAAGCA AGCCAGTGAG CAGCCCTGCC AGACTACTGC 180

CAGACTGAGA AACCAGAAG CTGGTAGTCA TGTGGGCTTG CNTTCTNTGC CAAACGACTG 240

GGAAACCAA ATNAGCCAC CTTGTGTTCT TCCTAGCTCC ACCCTCCCG TGCTGCTGTG 300

TTCTGCTCCT TCCNCACGGT TTCCCTGCTA TAGTTCCCAG CTGCTTGTA CGGGGCCNN 359

SEQ ID NO:5865

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06966

SEQUENCE DESCRIPTION:

GATCATGGCT AACGGGCACA GGCTTTCTTT TTTGGGTGAT GAAAATATTC TAAAATAACT 60  
GTAAAAATAT TGCACAACTC TGTNAACATG TGAAACCCA CTGAACTGTA TGCTCTAACT 120  
GTATGAATTG TATGGTATTT AAATTTNACC TCAATAAAGC TGTTATCAAA 170

SEQ ID NO:5866

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06967

SEQUENCE DESCRIPTION:

GATCAGAGCA AGAGAACTTC CAGAGATAAT GGATAGAATG AAAGAATATA TATCTATATA 60  
TATTTAACAT GTTGTITAGT AATCCCTATT TTAATTCAAT TCTCCATCTG TAAAATATTA 120  
GCTAACTGAA TTATTTCTGT GTTCTACTCT GGGCTCTCAC ATTAATACTC TGTTCAAAAA 180  
GTTTAAA 187

SEQ ID NO:5867

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06969

SEQUENCE DESCRIPTION:

GATCTTGGAC TTCCAGCCT CCAAACTGT GAGAAATAAA CTCCTGTTGT TTGTAAA 57

SEQ ID NO:5868

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06971

SEQUENCE DESCRIPTION:

GATCATGGTC AGCTCACACC CTAATAAGTC CACATCTTCT CAGTGTTTTA GCTGTTTTTT 60  
TCATTAGGNT TCCTTNTATT CTGTACCTTG CAGCCATGAC CAGTTCTGGC CAGGAGCTGG 120  
AGGAGCAGGC AGTGNGTGGG AGCTCCTNTT AGGTAGANTT TAACATGACT TCTGCCCCAG 180  
CTTNATCTGT CACACANGTN TGTGGCACCN CTAGTGCTAC TGCTAGGATA TCACCTACTC 240  
AGTTAGATTT TTCCNAAAAA NTAAGCTTTT AATTNATTTC TTTGGTGTN 289

SEQ ID NO:5869

SEQUENCE LENGTH:346

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06972

SEQUENCE DESCRIPTION:

GATCTCCTCT TCCACCTCTT CCTGGTTCCT TTGCGGGGAA AATTGCACTA AAACAGAACC 60  
 TTTTCTTAAT CCATGTTGGA AGGAAGCAAC AGTGAAGTCT ACCTGTTCTG GAGTTCTCCT 120  
 GGGTCTGCAG AAGGTTGGGA ATTTAGAAAA TAAGGCTGTT CTTTCATATT TTAATTTAAT 180  
 CTCTGTCAAT GGCCATCCCT CCCACAAAAA AACGTGGGTT AAGAGAACTT GCAGACTGGA 240  
 TATGCAAGCA AACGGGCANC TCTGGAGAAA ANTANGGNAN GGAATGCTGA CTTTCTCTTT 300  
 CTNTCTCTTT GTCCCCACAC CNNTTCCCAN CCAATTACT GGGGTN 346

SEQ ID NO:5870

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06973

SEQUENCE DESCRIPTION:

GATCCCGACC CTCACCAGTC CCATTTCCTT CCCTCCAGCT CTGCTTAGGC ATTTTGCCCC 60  
 TCACCCCAAT GTTCCACACC ATCGACAACC AAGGGGTGAG GTGGGGACAG GCCTCAGCAG 120  
 GGAATGGGGC GTATATGTTA GTGTGCTGC AACAATAAAG CCTGTTGCAT CTCTCATGCC 180  
 AGTGAAG 187

SEQ ID NO:5871

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06975

SEQUENCE DESCRIPTION:

GATCTNGGAC TTCCAGAAAA CAGAACTGTG AAAAGNCAAG TTTCTGTNGT TAAACCACC 60  
 CAATCTGAAG TATTTNGTTA TGGCAGTCCT NGGCAGACTA ATACAATATG CAACACATTT 120  
 ACAATANATA TACAN 135

SEQ ID NO:5872

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06977

SEQUENCE DESCRIPTION:

GATCAAATAA TGATGTTAAA TTCTTAAATC ATATTGCTA TGCAGCTGAA GATGATATTT 60  
 TGATTGTAT TTTGGGGGTA CCTGTGTTGA GTTGATAAAC ATTTCCATCT TCATTAAAC 120  
 TGCTTCCAAA CTAGTAAA 138

SEQ ID NO:5873

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06978

SEQUENCE DESCRIPTION:

GATCGGCGGG GCACAGTGGC TCGTGCCTGT AATCCCAGCA CTTTGGGAGG CCTAAGCAGG 60

CTGGTCGCTT GANCCCAAGA GTTCGAGACC AGCCTGGGCA ATACAGCGAG ACCCCATCTC 120  
AATTATATT ATTTAAAAAN TAATTAATGT AAGAGNAATT AAAACAGATT TTTAAANNNG 180  
NNAANNAN 189

SEQ ID NO:5874

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06979

SEQUENCE DESCRIPTION:

GATCTGACTC TTCATTNTA AGTTCCTTGT TACATCATGG TCATTNCTA GTTTTNNACC 60  
AGACTCCCAT CTCACAATAA AATGCATCAA CAAGCAA 98

SEQ ID NO:5875

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06981

SEQUENCE DESCRIPTION:

GATCTGCCGG CTCCCGCCCA GCCTGTGTNG AAAGAAGGCC CACGGGCACT AGGGGAGCCG 60  
AATTCTACAA TCCCGCTGGG GCGNCCGGGG CGGGAGAGAA AGCTGGTGCT GCAGTGGTGG 120  
CCCTNNGGGG CCATTCGATT CGCCTCAGTT GCTGCTGTAA TAAAAGTCTA CTTTTGCTA 180  
AA 182

SEQ ID NO:5876

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06982

SEQUENCE DESCRIPTION:

GATCTTGTTT TNCCTCATCT GTAAAAGNAG GTTAACAAAG CTTTCTGCC CACTTCTTGG 60  
GGAGAAGGGA ATAACATAAT TGGTAA 87

SEQ ID NO:5877

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06983

SEQUENCE DESCRIPTION:

GATCTTTGGC AGCGCATATG GCCTCTTTGG GGTATCGTC GCAATTNTTC AGACCTCCAG 60  
AGTGAAGATG GGTGACTAGA TGATATGTGT GGGTNGGGCC GNGCCTCACT TTTATNTATT 120  
GCTGGTTTTC CTGGGACAGC TGGAGCTGTG TCCTTTAGCC TTCAGAGGC TTNGTGTTCA 180  
GGGCCCTCCC TGCACTCCCC TCTTGCTGCG TGTTGATTG GAGGCACTGC AGTCCAGGNN 240  
NNGTCCTCAG TGCGGGGAGC AGGCTGCTGC TGCTGACTCT GTGCAGCTGN GCACCTGTTN 300  
NCNNCANCTG CACCN 315



SEQ ID NO:5878

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06984

SEQUENCE DESCRIPTION:

GATCTNTTTT TTTTGGTAG TTCCTCAGCT ATTCAGGAAG GTGTATTNT GCCAGTAATT 60  
ATCCCTATGC TAATACTTTT TAAACATTA CTAGTGAGTG CCCTAAAACA TTACTAGTGA 120  
GTGCCCTTTT NNTTACAGA AGAAATTGA TTGTTGTGAG CGATAATAAA ATTAACGTGG 180  
ANCTCTAAA 190

SEQ ID NO:5879

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06985

SEQUENCE DESCRIPTION:

GATCTCTATT ATNAGGCTAG ATGTATAGCC TCTACTCCCC CAGCTTCTTG CTCTTGACCC 60  
TGCACTGTAA GTTGCCCTTC TATTAGCAGC CAAGGAAAAG GGAAACATGA GCTTATCCAG 120  
AACGGTGGCA GAGTCTCCTT GGCAATCAAC CAACGTTGCT ATGAAATATG CCTCACACTG 180  
TATAGCTCAT TATAGGACGT CAGGTTTNTT GAAAAAAGTG GGCAAGNCAT GATTAATGAA 240  
TCAGAATCCT GTTTCATTGG TGACTTGGGT GGGGGCTNTT TGAATTTTAA AAANTNNTNG 300  
TNAGNTGTAG NNNNGTGTNT NN 322

SEQ ID NO:5880

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06986

SEQUENCE DESCRIPTION:

GATCATGGAA TACAAGATAA TTTCTCAGGA ATCAGATGGT CTTATTCCAC ACCTGCAGGA 60  
ATGTCAGCAT TGCAACCACC ATGGCAAATA TTGATTAAAT AANCAATTAC TATTTCCAGA 120  
TAAGTGCAA ANTCTTAGAN GAAATTGTCA TATCTTAGAC AATTTAGANG TGATGGAGGG 180  
TGGATGATGA GAAATTATCG CACCACTGCA CTCCAGCCTG GGCGACAGAG CAAGACTCTG 240  
TCTCAAA 247

SEQ ID NO:5881

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06987

SEQUENCE DESCRIPTION:

GATCCACAGT GTTGGGCACA ACTTTGACGT TTCTTAAAAA AAAAATTAA A 51

SEQ ID NO:5882

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06988

SEQUENCE DESCRIPTION:

GATCCTTGAT TGGTGAAGG ATACACAAAA TCAGGCTGCT TCAGAGGAAG TCATCTGCTC 60  
ACAGGAATCA GGGTGAAGGC CAAGGACGGC ACTCAAGAAT TGCCTGTCT CTAACAAAAA 120  
AGCATCTGCA ACGAACTTCC TTTAATTTT GAGTTCAGTG TCTGTGATAA TTAAGAAATG 180  
GCANTACCAT GTATTNCCC CAGAAGTAA GANATATTGC TGNACGGACC ANTAAAGTA 240  
ATTNAGCTC CCTCAAGNAN NATGNGGTGN GGGNGN 276

SEQ ID NO:5883

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06989

SEQUENCE DESCRIPTION:

GATCGGCCA CTTCTCTCTA GCCCAGGCAA CAGAAAGAGG CCCCATCTCA GAAA 54

SEQ ID NO:5884

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06990

SEQUENCE DESCRIPTION:

GATCCTTAAT TGCTACCACA TTTCAAACAA GAACTATGAC CAATTAACT TTACTGTTGT 60  
TGAAGTCCA AA 72

SEQ ID NO:5885

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06991

SEQUENCE DESCRIPTION:

GATCCNTTGG GAATCCAGTT GAAGTTCCCA AATACTTTAT AAGAGTTTAT CAGACATCTC 60  
TAATTTGGCC ATGTCCAGTT TATACAGTTT ACAAATATA GCAGATGCAA GATTATGGGG 120  
GAAATCCTAT ATTCAGAGTA CTCTATAAAT NTTNGTGTAT GTGTGTATGT GCGTGTGATT 180  
TACCAGAGAA CACTNAAAA NAACCAACTG ATNTTTNAA TCCTANTGTG TAGGTAAAG 240  
TGTCATGCCN TNNACCANTN CTAATGN 267

SEQ ID NO:5886

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06992

SEQUENCE DESCRIPTION:

5 GATCATAAAA ATAGCAGNGC ATGTTNCCTG ATGATTTTAC AGTGCATATT GTCATGGCCA 60  
GGGCTTAGAG GTAGGGGAAA AACATGTGGA CAGCTTTGTG ACAAGAGTCT CTCTTATAGT 120  
TTTCTTTCT AAAGTAACTT TTTCTGAGTA TGAATGTNNN NNNN 164

SEQ ID NO:5887

SEQUENCE LENGTH:341

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06993

SEQUENCE DESCRIPTION:

15 GATCCATGCA AATTGTCGCA TCCGACGGGT TAACTTCTCA GACAGACTCT ACTCAGANGA 60  
TGAGCTGCCG GCAGAGTTCA AACTGTATCT CCCAGTTCAG AACAAAGGCAA AGCAATAACT 120  
GGAATTGTGA CTCGAGGGAT AGACCCCTGG ATGTGACTCT NCTTTTAAA AGGAAACTAT 180  
GTGGAGGACG ATGCAAAANC ATATTTATCT TAGTTTGCTC TGCTGTAGTT CTGTTATTTA 240  
TACTTGGTGT TGCTTGTCTAT GGACACNGGT GAACATGCCG TAACTCTGTG ACTGCATTGT 300  
20 AAGTGCAGTG GGGGTAAGCA GTCCTGTGGC GTGGCGCATT N 341

SEQ ID NO:5888

SEQUENCE LENGTH:256

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06994

SEQUENCE DESCRIPTION:

30 GATCCTGGAC TGGGTACCTT ACATCAATGG CAAGTTTAAG AAGGNTAATT AATTACACAA 60  
ACCCCTCACA GACTGCTCTG GTGCCTGGTG GTGCTAGCTC CTCCCACCTC AGCACCTGCT 120  
GCATCTGGAG CAGCCCAAGC CTCAGGATGG NCAAGNGGAA ACCCACAGCT CAGCTTCAGG 180  
CTTCTTATGT TTCTGAAAAC AGCTTGGNTA TTTTAATGCA CGTTGCATTA AACCTCACTG 240  
AANCATAANG GGGAAA 256

35 SEQ ID NO:5889

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS06995

SEQUENCE DESCRIPTION:

GATCTTTGTA GGAATATATG TGTCAGTAAT NATGAGCTTC AATCCTGACA TTAATAACTT 60  
ACTGTNGAGC AGAGAAGAGT TGCTTGTAAC CCTTGTGCTT TTATATACTA NTTTTAAANC 120  
TTAAAGTGAT AGTGAGCTAT GAAGTACCAA TCATGTATGA TATGTGGATA CAAAGCACAG 180  
45 TATTATTAAA GTGTNATGTG GAAA 204

50 SEQ ID NO:5890

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS06996

SEQUENCE DESCRIPTION:

5 GATCAGCAAT AAAAAAAAC CTACAAAAA NCCTATATTC NTTAATTNTT GCTTTTACGG 60  
TGATATAGTG CATGCAAACC AGGAGCATT TGTGTCTTAA GAAAAATAAT CTTAGAACAG 120  
ATGGCTGTGA AAATTACACC CATGCACAGN ACANGCCACA GGAATAATNG GNN 173

10 SEQ ID NO:5891

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS06997

15 SEQUENCE DESCRIPTION:

GATCAAATAT TGGTTGAATG CCTATGTATG TCAGGCCCTG TGCTGAGCCA TGAGGATTAA 60  
AAAGATGAAT AANCATATCT TGTTTAGGAA ATGGATGTAT AAAAAATCA AGTGCAATAA 120  
AGTGTGTGTC CAAAAGCTGA CACAATGGAA AGGAAA 156

20 SEQ ID NO:5892

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS06998

SEQUENCE DESCRIPTION:

GATCGCTTGA ACCTGGGAGG CAGAATTTGC AATNAGCTGA GATTGCACCN TTGCACTCCN 60  
GCCTGGGTGA CAGAGTGACA CTCTGTTTGA AACAAACAAA 100

30 SEQ ID NO:5893

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS06999

SEQUENCE DESCRIPTION:

GATCACTTGA GCTCAGGAGT CCTAAACCAG CCTGGGCAAC ATAGTGATAC CTTGTCTCTA 60  
CCAAA 65

40 SEQ ID NO:5894

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS07000

SEQUENCE DESCRIPTION:

GATCTTGAAT AATTCATAAT TCTTCCACAG TAGAAATAAA ATAATTNCTG GCTAGTTATT 60  
TTCTTAAAAA TAAAAAAAT TTGAAAACCT CAAA 94

50 SEQ ID NO:5895

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07001

SEQUENCE DESCRIPTION:

GATCCCTCTT TTCCAGAAAA TTCTGTGGAA TTTTCTGTA GGACTTTGTT CTCCACAAGC 60  
 TTGAATTAAA GCAGGATTCA GTTTGCAAA 89

SEQ ID NO:5896

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07002

SEQUENCE DESCRIPTION:

GATCAGCTGA AGTGTGTTTT AGACCCAAAC CATCTGGCCC CTTCGTTTTG CTCAGAGGAA 60  
 GTAAATNTNC ACTTAAATGA AATTGAAAAC GCCATGTGGC ACCACAAAAG AGCTCTCTGT 120  
 ACTTNCCCCA TGCTGCCTCA AAAGTNCCTGT AAGTTTCGGG GTCAGTGTCC CACCCTTCAC 180  
 TTCCCGANNN NNGGGN 196

SEQ ID NO:5897

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07003

SEQUENCE DESCRIPTION:

GATCCCAGTT TGCTTGCCA AATAAACTCT GTTTATGTGA ATTTATTAAA CGCAAA 56

SEQ ID NO:5898

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07004

SEQUENCE DESCRIPTION:

GATCCCAGCT TTTTCCCTC TCCCACAAAA CCAGGTAGTG AAGTTATATT ACCAGTTACA 60  
 GCAAAATACT TTGTGTTTCA CAAGCAACAA TAAATGTAGA TTCTTTATAC TGAAGCTATT 120  
 GACTTGTAGT GTGTTGGTGA AATGCATGCA GGAAAATNCT GTTACCATAA AGANCGGTAA 180  
 ACCACATTAC AATCAAGCCA AAAGAATAAA GGTTTCGCTT TTNTNTTGT ATTNATTGT 240  
 TGTCTTTGTT TCTATCTNNG ANATGCCATT TAAAGGTAGA TTTCTATCAT GTAN 294

SEQ ID NO:5899

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07005

SEQUENCE DESCRIPTION:

GATCTCCCTA CTCCATTNNN CCCTTTAATT NAAGTGGCCA CATGTATATG TCTTCCCTGC 60  
TGTGTTAGGA AAATGGGGGC TGGATATCCC AAGAATCAGA GGTTATATAN AAN 113

5 SEQ ID NO:5900  
SEQUENCE LENGTH:171  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS07006

## SEQUENCE DESCRIPTION:

GATCGCTTTT GTGACTGTCC ATCTGTCCTT GACAGTGGCT GTCATATTGA CTCCTTTGNT 60  
GNTTTGTTGG TATTGGGGAC ATTTCCACG GCTGAGTTNT TTTTGACTGA CATGTTTATG 120  
15 ACATAGACGT NGTTTTCGCA TCCNTGACTT AAAGTACTT GNACNCCNTT N 171

20 SEQ ID NO:5901  
SEQUENCE LENGTH:76  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07007

## SEQUENCE DESCRIPTION:

GATCTACTGT AAAAAGAGGA TTAAGNAAAA TAAATNAGA GCAATTATAT ATATAATTNT 60  
25 ATATCATACA CAGAAA 76

30 SEQ ID NO:5902  
SEQUENCE LENGTH:118  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07008

## SEQUENCE DESCRIPTION:

GATCACGGGA GCAATGCTGT ACGGTTTTGT ACACTGGTGG TTTGTTTCCT AGAAAACCCA 60  
35 TTGTNTCTCT GGATTCTAG CACATTACTA AAAGAGCCTC TNCITTTGTA ACATGAAA 118

40 SEQ ID NO:5903  
SEQUENCE LENGTH:185  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07009

## SEQUENCE DESCRIPTION:

GATCANNCTG ANCCAATTTA CCAAGCATT TTAAGGAGGA ATAATNCCAT ACCATGTAAA 60  
45 ATACCATGAT ATGCTGATTA TAATACATTA ACAAATTTTT AAGTTGCGTT CACTAAATNC 120  
TGTCTGTTT CTTCAAAATA ATATAGCTTA AATTGCATGN TAATNGTATA TCTTACCTNT 180  
TTNGN 185

50 SEQ ID NO:5904  
SEQUENCE LENGTH:134  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07011

SEQUENCE DESCRIPTION:

5 GATCTACCCA ACTCTGTCAT CTGTAACAAC CAGTGATAAC TCTCTTGTCT TGTA AAAAGG 60  
GTTTATACAT AACTTGTACA TGGTTTCATT TTGTATTNC CGCAGATTAA AAATTTATGT 120  
ATTCTNTTC TAAA 134

10 SEQ ID NO:5905

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07012

15 SEQUENCE DESCRIPTION:

20 GATCGAATTN CNACCCCTAA NCTTGTCGGG ACGTATGGTC CAAATTCANA TTAAGGTGGT 60  
CACCCAACCC GAGATGTCAG GAAAGGCCTT CTGCAGAGAA AATNTCCCC CACCCGCCAT 120  
CTGCAGCCAG GTGTGTGCCA CACGGCAGCC TTCCCGAAAC ATAGTATGGA TTTTAAAAAT 180  
GTGTTTATTT TTNTNTCTCA ACCACTTTAT AACGTATTC TCAATTTANN TTGTAATGTC 240  
TTGTNTTGGG GNGTTGCTGG GTATCCTTNG TTATGCTTCC CACTGTTNTT NTCACN 297

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SEQ ID NO:5906

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07013

SEQUENCE DESCRIPTION:

GATCTAGAAT GGGGCTGCAA GNCGGTCCCC ATTTTGGATG GGTCACATTC AGACACCACA 60  
 CTATGGTTGC ATCACCTGTC ACACCGACCT AGACAGCTGG ATGCCATTTG GNGTAGAATA 120  
 ACCAGACTGG TGAGTAANCT AGAAATCATA TTACGTGAAG AGTGGCAAAA GGCCTGAGAN 180  
 AGTTTAGTTT GGNAACATG ACTTANAAGG GGCATCACTG CCCTCNCAT TTNTNTNANG 240  
 GCCTCATTTT CNGN 254

SEQ ID NO:5907

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07014

SEQUENCE DESCRIPTION:

GATCCATGAA GGAATCGGGA GTGGATGGAA TCGGGTAAAA CTGTCCTGGG GCCGGACCCG 60  
 TNGCCCAAAG TCCGGACCNN GACCNAAAA ACGCTTCCAT CTTAGTCACG TTAGCAGAAA 120

SEQ ID NO:5908

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07015

SEQUENCE DESCRIPTION:

GATCCCAATT TTGTAAAAAT ATCTGTAATA TGTAAGCATA GGTATTTGTA TATCTTAAGA 60  
 AAAAAAGCCT AGAAATAAAG CCACAAAAAT AAA 93

SEQ ID NO:5909

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07016

SEQUENCE DESCRIPTION:

GATCTCAATN TGCAAACTCC TTGGNCTCCA GACCCCTGTC TGGNTGGNAC TCCTAGCAGT 60  
 GTGTGGTTTC ATCAGGAAAT CCTTGCAGCA GGGGNTTAGA TGGTTCCTTC AGGAGGTGGN 120  
 GAGCCTCCAT AGCATTGAAG GCCAGCCTGC ATCTCGCGGT GTGTGTCCAC TTCTCCCCTC 180  
 ACTTTCCCCT NACCCATCCN TTTAAAGTGA TTGGCTGTGA GGAGCACAGA GGNGTGGCAA 240  
 TTCCATCTGT TNATGGGGTC AGAAGACATA GCCGNCATGG NGATTTCACA ATTNACCNGN 300  
 GTAAAN 306

SEQ ID NO:5910



SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07017

SEQUENCE DESCRIPTION:

GATCATATAG AGTAGTTAAG ACAACTGTAA CAGCATTTTT TGAAATACAT TGTAATAATA 60  
TAAAAGGTAA CATAATTAAA 80

SEQ ID NO:5911

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07018

SEQUENCE DESCRIPTION:

GATCTTAAGC TCTGCTCTCA GCAGATTTC A GGTGTACCAT TTGTAACTG TACTGAAGGT 60  
GTGTCCTCAA GAAGAAAGTG TTCAAATTAA AAAAGCTGCT GCCAAGTAA 110

SEQ ID NO:5912

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07020

SEQUENCE DESCRIPTION:

GATCGGGAGG ACTGTGGCCA GCAATTAACA CCATGTAGAC TTCCTTAGTT CTTAAGTGGT 60  
TGAATTCGCT GNTTGTCTG TAACGTTATA AATAGTNNAT ATCTGAAGAC GGAGAGCCTG 120  
TANTATTCTT CAGATTAAAT GAAGCGTGAG ACACTTAA 159

SEQ ID NO:5913

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07021

SEQUENCE DESCRIPTION:

GATCTCTCCC ATGCCTTTTA AGCAATTAGA ACTAGATAAT GCAGCCATTT GTCACCCAAT 60  
TAAATTTGAA AGGCCAGAAA TGCATGGATT AGCACTTCAG CTTTGTCTGC AGTCAAAGCA 120  
ATTGTTACTT AGATAGAAGG ACAGTTAAAN TGAAAAATGA ATTTGNTAA AANTGCGGNN 180  
GTATAGATAA TATTCATT C TNCTTTTAA TGCTTAAACA CCCTGTATTC TGTATTTNAC 240  
TTGTATCATA NTTTTATTG CTCATTCCTA TTTCCCTGNG ATACTTATTN CTTNCACAAT 300  
ATTTCTTCAN GTGGATATGT NCTTTAANTN 330

SEQ ID NO:5914

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07022

## SEQUENCE DESCRIPTION:

GATCATAGCC CTNNGCCTGG CGGCACAGCA GCACTTGCGT TCTCGGGGCT GTCGATTNCC 60  
TGCCACCTGG CCAGATAACC TCAAGATTTC CACCTTTTCT TTTCAGCTTG ATTGCATTG 120  
ACTATATTN ACAGCCAGTG ATTGTAGTTT CATGTTAATA TGTGGCAAAA TATTTTGTGTA 180  
ATNATTTNCT AATCCCTTTC TGAGTACTCT GGGGCCCTGC ATTTATNAGG CACCTACCTT 240  
CATTTTGCTA ACGCTTANNC TGAATAAAAG NTTTTTGATT CCTTAANAAA AGGGNNNGN 299

SEQ ID NO:5915

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07023

## SEQUENCE DESCRIPTION:

GATCCTTTGT CCAGAAGAAG CCCATGGAAT ATTGAATGTA ATACATTTAG TCAATTAANT 60  
TTTAAGNAGA TTCTTATNTA ATAAA 85

SEQ ID NO:5916

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07025

## SEQUENCE DESCRIPTION:

GATCCAGCTC AGGGGAGCCC TCCTCCTGAC TTTGGAGACC TCCTTCCAGA AAGACTGCTC 60  
GGACTATGGA CTCTGAGCTC TTAAGTTGCA CCCGCTGTAA TACAAATNAG TTGTTTGCCT 120  
GAATTCCAAG AACTGTCTCT GTGGTCTAGG CTGTCTGAAA TTTCTGTTGA GGGTAAGAGA 180  
ATAAGGAAA 189

SEQ ID NO:5917

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07026

## SEQUENCE DESCRIPTION:

GATCCCTAGG GATTNTTCAT CTTAAGACTC AAAAGGCTTA ATACCAGGAA CCACCTTGGC 60  
AAGATATTTA CCCACCGGCC ATCTCTGTTT ACTCATGAAT GTTAAATGTT AAAACGCAGC 120  
GCTCTAACCC TGCNTNNNAT TTAATTGCAA ATGTCTGTAA TCTGTAATTG TNATGCCTCT 180  
GATGGAATAA NTTATCTTTT TCAGTCTCCT CTAAA 215

SEQ ID NO:5918

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07027

## SEQUENCE DESCRIPTION:

GATCGGATTG ATTAATAAAC AAATNCTCTG GAATTTTINC GTTCATGCTT TTCCGTATTC 60

TTTATGGCTT TTAAATAAAT ATACAATGGT TAATAGTAAA

100

SEQ ID NO:5919

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07028

SEQUENCE DESCRIPTION:

GATCAGGGGT CCGGCTGTCC TTCTGTCCTG CTGCAGACTA AAGGTCTGGC CAATGTCTTG 60  
 CCCACCCCG CCAGCCGCGA TACGGCGCAG TTCCTATATT CATGTTATTT ATTGTGTACT 120  
 GACTCCATCT GCCCCGTCAA ATAAAAAACC ACAAGGTTCG AAA 163

SEQ ID NO:5920

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07029

SEQUENCE DESCRIPTION:

GATCACTGCT GCTAGCTGAC TGGACCTCCC CATTGGAAGT TTGTAATTTT NCTTTGGCAA 60  
 AGTTTCATTG ACTAGTAGAA CTCATTCTGT TTTAGTGTAT ATTTCAATAT AAATGTAAAC 120  
 ATTTTGCTCA AA 132

SEQ ID NO:5921

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07030

SEQUENCE DESCRIPTION:

GATCCTAAGG AAGGAAAAAG AAAGTGTTAA AAATTAATAA AGGTTTTTTT GAATCCCGTG 60  
 TCCTTCAAGT GCTTTCTAAC TTTGAGAGGA AGAAATTGAC CACCTGGACT ATGGAACGTG 120  
 GCGTAACAGC TTTGAAAGTG TATTTAAAN TTAANTCTAT ATGCCTTTAA NTCAGTGAAT 180  
 TGGAAACATA TTACATGNNG TTNATGATT TNCCTCAAAT ATANTAANTN GTTTCCTTTC 240  
 CAGTAGAAA 249

SEQ ID NO:5922

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07031

SEQUENCE DESCRIPTION:

GATCTGCAAG TAGCCTAAAA ATGCGATTGC TGGTAAACCT GGCCTCAAAT TTCATACTAC 60  
 CATAACTNNT TTTATATATT GCCACTAATT TTGACTGGAT TTAATAGCAC TTTATTGTAC 120  
 AACTACAAAA AAAAAANTNTA TTCCTGGANT TGTGCGCNGT GTAATTNCTC TAATGTNCTG 180  
 GTGCTTTNCA N 191

# EP 0 679 716 A1

SEQ ID NO:5923

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07032

SEQUENCE DESCRIPTION:

GATCTTATTT CATGAAGGTT GTATAAATGA AATCATTCAG TAATGTATCT TTTAAGACA 60  
GGTTTTTTTT TTTCTCTCAG CACAATTTCC TTGAGGTTCA TCCAGGTTGT TACCCATAAT 120  
ACCAGTTTGT NAGTCTTTAT TGCNGTAGTC TATAGCATGC TTATATCACA GTCTGNCCAA 180  
CCATTCACCC NTNGATGGGC ATATGGGCAT TNCNGTTTG GNGCTATTNC AANTAN 236

SEQ ID NO:5924

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07033

SEQUENCE DESCRIPTION:

GATCTNTTTC ATAGTGTTCA AANCTGTATT ATTATATGTA GAGGGAAATA ATTTTCTCAA 60  
CACTAATCGT TAATAACTAT TGTATTAAAT NGTCATNANG N 101

SEQ ID NO:5925

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07034

SEQUENCE DESCRIPTION:

GATCTGCAGT TTCCCCTTTT NTCCCCTCTG AAGAGTGGTT CTTATGTGCA ATCTGCAGTA 60  
ACCTTGAAGT CCAGAGCTGC ACTATAGAGG AGAATGCATG CCACTATGAC AGCAGTATGC 120  
CAAGCTTTGT NTTATCTCC TAATAAACGT TAAGACCTTT GGTGTAATAA ANGCAGCAGC 180  
ATTCACCAAC AAA 193

SEQ ID NO:5926

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07035

SEQUENCE DESCRIPTION:

GATCTGGGGT AGGGGGCACC CTACAGTGGG ACCCNTCCCN CATTATTCTT TCTNTCCAGC 60  
CCCTCCCTCC CACTGGAGCA GCTCCAGAGN CATTCTCAC CCCCCTNACC TCTCCAGCC 120  
AGGGCTGAGA GGATTGAGG TGGCTGGGAG GGTTCAGG CCCCCTGCC CTTNCCCACA 180  
AACTGGGTGN TAGGGCGGAC TTACCTGGCC CAGCCCTGCC TCCNTNAGCC AACCAGNCC 240  
NTNGGGCTGT N 251

SEQ ID NO:5927

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07036

SEQUENCE DESCRIPTION:

GATCTCGATA TTTCAAATGG GCTTTNNATG CACTGTTGCC AAGAAAGGCT TTCCTGATT 60  
TTTNACAAN TNAATTTTG CACACTTTCA TTGGTGCTT TCGGCAACTT ACATTGAAAN 120  
TGAGCTATTG TN 132

SEQ ID NO:5928

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07037

SEQUENCE DESCRIPTION:

GATCCCTGGG TTGCCCTGTC CCAACCTGCT TGTTAGGTGC TTTCCCATAG NAGGCCCTTC 60  
TTGAGAAACA ATAACTAGG TAGAACTAAA 90

SEQ ID NO:5929

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07038

SEQUENCE DESCRIPTION:

GATCTCAAAA CTCATTGTT GTACCATATA TNATGGTTTT NTGTCTATAT CATATATTC 60  
CCTACTTATG TGTTTAAATN CTATTTNGTN ATGTCAATCT CTCTGATGCC ACCTATTN 119

SEQ ID NO:5930

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07039

SEQUENCE DESCRIPTION:

GATCGGGGCC AGAGGCAGAA CCCTGGTGAG GAAGCTCCAG TCCTGCTCTC TACCCAGCCC 60  
ATCTTGCCCTC CATGGTGCTT CTGGAGGCCT CTGGGCCTCC TCTAACAGGG GCTGGTGGGC 120  
ACCAAGAGNC AATGGAGTAG ACCCCTGGNT GGTAAGGGNC AAGTNCCACC GGTGCTTCT 180  
GGGAAGGGGT TTCTAACACT AGTTTGTGTG CTGTGGTTCC TGGGGTGCCC TCCACTGCCC 240  
TCTNTTCAGG AN 252

SEQ ID NO:5931

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07040

SEQUENCE DESCRIPTION:

GATCCCACTG CAGTGGTGCC TACATTTATC ATCATGGCTC CTCTTGAATA AAATCTACCT 60

TACCATCTTC AACAAA

76

SEQ ID NO:5932

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07041

SEQUENCE DESCRIPTION:

GATCAGCACA GTAATGCCCA ACAATATTGT TTTAAACAA AAAATGTAAA CATTCAAAAG 60  
AATCTCTCTA AATCACTGAT TAATCATTG GACTGAAAAC AAA 103

SEQ ID NO:5933

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07043

SEQUENCE DESCRIPTION:

GATCTACCCG NCTNGGCTC CCAAAGTGCT GGCATTACAG GTGTGAGNCA CCGTGCCCGG 60  
CACCAGNATC CTTTGGTATA GCCAAGCCTT TTGGTTACCG NCTCATGAAG AATATGCTTC 120  
CCGCATTGTC CTAGTCCCAG TTGTATTCTC ACAGGTGTTA TGNGGGGGGC ACAATCCAAA 180  
TNATAAACCT GGTTCATGNC CAACANATT NTGCTAAATA GGGAGGNGGG N 231

SEQ ID NO:5934

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07044

SEQUENCE DESCRIPTION:

GATCTGAGCC CAGCGTACAG AGAAGGCTCT GTGCAGACAC TGCTCACACC TCCAGCTCCC 60  
AGCTCACCTG CCCACAGGT GCCAGGNTAC CTNTTNTANT GGCCAGCAGG GCCCTNACCA 120  
TCCTCAGCCT GCNTTCCAGT CGCCCATTCT TTCCATTCTG CGGCTCGTGC TTAAAAAGCA 180  
ACCAGCCAAC CNTTTNTGAT ATAGTAGGGG ACTTGAAAGG GGCTAAGAAG ACTGANGATG 240  
GTCTGCCACC TTAAACCACA AGGNTTNGGG CTTTGGTTN 279

SEQ ID NO:5935

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07046

SEQUENCE DESCRIPTION:

GATCTAGGAG AAGGGNCTCA TGCGGACCCT CACATGGGCA GAAAAATGGT GGTCATTGGC 60  
CGACATCACA GTTTTCNGT TTCCACCCCA GCTAAAAACC GTTGTGTTGCT TTAANTTTNN 120  
ATAAACTGGA ATCCTTTCAC CCGTCTCTAC AGCTAACCT CACANGCATG AGGTGCTGTG 180  
GCTGTNCCTT ATCCTAATGA TGCGCTNNGG NCCCGTAAAT GTNAACACTC ATGAN 235

SEQ ID NO:5936

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07047

SEQUENCE DESCRIPTION:

GATCAGTTAC ATTCATCAGT TGGTGAGTTT TGAAGAATAA CTACATTNA TTTCAAAC TA 60

ACAAATGTAT ACGGTTTTAG TTCAGTGTTG AAGAATTNA ATACAATATT AANTNNCTN 119

SEQ ID NO:5937

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07048

SEQUENCE DESCRIPTION:

GATCCCTTTT NAAAAATATA TGTATGCATG TNTGCATTAA AGAGTCTGAA AGGATACTTG 60

CCAAAGTGTA AAAGCATTTA TCTCTGGGAG GTGAGATTG GAGCAATTAT ATTNCTTTT 120

TGCATATCTG TAACTNCTNA TTTCCCNCAA TGNGCATGTA GTGTCTGTAA AATTTCCAG 180

GGAATAANCA NTGATGTTCA CAATATATAT TNN 213

SEQ ID NO:5938

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07049

SEQUENCE DESCRIPTION:

GATCCAGACC ATCCTGGCTA ACATGATGAA ACCCTGTTGC NTGTNGTACC AACTACTTGG 60

GAGGCTGAGG CAGGAGAATG GCATGAACTC GGGAGGCGGA NTTGCAGTGA GCCTCCAGCC 120

TGGGCAACAG AGTGAGACTC TCTCAA 147

SEQ ID NO:5939

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07050

SEQUENCE DESCRIPTION:

GATCCTGGGA GCCTCTGTTC TTTGCGCATT TCAGACACAG TCTGTGTGGC GAGGAGTGTG 60

ANGGNAGGAG CCTNGGGTGC AAGCCCGTGT NTTTGGCCTC TTTCTCGTG AAGACGATGT 120

GTCCCCGTCA GAAAAAGTGG GCTCNCNTCTG CAGCCCGTG AGCTGAGCCC AGGCTGCGTA 180

GTGACCACAA GCTTATGTGN AGCACTGCTC AGGGAGGNTN TCAGGAATTC CCCTCACCTC 240

GGAAAGGANC TTCTCAGTTT TTATTGGGGG TGTNTAAATT TNCTTNCATA TNGTTCATN 299

SEQ ID NO:5940

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07053

SEQUENCE DESCRIPTION:

GATCCTTCAG GCAGTAAGGG AGAGTTTTGC CTCCTTACAC AGTGGCCTTT GCTTGCACCT 60  
CCAGCTGGAG ATGGGTGTGC CCCAGAAGTA AGCTTTGCAT CTCTTACAAG AGGGGAGCTA 120  
CAGGGGCAGC CGTGGCCTAG GCCCAAACCTC TGCTCTGAGA AAATAAATAT CTGTACCACC 180  
TGTA AAA 186

SEQ ID NO:5941

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07054

SEQUENCE DESCRIPTION:

GATCCGGTNA TGGTCTGGGC AGAGGCTGGG TCAGGAGTCC CAAAGGTCAG TGACAGTTTC 60  
TCAGAAGAGG CCCAGCGTCC ACCTCTCTCC CAGGGCCAGA CACCTCTTCC TGGCTCCCCC 120  
ATCCCCCTAT GGGCTCCAG CNCCTGCAC CCTCATTGCT GNNNAGATTA AAGCCTCTGT 180  
TTTGCACCTG TCAAA 195

SEQ ID NO:5942

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07055

SEQUENCE DESCRIPTION:

GATCATTCAC TGTTTNGTT TAAAACTGG TCAGTACTAT GAAGCTTCTG TGGTTTGTAT 60  
GATGTTTTAA CTTTCACTTT AAACTGCATA GAATAAATTA AATTGAAAAC ANCAAA 116

SEQ ID NO:5943

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07056

SEQUENCE DESCRIPTION:

GATCCGNAAG CNAGANACCC TGCAGGCTGG CGGGGACCCA NGGGAAGGC CTTCCCAGGC 60  
CCTTCTAACCC CCTGTGGCCC TGGACTTTCC TTGTNTGGAC TCACCCAGG CCTGGN 116

SEQ ID NO:5944

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07057

SEQUENCE DESCRIPTION:

GATCATAATC ACTGCCTTAC CNNCCTCAGC GTTGTNGTAA GGAAGTGTG TGTGGAAGTT 60  
TTTAATAAAC TTTGATGCT AGTNTACTTA GGGGGTGTNC CAGGTGTCTT TAATGGGGCC 120



TTCCAGACCC ACTCCCCACC CTTNTCCCCT TCCTTTGCCC GGGNACGNCG AACTCTCTN 179

SEQ ID NO:5945

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07058

SEQUENCE DESCRIPTION:

GATCTAGATT AGCAATATAA AGAAGCATAG TGGTACTCTG TTTCACACTT TCAGTAGATT 60  
TATTAGAAGT CAAATNCTAT TCAACAGACA CTTATTAGGA TATACAACTA ATTTANGAAT 120  
AAAATTCCAG GCACAATATA TTTNNNTNAA NTGGTATTTG TNAGTN 166

SEQ ID NO:5946

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07059

SEQUENCE DESCRIPTION:

GATCTTTTGT GACTACAACT TCTNTTGTAATAAATGATAT ATGGTATTNC CATCGTCAGT 60  
TACCGAGTAT AGCCACTGGG TATCACTACT TTGTGTAAAGTGCCCTTCGC ACTTTAAGTA 120  
CATTACTTAA ATGTTGCTTT TAGCTTTGAT AAATTGAAAA TATTTNAATG GGNNGGGGNN 180  
TTGAAATTGA AAACACTGTA AAATAGGTTG GNGTGTGAGC NNTATTANGN 230

SEQ ID NO:5947

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07060

SEQUENCE DESCRIPTION:

GATCCGCCTA CTTTGGCCTC CCAAAGTGCT GGGATTACAG GCATGAGCCA CCATGCCCAG 60  
CCAGNGATTT AATTNTTAAT AACTAATTTN AGGGCACAAT TTGACCTCCA TTGNCAGCCT 120  
GTTTGTATTA CTTAATGTGA ATATNTGTGT GTTTTGCCAN GGGNTATTGA NGTATTN 177

SEQ ID NO:5948

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07061

SEQUENCE DESCRIPTION:

GATCTCCAGG CCCAGCCTGG CCCCAAATAT TCTTTCCTTT CATCCTCAGC AAGTGCTGAG 60  
TCTGTGAATA AAGCCACATA ACCAGCGGGC ACTAAA 96

SEQ ID NO:5949

SEQUENCE LENGTH:191

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07062

SEQUENCE DESCRIPTION:

GATCATAAAG CCACCGGCCA CTGCCACGCA TGTGACACCT GTGCCATCGT GCTCCCTCCT 60  
GATGGGCACC GTGGTGGAGG AAGTCACCCA GCTGTTTCTC AGTCCCAGAG GCCGGTGGCT 120  
GGTTTAAAC TTGTGTTGAC TGTGATACT TATTACTGT ATAAATATAA TTNATCATTT 180  
GTACCATGAA A 191

SEQ ID NO:5950

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07063

SEQUENCE DESCRIPTION:

GATCCAACCTG GGAGAACCTC AGCCAATGCT GGAAGNATGA TTGAAGTACC TCTCTTTNT 60  
NACTCTTGTA CAGCTTAATG TGCAATAAAG GAAAAGTTAT ATCTGTAAA 109

SEQ ID NO:5951

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07065

SEQUENCE DESCRIPTION:

GATCGACCTG AAATCCTCA CCAAAGTNCT CGNNCCGGAG CACGAAGTCC GGGAGGATGA 60  
TGTCGACTGG GACTGGGACC ATCTGTTCAC TGAGGTGTCC TTAGAGGTCC TCACTGAGTG 120  
GGACCCACTG CAGACGGAGA AGGAGNACCC TCGNGGCAG GCCATNCACA CCTNAGCCCG 180  
TCACCCATGC TCTAGACATN AAGAANTGCA ANGGGN 216

SEQ ID NO:5952

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07066

SEQUENCE DESCRIPTION:

GATCCACCAA AATAAATGAT TTTCTACATT TTCATTGGA CTAAATCCCA CGAATGACAA 60  
CTACCACCTT TTTTCCTTT TTAATTAATA CTAAATATTG TGATTTCTTA TTTGAGGTTC 120  
AAAATGACCT GCTTGAAACT TTGATACATA TTGGAATACA TTATGTTAAT AAATTTGTAG 180  
CTTTTGTGA AA 192

SEQ ID NO:5953

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07067

SEQUENCE DESCRIPTION:

GATCACACCC TGGAACAATT GGNGGATTGC TTGCTGCCCT GCATCTTAAG GCGTATTCTA 60  
GCAGCAAAGC TTGTNATGCA CTGACTTGGG GCAAGTAAAA CTGATGCTGA GGACAAAGGG 120  
AGANGATGTT CCTCGCCCAG GGAAATNAAA ACTTTNCTNA TTCACCTTGC TTGTGCTTAA 180  
NCACCTATGT NCATCTAGTG TAGAATACAT GGCTACTTGT TTGTAATTNT NTNATTGGTG 240  
GAATTAAAGT AATTTTCCCT TATCTTTGAN CTTTTATTTA GAGAACTNAA ANAAAGCN 298

SEQ ID NO:5954

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07068

SEQUENCE DESCRIPTION:

GATCTNCAGG GGNATGTTTT ACCATCTGNA TCCAGCCTCC TGCTAACTCC TAGCTGACTC 60  
AGCATAGATT GTATAAANTA CCTTTGTAAC GGCTCTTAGC ACACTCACAG ATGTTTGAGG 120  
CTTTCAGAAG CTCTTCTAAA AAATGATACA CACCTTTCAC AAGGGCAAAC TTTTTCCTTT 180  
TTCCCTGTGT ATTCTAGTGA ATGAANTCTC AAGANTCAGT AGANCNAATG ACNTTGGNAT 240  
GTAATGNTNN 250

SEQ ID NO:5955

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07069

SEQUENCE DESCRIPTION:

GATCCGTNAA TNCNCGGAAT GGCAGGGGAA GCCTTGCACT AGGTTGCAGA GAAGCATCCT 60  
CCACATCCTG TGTCAGAAAC CCTGGTCTCC GTGGCACTTG TAACTACCG TNCTGTCTNC 120  
TGGTCTGTNT GTGTN 135

SEQ ID NO:5956

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07071

SEQUENCE DESCRIPTION:

GATCTAGAAT TGACATTTTG CCTTCTTGTT TCCAGGTGTT TCTATTTTTT CTATTCTTTC 60  
AGAGAAATCT CATATTTTCG TGTATTTATT GCTGTACTA CTATATTTAC TGCTGAAAAC 120  
TGTAACAACC TGAAGATTTG TAAATGTGA AACATAGTTC ATTAAAAATA ATAAAAATAA 180  
TCTAAAATGT AAA 193

SEQ ID NO:5957

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07072

SEQUENCE DESCRIPTION:

GATCCTCCAA AGGCCTGCCC CATGNATTTA ACAGTAATAC AGGAAGCATG GCAGGCACCA 60  
 TGCAAACCAA GGATGGATGG TGCAGTCCCT GTGTCAGTGG GCGGTGTTT CCTGCTGGCC 120  
 5 TGAATCACT CATCACCTGA TTGATTGGCT CTGTGGTCCT GGGCAGGTGC CTCATAGGTG 180  
 TGTGGNTATG ATGACGTTTC NNTAAAATGT ATGTNTTTAA CANATACTNA ATNGTATTAN 240  
 GGTCATGTAC CAATGGNTTT NATAATGTTT NTN 273

SEQ ID NO:5958

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07074

SEQUENCE DESCRIPTION:

15 GATCAGAAAG NATTAATAT CACTACCACA TGAGTTAAAA CAAAAAATGG AATAAAAAANC 60  
 AAAAGTGGTG TCTATGTTAT CAGTGGNTTA CTTGATAGGN CATTNAN 108

SEQ ID NO:5959

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07075

SEQUENCE DESCRIPTION:

25 GATCTTCACA AGGNTTGTAT TGGCCACATC CACGTCCTCC GAGCCTACAT CAAGACCCAA 60  
 GTGAACAAAG AGCTGGAGCA GCTCCAGGGG CTGGTGGAGG AGCGGCTCAA GGCCAGCGAG 120  
 GAAAGGCTCA GCAGCAAGTT GACTGCACTA GAGCGGCCCT TCCAGCTACC TCCGGGTAAA 180  
 GGCAAGAGCA AGACCAAGTG ACCCCCAACA TTTCCCAA TAAAGGTCTG GGCCAGANTG 240  
 30 GCACCATCCC TGCAAA 256

SEQ ID NO:5960

SEQUENCE LENGTH:262

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07076

SEQUENCE DESCRIPTION:

40 GATCTAGTCA TCTGGTTAAG GATTTTAAGC AGATGCAACT ATAAACCCAA GAACTGTAT 60  
 TACTATTACT GTTGGTCATA CTAAACCTGT CTATTTCTG AAGTATATGA CCCACAAGGA 120  
 TGTGAATAA CTAGGAGAAA CTGTTTTTGT AACTGTACA TCCTTAGTAT TTTTACACGT 180  
 ATATGATAGG GATGAACATG ATTTTNCCTC GTACAGACAG CTTANNTAAN GCACTATGTC 240  
 ANTCTGCAAA ANAGNNNNNN NN 262

SEQ ID NO:5961

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07079

SEQUENCE DESCRIPTION:

GATCTCAGCT CACTGCAACT NNTGCCACCT GGGCTTAAGC CATCCTCCCA CTCAGCATC 60  
CCAAATAGCT GGGACTGCAG GCACACACCA CCACACCCAG CTAATTTTNG TATTTTTTGT 120  
AGAGACGGGA TTTCACCATG TTGCCCAGGC TGGTGTGAA CTCATGAGCT CAAGTAATCT 180  
GNTGGCCTTG GCCTCCCAAA GTGCTGAGAT TATAGGCGTG AGCACTGCAT CCAGCTCACT 240  
CCTNATTTCT TTCTAGCCCC AAAGGGGTTG AGTCAGCAA TCCTNCAGCC TTTTN 295

SEQ ID NO:5962

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07080

SEQUENCE DESCRIPTION:

GATCCTGGAA TGTTGCTGG AGAAATTTAA AATACNGGGG TTTTTNTTT AATGGTGCCT 60  
ATTTAGAGTT GGAAGTTGAA CAGCTGTTGC ATTACATACT TTTCCTTTT NATTGAAATT 120  
TTGAAATCAA ACGTCTTGAT TTTCCTNTCC TGTGAATTG CTATGTNCAG GATGTCCTAG 180  
GGGGTGGGGG CAGGGACTCT TTTCGTAATA AGCACTTGTN TTAATNTGGT TGTGTGGNGT 240  
ATAAANGGCT ACACCCTTAT TATAAAAANN NN 272

SEQ ID NO:5963

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07081

SEQUENCE DESCRIPTION:

GATCTGTCGT CTTCAAAAAA ATGGCAAAGT GGGAAATGTG GGAGGGGAAA AACTTCAGA 60  
ATAAAAGAGA TTTAAGAGAT GTATCAACAA A 91

SEQ ID NO:5964

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07082

SEQUENCE DESCRIPTION:

GATCAGGTTG TCTGCATTTG TTGGTGTAAG TGAACATCAT CACAGTTATC CTGAGTTGAG 60  
TTTAAGCCAA ATANATGCAT AGAAAAGGGT CTCCTATTA ATGGAAGANG GTAATTTTAA 120  
GGATGTGTAT TATTTAGTT TTGTATGTTT AACTNTNATT NAATAAAGTG TTTTAAAAAT 180  
CNCAAAAATN ANNN 194

SEQ ID NO:5965

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07083

SEQUENCE DESCRIPTION:

GATCTGCCTG AAGAAAATAT CTGTTTTCTA TATAAAAAA TTTTTTAAAA TAATTGTAAA 60

5 GTTAGATTTA AAATTGTAAA ATATAAAATC ACAAAGGAAT GTACCTTATG AATGTTGTTG 120  
ACATTTTATG AAATTATGTG GATTCATATT ACTGTTACAA GATAGANTTG AATGCAAAAA 180  
GTCCAAAACC TCAATAAANT TTGAGGAAAA CGTGTTATTA TGTAAATTGAN NTANAANCAT 240  
TTTATAATTG TGCANGTNAN NNNNAN 266

SEQ ID NO:5966

SEQUENCE LENGTH:256

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07084

SEQUENCE DESCRIPTION:

15 GATCCTTTTN AGTTTTTCCA GGTGAGAAAT CCTATCAATT ATGTNATAAT NATATGTTTT 60  
CCTNTTCAA AATTATAACA TAATTCCTGA CTGCATGGGT TAAACATTTN CATAACAGTG 120  
CTAAATAATA AAGGTGGCAG TGGCATTTTT GTCTTGTTTC TCATTTTAGC CAGAATGTGT 180  
TTGCTACAGC AATCCAAAT TGTGTTTTGT GAAAAANAAA TATTCTNCTT NGGAGACANG 240  
GNNTNTACAT TTGCAN 256

20 SEQ ID NO:5967

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS07085

SEQUENCE DESCRIPTION:

GATCAGAAC A GGCTTAAATT GATGCTATAG AACCAATTAC TCTGTATTAT CTTTGCAACT 60  
CTTTTGTAAG TCTAAAATTG TTTGGNAATA AAAGTTTATT TTAAANNTTA AAAAAANANN 119

30 SEQ ID NO:5968

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS07086

SEQUENCE DESCRIPTION:

GATCTTCTAA TCGACAATCT ACATCATAGT GACCACCAGT AATCACCTGT AAGAGATTAA 60  
AAAAGAAAAA TCACTGTGAA AAGTGTGAAA AATTAATCAG ATTTAATCAG ATTTCTTATT 120  
AAAATGGCAA TAAGGTGATG GGCAA 146

40 SEQ ID NO:5969

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS07087

SEQUENCE DESCRIPTION:

50 GATCTGGTTA AGTGTGCGGC ATCTCATCCC CCACTCTNTC CCTTCTTGCT CCTGCTTCCC 60  
CCTTATNACT TGCCAGCTCC TGCTTCACCT TCCACCATGA GTAAAAGCTC CCTGAGGCCT 120  
CCCCAGAAGC CAAGCAGATG CCAACACCAC GCTTCCTGCA GCCTGCAGAN CTGTGAACCA 180

ATTAAACCTC TTTTCTTTAT AAA

203

SEQ ID NO:5970

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07088

SEQUENCE DESCRIPTION:

GATCTTCCAA AAATTTATTA AGTGTTTACT TTAAAGTGG AAACAATGTT TTTAAGAGGT 60  
 GATATAAAGA AA 72

SEQ ID NO:5971

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07089

SEQUENCE DESCRIPTION:

GATCCCTAGC TTGTTTTCTG TCAGTCATNC ATTGTAAGTA GCACATNGCA ACAACAATCA 60  
 TGCTTATGAN CAATACAGTC ACTAGGTNTT AGTTTTNTTT AAATAN 106

SEQ ID NO:5972

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07091

SEQUENCE DESCRIPTION:

GATCTGTGTG ACTGATGGGC AGGGCTCAAT GATGCCCAT TACTGCTCAC 60  
 ACCACTGACC TGGACCCNAA CAAAAAGCTG ATTGTCTTTT TAAAAGTTAT TATTTTGCCC 120  
 TGAGCAAATT GCATTTTANT TGGGGCAGTT GGAGTGTTGA NTTCTGGCA GCATTGTGAA 180  
 GNNGACCNNG GTGGANGTTT NCTGTCCCNG GN 212

SEQ ID NO:5973

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07093

SEQUENCE DESCRIPTION:

GATCTACCCA CCTGGCATC CTAAAGTGCT GGGATTACAG GCGTGANTAC CAAGCCCGGC 60  
 TTTTTTTGTT TTGACATGGA GTTTCGNTCT TGTCACCCAG GCAGGAGTGC AGTGGCGTTA 120  
 TCTNGGTTCA CTGCAACATN CGCCTCCTGG NTTCAAGTGA TTCTCCTGCC TGAGCCTCCC 180  
 ANGNACCTGG GNTTACAGGT GCTCCNACCA AGNTN 215

SEQ ID NO:5974

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07094

SEQUENCE DESCRIPTION:

GATCTGGAGG TTTACAGAAG CCTTTACCCA TCCTGAGACT CAGTTCCTGCT GTTGGTCTNC 60  
AGAGAAAGTGT CTGCACCTGC TGAGANGNAA TCACACCACT GCACTCTAGA CTGGGCAACA 120  
GNGCGAGACT CTGTCTCAAA 140

SEQ ID NO:5975

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07095

SEQUENCE DESCRIPTION:

GATCTGTGA AGAACTCAGC TGCTGGAAAC CATGCAAAAT GTTTTGAATT GCCCTTAAAA 60  
TATGGAAAAT GTTTTCTGAA TGCTTTATAT TCTTNTGCT GTAAATTAAA AATGANGAAA 120  
ATTTCCCAT AAA 133

SEQ ID NO:5976

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07096

SEQUENCE DESCRIPTION:

GATCCCTGCC CTTTGGCACA TCCACTGAAA GGCCAAACAG CAAGTCCGAG TGAGTTTTAA 60  
ATATTAATTA ATCACCTTT ATTTTACA CTTGAGAGTG ATTGTAATAA AGGCTGTCAT 120  
TAATAAACTT GGTTCTACCT TAAA 144

SEQ ID NO:5977

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07097

SEQUENCE DESCRIPTION:

GATCTAGAAA TTGCCCTCCT TTTACCCCTA CCATGAGCCC TACCAAAACC AAACCTANCC 60  
CTGGGCAACT AANTAAGGT ATTGGACATN CCCTTCTNAA TTAATNATCC AATN 114

SEQ ID NO:5978

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07098

SEQUENCE DESCRIPTION:

GATCTGACTT CAGACAGAAA CCAATACCAG CTCCTTTTC CTTTAAACNT TTGAAGAGTG 60  
TTGATTGTGTT ACTATATTAC GTATGCAAAA CTGGAGAGNG TATNGNTNGA TN 112



SEQ ID NO:5979

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07099

SEQUENCE DESCRIPTION:

GATCCGTCCTAACAATAA GGAGGCGTCC TTGCCCTATT ACTATCCATC CGTCAATCCG 60

TAGCAATAAT CCCCATCCTN CGATTATATC CAAACAACAG ANGATTGAT ATNNTNGCCC 120

NACGTAAGGG N 131

SEQ ID NO:5980

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07100

SEQUENCE DESCRIPTION:

GATCATGTAG GACGNGGCAT CTGCCCCTG GTAGAGAGGA CGAATNTTCC AAAACANTGG 60

GCTCTACGGN AAAAAGAAGT AGGTTAGTCA CCTTCTGGAC CCTGTCTAAC TCGTTTGCTN 120

AANAGN 126

SEQ ID NO:5981

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07101

SEQUENCE DESCRIPTION:

GATCTTATTT AACCAAAGAC TATTTATTC CTGATATGAT TTGTGTGCTT GATTAAAATG 60

GNANTTAATG ATATTGAAA 79

SEQ ID NO:5982

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07102

SEQUENCE DESCRIPTION:

GATCAACAGG CTTATTAGAA GAATGAACTA AGGTGAGAGA CCTCATCCTG AGAAAGGTTG 60

AGTTAATGTT AGAGTATAAG TGGTGGTAAT CTTGAATACT TTTCCATTA AATATTGATG 120

GGGGTTTGAN TTTAATCAG TGCTTTTNTG GGNAGTGGGG GTCAACTATC TTAATGATTA 180

CAGTTGGTTT GTTACTGCT TTTGAGGACC TTTCTGGAGG AAAGGAAAAG CCTGTTTTGG 240

GGAGTCTTTA AAGATGGAAG TTGGGTGGTC N 271

SEQ ID NO:5983

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07103

SEQUENCE DESCRIPTION:

GATCAATATG TGACTGGAAC CATTGGCGAG GATGAAGATT TGATAAAGTG GAAGGCACTG 60  
TTTGAGGAAG TCCCTGAGTT ACTCACTGAG GCAGAGGAGG ANGNATTGGN TTNNGAACCT 120  
GCNTN 125

SEQ ID NO:5984

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07104

SEQUENCE DESCRIPTION:

GATCTNATTG TATTGTCGAA GGACTATTTT TNAACCTGTC CAAATAAACT CTGCAAAGNA 60  
TTTCCACAAG AAA 73

SEQ ID NO:5985

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07105

SEQUENCE DESCRIPTION:

GATCCTGCCC TGCTCTCAGC CATAGTGAAG GACCAGCCCT AGGAGTCTGC GAGAGCCTCC 60  
TTGGTTCCAT CGTGAAGCCA TAAACAGGAA TGCCTTTGGC AATAGCCTTG AGCCTAGAGG 120  
GCCCTCTNAT GCCCCACTGA GGTGCTGTTG GTTTATTGCT GGCANCGTGA ATTCTCTCAG 180  
GGGTCTAGGA GGGGCATTTT GGAGACTGCC TGACANCACC NCTATCCCCT GCCTCCCN 240  
CTNAGAAGAG GGTGGAAGNA TGAAATGAAA GCTATGGGNC TTTTGGGAGG NTAACCCAGN 300  
GTCTATTCTA GGGTTNGNGG AAGTGNNTAA N 331

SEQ ID NO:5986

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07106

SEQUENCE DESCRIPTION:

GATCCCCTGG CCTGGTGCCC ACCTGCCTC GCAAGCGCTC GCCACCCTCA CGTGGCTCAC 60  
CTGCTGTTGA GCCTTGCTGT GTCAATAAAC GGTGTTGAGGA TTGCAA 107

SEQ ID NO:5987

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07108

SEQUENCE DESCRIPTION:

GATCAGATAT ATCCACAACG NGTTTAAGAT TTTCAATATT CTTAGAGAAA ATCAATAAAG 60  
TCAATAACTA CTCACCATG AAA 83

SEQ ID NO:5988

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07110

SEQUENCE DESCRIPTION:

GATCAAAAAT TGTGGACATA TCTGCAAATN ACTACCTATA GCCTCATGAA AGTACATTTC 60  
ACAAAATGTA AANNCAATG AACACTAAAT TTAAGAGCAG TTACAGTGTG ACTCACTCAT 120  
GTTTAAAAAA ANTCGGNGAG CTA AAAAANTA CGTCTAN 157

SEQ ID NO:5989

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07111

SEQUENCE DESCRIPTION:

GATCGAGTCT GCTCTGACCT CTCAATCTCC TTCTCTCCCC AGGCTGCTGC TCCTGCTGCC 60  
CTGTGGGCTG TGCCAAGTGT GCCCAGGGCT GCATCTGCAA AGGGGCATCG GAGAAGTGCA 120  
GCTGCTGCGC CTGATGTCGG GACAGCCCTG CTCCCAAGTA CAAATAGAGT GACCCGTAAA 180  
ATCCAGGATT TTTTGT TTTT TGCTACAATC TTGACCCCTT TGCTACATTC CTTTTTINCT 240  
GTGAAATATG TGAATAATAA TTAAACACTT AGACTTGAAA 280

SEQ ID NO:5990

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07112

SEQUENCE DESCRIPTION:

GATCTCCAAG CAGGAATATG AGGAGGGCGG GAAGCAGTGC GTGGAGCGAA AGTNCCCCTG 60  
ATGGCACTCC TCCCCACACA CCTGCTCCCA AGCTCAGATG GAAGTCCCTT AACCCCATG 120  
CCACATTGCC CCCCTCCTCC TTCCCTCTT GTCCTCATT ATGGTGATGT TTCTGGGTTG 180  
AAAGAAGTAA AAATGTTTAA AGAAA 205

SEQ ID NO:5991

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07113

SEQUENCE DESCRIPTION:

GATCTTTAGC AGTCTCTTCT AGTTTCCTG GATTTCCTG ATTTATTANT TAGGGAAAAAT 60  
GAAAAGAGGA CCTTCTGTC CGCCTGCACT GCTTACTGGT AAATAAAC AAATTATGC 120  
TGCCAAA 127

SEQ ID NO:5992

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07114

SEQUENCE DESCRIPTION:

GATCGCTTGA GCCTGGGTAG AGGCTGCTGT GAGCTGAAAT GCGGCCNCTG CACTCCAGCC 60  
TGGGTAACAG AGCGAGNCCC CGACTCAATA AATAAATAAG GATGGATAAA TTGTAGCGTA 120  
TGCACCATTG ATTATGCTAA GACATTTTAA AGTAATTATG AGAAACGCTC TACTAATGAT 180  
TTGTTTTTAT TTGTATTTTN CTGCTTATTA GACAAATATA TNCTCATTTT AAAANGGAAA 240

SEQ ID NO:5993

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07115

SEQUENCE DESCRIPTION:

GATCAGAACG AGCTGTTAGA ATTCAGAGTG CTAGAACTCG AAGTAAGAGA CTCTATCTGT 60  
TGAAACTCT CAAACGGAGC AGACATTCTC TTTGAACCCA AACTGAAATT CATGTAAAGC 120  
TCTCAGATGT TTTCAAGCAT GTGTAAAGGG GACATGTTAT AGTTTCTTTC TTTCTTTCTT 180  
TCTNTNTTTT TTTAAANCTG TATGTNCAGA ATANTTNCNC TGCCTTAATG TGTNCTGGNG 240  
AGCGTGCTCA CCCAGGNCTN TGGCCATGTN CCAGAGCTAA TATATTTNTT GCCTATGGCT 300  
TNGTNTGGCA CTTAATGAAT ANTTGTGN 328

SEQ ID NO:5994

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07116

SEQUENCE DESCRIPTION:

GATCTTCAAA ATCCAGGAGG GAACCGAGAT AACACAAGTA CAGGTGTGCA AAATTACTTA 60  
GTAAACTAT TTNTCTATT ACTCCTTTT TGCAAGTACA TACATTAAAT GATAANTTNA 120  
TTGTGAAGTT AATAAANTGC CCATAGCTGT TCTATTACCT TCAGAACTA TTTTCATAAT 180  
TGANAAANAC TTGGNGTAAG TACATGTGTT ATATANCACC TACCCTAGNT GCTCAAGTGC 240  
GTNNNGGAGN 250

SEQ ID NO:5995

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07117

SEQUENCE DESCRIPTION:

GATCCTCCTT CCTCAGCTAC TCAGGAGGCT GAGGCAGGNG AATGGCATGA ACCCAGGAGG 60  
CAGAGCTTGC AGGGAGCCAA GATTGTGCCA TGGCACTCCA GCCTCGGCGA CAGAGCAAGA 120  
CTCCGTCTCA AA 132

SEQ ID NO:5996  
SEQUENCE LENGTH:78  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07118  
SEQUENCE DESCRIPTION:  
GATCCTATAG GGAGGNCATT TCCTGTCCTG GAATTAGTAT TTCTAAAATG TGNATAAACT 60  
TGTTTTATAA AAAGCAAA 78

SEQ ID NO:5997  
SEQUENCE LENGTH:118  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07119  
SEQUENCE DESCRIPTION:  
GATCAGAAAG TGTTATTTAA CAGAACTAC ATACATTTTT NATGTCTCTC TGGACCCTTT 60  
GATTCTAAGT AAATTNCAG TAAGTNAGCA GTAATAGACT ATCCTNTTCA NCTATGAN 118

SEQ ID NO:5998  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07120  
SEQUENCE DESCRIPTION:  
GATCAAAAAG AGGAACTTG AAATGTGATG GTGTTTATAA TAAAAGATGG TAAACTAAA 60

SEQ ID NO:5999  
SEQUENCE LENGTH:127  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07121  
SEQUENCE DESCRIPTION:  
GATCTCCTTC AGAATTTTGG TCTTGACTTT GAATCTTTGC CTGTTTGTCT AAACATTGTA 60  
CTAACATTCT GTTTGAATTT GGAAGTATTC TAATACAAGA TTTGAATAAA GTTTATCCTT 120  
AAATAAA 127

SEQ ID NO:6000  
SEQUENCE LENGTH:195  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07122  
SEQUENCE DESCRIPTION:  
GATCCTGGAG CTGGAGCATG AGTGTCTGAC AATCAGAAGC ATGATGTCCA ATGTCNNGAT 60  
GGCCAGAATG AATGTAATAG TTCAGACCAA TGCCTGNCCA CTGCTCCTTT ATGACTGCAC 120  
TTCTAGCCAG TAGCTCTGCA CAAGTNAGCT CTGTAGAAGT AGGANCTTGG GCTTAAGTCN 180

TGNGCTNTNT CTCCN

195

SEQ ID NO:6001

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07123

SEQUENCE DESCRIPTION:

GATCCCAGCA TGGGGTGAGC ATGAAAGAGT GGCAAACAGA GTGGCATAAG ACAGATAAAA 60  
TACAAAAGGC AATTACAAA GGACCAGGAC CGCAGAGGCA GAGATAAACC AGTGGGCTCA 120  
GACTTCTGAG CGTCTCAGAN AAANNNAAN AAANN 156

SEQ ID NO:6002

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07124

SEQUENCE DESCRIPTION:

GATCTGTCTA GCTTATTAAG GATGAACTG AATTGGAAAA ATAGCTCCAT TTTTGGTGC 60  
TTGGGAAGCA CAGTGACCAA AAAAGTTGTA TGGCTGCTTA TTCATTAGTC TTTCTACTG 120  
ATGTCAAATC CATGGTACCT AGAGTTAAAT AAAATTCCAA TGCTCTTACT CTTTAAA 177

SEQ ID NO:6003

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07125

SEQUENCE DESCRIPTION:

GATCCAGTTG GGAATAAGT ACATCGTATC GGTTCCTGTT CAGATGACAT GGGGAAGATG 60  
ATGGTTCAGC CACTGGTACT ACGAGAATGT TTGTATTACC CACATTTGAA TTNATTGCT 120  
ATGATTTTNA TGAAGATTAA AAATATATAC ACAGTTCCTG GTATGTTGAG GTTGTCTTTA 180  
TTATTCTTAC TCAGAAAGGA AAATTTGTAA ATATGTTTGT GTGGCTCAAA CTGATACTAT 240  
TCTTACANCT GGANCATTGA AAATNCAGAG GGCTGTATTT GGNTATTAGN GAGGNCTCCG 300  
AATGN 305

SEQ ID NO:6004

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07126

SEQUENCE DESCRIPTION:

GATCCTCAGG CTGGTATACG GCGCAATGTT GCATCAGCTN TGGGCAACTT GGGNCCTGAA 60  
GGTTTGGGAG AGGAGCTGTT ACAGTGCAGG GTACCCAGC GGCTCCTAGA AATGGCATNT 120  
GGAGACCCTC AGCCAAATGT GAAGNAGGCT GCCCTCATTG CCTCCGGAG CCTGCAACAG 180  
GAGCCTGNCA TCCATCAGGT ACTGGTGTNC CTGGGTGCCA GTGAGAACT ATCCTTGCTC 240

TCTNTGGGGG GNTCAGTCAC TGCCACACAG CAGTNCTAGG CTTGNCTGT GCCAAAACAA 300  
TTGNANN 307

5 SEQ ID NO:6005  
SEQUENCE LENGTH:215  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS07127  
SEQUENCE DESCRIPTION:  
GATCTCTCTC CGGCCCCCTA GAAGCCCTCT CCTCACTGCA GCCCTGGTGC TCTGGGGAAG 60  
GAGGGGCATT GACAGGTGGT TTGACTGTTC ACCCAGCAGC CCCGCTTCCC CACTGGTTTC 120  
TCTCCTGGCT GCCGGCGGNG GTAGGCTGGG AAAGCTTCCC CNTCACCTAG GNCGGGCCAG 180  
15 CACCGGCCNG GGNCNNAAGA GGTCNCCTNN ATCCN 215

SEQ ID NO:6006  
SEQUENCE LENGTH:273  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS07128  
SEQUENCE DESCRIPTION:  
GATCCGAGGG GAAATNTTTA GAGCCCTCAG GAGGAGGAAG AGACCGAGTT TTAGGAAAAA 60  
25 CATCAAAGCT GGATAGGTTG GGCAGAAGAG CTGGGGATAG CATTAGAGA GGCTGAGAGT 120  
CCTGGGTTCT GGNTTATCAC GTGTGAGNGA AACNGGAGGT TGCTANTTGT AGGTGGGCGT 180  
CAGGNTNGA GTGNTGCTTC CAGANGTTTC TGCAAGTGGG CCGGGTCTAA GNTAGGGCAT 240  
GTTACGCCAG ANGTTTNAGG GNCACCTAGGT AGN 273

30 SEQ ID NO:6007  
SEQUENCE LENGTH:250  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS07129  
SEQUENCE DESCRIPTION:  
GATCACAGGG AAAAACCGAC CGAGCTCAGG AAGCCTAATC CAGGTGGTAA CCACAGAAGG 60  
AAGGACGGAA CTCACCCAG CATATTTTGA GGCCTCATCT CAGTGCCTAT NAGGGGCCCTG 120  
CCAGNAAGGT CACTAACCTG GTCTCAGTGT GGCCTTGTCC AGCCTTGTGT TTNCTGTTAA 180  
40 CCCCGNTTGT TGGTACGAGN TATTGNNTCC TATATTACGG ANACAGANCC NTGNTTTCGG 240  
NTTTTGCATN 250

45 SEQ ID NO:6008  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07130  
SEQUENCE DESCRIPTION:  
50 GATCCCAGTN AGTCATGAGC CTCAACCCCC TCCAGCCAC TGGGGCTCTN ACCTCCACAT 60

55

GTGGGTAGAA GCTTNCCTGC CCCCTTTNCC TCCAGGAAGC CCTNAN

106

SEQ ID NO:6009

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07131

SEQUENCE DESCRIPTION:

GATCGCCTGA GCCCATGAGG CCAAGGCTGC AGTGAGCCAT GGTCACGCCA CTGNATTCCA 60  
GCCTGAGTGA CAGAGCAAGA CCCTGTTGAA AACACAACA ACANCAAA 108

SEQ ID NO:6010

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07132

SEQUENCE DESCRIPTION:

GATCTAAAAC TATTTTCTG TATAATATT ATTTGCCGAA AGTTTGTTTA TATTNAGAAG 60  
TCTGACTATG ATGAATAAAT CTTAAATGCT TTGTTTAATT GAAAAACAAA AATCACCAAT 120  
ATCCAAGACA TGAAGATATC AGTTCAACAA ATACTGTAGT TANGNGACTA NCTCTCCACT 180  
TNTATGGGAA CTACATTCA CTCTTGTTT TCAGGATATA GCAGCACTTC ACCGAGATAT 240  
TCTTTCAGCC ATANCACTGG TAACATTCT NCTNAATCTN TCTGTAGCAC TTANAGGANT 300  
TCCCTCATTG GNTNCCTTC AGTGTTNCG GGNGN 335

SEQ ID NO:6011

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07133

SEQUENCE DESCRIPTION:

GATCCAAAGT AGCTGGGATT ACAGNCATGA TACCACANCA CAGTCATTG AATNTATCAT 60  
TACTTAGTAC TCNTATTTT TTCCCTGCTG CTCTTATGC ANTGAAGTCC TN 112

SEQ ID NO:6012

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07134

SEQUENCE DESCRIPTION:

GATCTCCTTT TGATTAATTT ATAGAGTTTT TGATTATATG TCTTTGTATG ANCTTTTTAG 60  
TTATTGCTCA AATATCACAT TTNATATTTA TAACACAGGC TACTGATGTT GACATTTTAA 120  
CAGTTCAAGT GAAGTGTAGA AATCTTACCC ATTATCCCTC CCTATTAATN NNNTANTGGT 180  
CTTAAATGTC TTTCCCTACA TATATTTNTA ACANGTATAT GAGATAGCCT TACAGTTTGT 240  
NCTTTAACTA TCAATCATGC ATTAGGNNAC TCAAGNGGN 279



SEQ ID NO:6013

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07135

SEQUENCE DESCRIPTION:

GATCTGGGAC TGGCAGGTTA TTAATCGAGA TACACTTGTT AGGAGGGACA GGGTTCCCT 60

AAGGCACTTT TAAAGATACT CTGTAAGAAC CATTACAAT AAATTACTG TCAATCAA 119

SEQ ID NO:6014

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07136

SEQUENCE DESCRIPTION:

GATCGAGGTT GTTTGCAACG ACCGTCTGGG GAAGAAGGTC CGCGTTAAAT GCAACACGGA 60

TGATACCATC GGGGACCTTA AGAAGCTGAT TGCAGCCCAA ACTGGTACCC GTTGGAACAA 120

GATTGTCTCG AAGAAGTGGT ACACGATTTT TGGGGACCAC GTGTCTCTGG GGGACTATGA 180

AATCCACGAT GGGATGAACC TGGAGCTTTA TTATCAATAG ATGAGAATGC TCATCTTCCT 240

GNTGNGGGNT TTNCTNTTCG NTNCTGGATN CNCCACACTG GGGNTAGATG CTTGNTTGTA 300

AANNCTTNC CTTN 315

SEQ ID NO:6015

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07137

SEQUENCE DESCRIPTION:

GATCCTAAGT AGAACCAGGT AATTGTCTCT TTTTCTAATA AGGAATTGG GTAATTTTNA 60

ATTTTNGTT TTTTAAAAA TAACCTAGAC TATGCAAAAC ATCAAAGTGA ATTTCCCATG 120

ANTGTTTTTA ATATTCTCAT CTCAACATTG TGATATATGC TACTAAAANC CTTNCATAT 180

ACATCTNACC TCATTTCAGG TGANTNATTN TAATCTNN 218

SEQ ID NO:6016

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07138

SEQUENCE DESCRIPTION:

GATCAGAGCA GAACTAAATN AAATTAGAAT AAAGTTAAAC AATTAAAAAG AAA 53

SEQ ID NO:6017

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07139

SEQUENCE DESCRIPTION:

5 GATCGACTTA TACCTATGCT AAAGTTAACG GTCTGAGAAG GTAGATTAGT GGTTCCTAG 60  
GGCTAGGGAG TGGGTTTGGG GGTGGGGAAT AGAAAGTGAC TGGTCATGGT TATAGGCTTT 120  
TTTGTAGCAC CATAAAGATA GTTTAAATTT AGATTGTGGT GGTGATTGCA CCACCCTATG 180  
ATTTGCATGG TATGTGANTT ATATCTTAAT AAAGCTGTTT AANANGTCAA A 231

SEQ ID NO:6018

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07140

15 SEQUENCE DESCRIPTION:

20 GATCCGCTCC TAACCTGCGA CCGCAGCTGA CCTTCTCCTG CCACTAGCCC GNCCCTGNCC 60  
TTAACANACG GGATGAAGTT TCCTTTTCTG TGC GCGGCGC TGTTCATA GGCAGAGCGG 120  
GTGTNAGACT GAGGATTTTCG CTTCCCTCC AAGACGCTGG GGGTCTTGGC TGCTGCCTTA 180  
CTTNCNNGGG GCTCCTGCTG ACTTCGGAGG GCGGATGCA GAGCCCAGGG NCCCCACCGG 240  
AAGATGTGTA CAGCTGGTCT TTA CTCCATC GGCAGGGCCC GAGCCCAGGG ACCAGTGA CT 300  
TNGGCCTGGA CCTNCCGGTC TAACTGCAAG CATCTTCCCC AGGGCAAAGG NTTNTGGGG 360  
GAACGNGAGG TTTNATNTTN 380

25 SEQ ID NO:6019

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07141

30 SEQUENCE DESCRIPTION:

35 GATCTATTTT GTGTGTTTG AAACCTTAGGT GCAATNTCCC CTGGAAAAAG CTAAAGAAAT 60  
GTATATGTTT AATNACATTT TAAAATAAAA TATTATATAT ATGTAAA 107

35 SEQ ID NO:6020

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07142

40 SEQUENCE DESCRIPTION:

45 GATCGATTTG ATAAAATTAA ACAAAGTGCT TTTAATGGAA AAAAAAAGA AA 52

45 SEQ ID NO:6021

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07143

50 SEQUENCE DESCRIPTION:

55 GATCCACTGT AATAGTCCAG-TTTGGGGTGC-AGACAAGTGT GAAGA ACTTC TGAAAAAGAC 60

AGTGA AAAAC TGCTTGGCCC TGGCTGTTGA TAAGAAGCTG AAATCCATTG CATTTCATC 120  
CATCGGCAGC GGCAGGAACG GTTTCCAAA GCAGACAGCA GCTCAGCTGA TTCTGAAGGC 180  
CATCTCCAGT TACTTCGTGT CTACAATGTC CTCTCCNTC AAAACGGTGT ACTTCGTGCT 240  
TTTNGACAGC GAGAGTATAG GCATCTNTGT GCAGGANATG GCCAAGCTGN GCGCCGNNN 300  
NGGCTNGNC AATGNCAGGA CCNGNTTGCA CCATGGTACC GNACCTTNAG TTTNN 355

SEQ ID NO:6022

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07144

SEQUENCE DESCRIPTION:

GATCTTGAG CTNCTGGAGA AGCAGGNCTG CNAGCTGCTC AACCGNTTC AGGACTAGCC 60  
CCCGCAGGCT CGTGC GCCAC CCCGTCCTGG TGAATAAACG CACTCCCTGT GCCTCAGACA 120  
AA 122

SEQ ID NO:6023

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07145

SEQUENCE DESCRIPTION:

GATCCGATAA TGTACCATGT GCCTGCTGGT TTGGCCTGTG CTGTTTCTGC TTTTGCCCC 60  
TNACTTCCTG TGCTAGAGAA AGCCTTATTG GTGTTGGTGG TGGTGATGGG AGGGAAAAGG 120  
GTGGTCCTTT GGGACTCTTG ATAAAAATNT TATCATTTGA AA 162

SEQ ID NO:6024

SEQUENCE LENGTH:179

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07146

SEQUENCE DESCRIPTION:

GATCCAGGCC AATGCATGGC TATTGCTGTA AATCTTGATG TTTATTTCTG CCTTGTAAG 60  
TTCTATCAGC GCCTACCTGG AATTTAAAT TCAGTAGACA AATTAATTGG TCCTCTGCAC 120  
AACTTTTTTA ATAAGTAGAT TATTTNCAA NGGGNTTNGA NCAANTTTNA TTGANTCTN 179

SEQ ID NO:6025

SEQUENCE LENGTH:403

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07147

SEQUENCE DESCRIPTION:

GATCAGAGTG GCTGGAGCAG AGTGAATNAG GAGGGAAGCT GAGTAGCAGG TATCTGAGAA 60  
GCAATGCAGC CCGCAGCTTA ACTTCAACAT GCTTTTAAAC TTTTNNCCA TTCTNTTGAG 120  
TTTCAAGATA TAACCTTGAG GAAACTCAAA ATCCTTTCTC CTTAGCCTTA AAATAGACTC 180

CACGTCCTC CCCTTTNTCA CCAGATATGC TCCCTTTNCA TTTATCTAAC TGTATGCTAC 240  
 TATTTAATTG TGTGATGTCT TAGANGTTTC AGTGGCTAAT CTTGAGACAG ACCAAGNCTG 300  
 GAGACCCAGC TGGCAANCCT TCCANNATTT ANCTTCAAAA TTGGCTAATT NANCAACCNG 360  
 GCCCTTNGTT NNAAATTATG GTNATTCCGG GGGNCCCGGN TGN 403

SEQ ID NO:6026

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07150

SEQUENCE DESCRIPTION:

GATCTTGCTG CAGCCACAGT GCAGTCCACA TTAAGTCTAC AGACCAAACC ATTTGTATCT 60  
 GGCATCACTT ACTAACACAC GACATGCAGA AAAGCCGCAT GTNGTGTGTT AGTATACANG 120  
 AAGGAATAGA AAAGTATAC TGTTTTAAAT ANTCTGTAAT TTCAATTTT TTNTTTTNN 180  
 GCTGAANTGG GTCNTNTN 198

SEQ ID NO:6027

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07151

SEQUENCE DESCRIPTION:

GATCATAACT CTTTNTTGAA CTAGAGTATT TTTGCAGCAT TCCTTGTCAT CAGAAACATG 60  
 GTTAAAGTTT AAAAGTAGAA GCAGCAGAAA ACTAGCTTGT AAAATTATC CAAGTAGAGT 120  
 GCAGGCTAGG CTGTCTTGGG GAAATAAACA TTAAANCTTA AAGCAATGTT TTACATGGAA 180  
 ANNNNANNNN 190

SEQ ID NO:6028

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07152

SEQUENCE DESCRIPTION:

GATCTTGTCG CATTNTTGAC CTTGGACCTG CTTGGTTAAG GAGGGAGTGG GCCAAACCAG 60  
 AGTGCCAGGA GCTAATGGAG CCAGGCCTGA CTCCTAGGAG TGGTCCAAAG GCCTTCAGCC 120  
 TAGATGGTGC AAAGNTGGGG CCAGCCTGTT TTCACCGNA CCNGNGCCTG TGACACCAAG 180  
 ACCCACCCCA ATCCCAGNNT TNACACAGTA TTNTCCN 217

SEQ ID NO:6029

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07153

SEQUENCE DESCRIPTION:

GATCGGAGCC TACTTCCCTC CGCTCAGCCT NGAGGAGCTG AGNCCCTACT TCAGGGACCG 60

TGGGTGGCCT CTGCCCCGGC CCCTCTAGAC GTGCACCAGA AATAAAGGCG AAGACCCAGC 120  
CCCTCGGCGG CTCAA 136

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SEQ ID NO:6030  
SEQUENCE LENGTH:278  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07154

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SEQUENCE DESCRIPTION:  
GATCCAAACC CAAGTCTTGA GCAATGTTTT TCTCAAAAAG CTGCTATCCA ATNATATAGG 60  
AAAATACATT GTGTTTCCT AAACACACTT TTCTTTTAA ATGTGCTTCA TTGTTTGATT 120  
TGGTCCTGCC TAAATTCAC AGGCTAGGNC AATGAAGGCT GAATCANNGN CANTTCATCC 180  
ACCAATATCA TGTGTAGATA TTATGTATAG AAAGTANAGT AANTTATGGC TCTAACTTCT 240  
GTGTTGCTGT NTATCCTGN TTTTNTCGG GGGTGNTN 278

15

SEQ ID NO:6031  
SEQUENCE LENGTH:65  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07156

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SEQUENCE DESCRIPTION:  
GATCAGTTGA TGTACACTTG TATTATTAAA GCACTCAATA AATCACTGTG GCTGATAACT 60  
GCAAA 65

25

SEQ ID NO:6032  
SEQUENCE LENGTH:161  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07157

30

SEQUENCE DESCRIPTION:  
GATCCACATG GCACGGTGAC TGTAGTTAAT GCATTTTATA TGTCAAAATT CCTTANATAG 60  
TAGATTTTAA ATAATCTCAC CACAAAAAAG TAGATGTGTT GGTGATGGAT ATCTTANTTN 120  
GCTTAANGTA NTTGTNTCAC CAATGTATAC ATNTATCAGN N 161

35

SEQ ID NO:6033  
SEQUENCE LENGTH:130  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07158

40

SEQUENCE DESCRIPTION:  
GATCATCTTT ACAGTTCCTC GGGAAATNT GAATGTCCTG CGTTTTGTTT TCTTTACTGT 60  
ATGAAACAG GAAAATAAAA GAGAAATTTA GAAAATACAG CTCATTACAA TAAANNNTTT 120  
GGNTTTCAAA 130

45

SEQ ID NO:6034

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SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07160

SEQUENCE DESCRIPTION:

GATCTGGCCC AAGCTGGGCT CCCTNNAAGC CAAGAGAGCC TCTNATNGAC CCCGCCTGCC 60

CGAATGAAAT CCGAACAGTT GGGGCTGTTC ATGGCAAGTG GGGCTGGTTT TTCATNTCCA 120

TTGGTTATTT AAAGTTTCCN TAAAAATAAA CGATTTTAAG TTAAG 165

SEQ ID NO:6035

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07161

SEQUENCE DESCRIPTION:

GATCTGGGGT CTGTTTGTG CATTACTTTG TTCACTCCTT CTTCATTTA TTCATTCAAT 60

AAACATTTAT TGGGAAA 77

SEQ ID NO:6036

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07162

SEQUENCE DESCRIPTION:

GATCCGGCTT GCCCAGAAAG AGAAGACAGC CATGGAAGTG GAAGCCCCTT CAAAGCCAGC 60

CAGGACTAGT GAACCACAGC TCAAAAGGCA AAAGAAGACA AAAGCCCCC AGGATGTAGA 120

AATGAAGGAC CTTGAAGATG AGAGCTAAAC CTCTTCCACT AGAAGATTCT CAACTGGAGC 180

CAGCCTTCNG GCTCAGTGGT TGTTTCAGAG GACTTTGACA AAAGCAAGGC CCCTTTTCAC 240

TCTCCAGATT TCCTCCTACC TAATGGCCTA CTGACCTCCC CTTAGAGGGA TGTNTTTGGG 300

NGGGAAGNTN 310

SEQ ID NO:6037

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07163

SEQUENCE DESCRIPTION:

GATCCAGAAC ACTTCAAGAA CTCGTCAAAC AGCTCGATAA GCCTTTTTGA CTGTNTACAT 60

CTGTACCGGG AATAACATTC CTAGGCTGAA ATTTCCACAA AGANTAGAAC CTGTACCCAG 120

TTCTTCAGGC TGATTTCCTT GACCTCTTGG GCATTTGTAT TTGTAGTAAA GTATTGCAGA 180

GATTCTAAG TATTTTNNNA GCAGCCATNA AAAATTGGNC TTTGTNTTNG TTGATTCATN 240

NGGAGGGCAA GTTGGGGANT AGACTTCAGT NGANCTCGGT ATGGNTGN 288

SEQ ID NO:6038

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07164

SEQUENCE DESCRIPTION:

GATCACGCCA CTGCACTCCA GCCTGGGCAC CAGAGTGAGA CACTGTTTAA A

51

SEQ ID NO:6039

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07165

SEQUENCE DESCRIPTION:

GATCTGGGCA GGGAACATCA CATACCAGGG CTGTCTGTCG GGGGGGTGGA GGGCTGGGGG 60

AGGGATAGCA TTAGGGGAAA TACCTAATGT AAATNACAAG TTGATGGGTG CAGCAAACCA 120

ACATGGCACA TGTATACCTA TGTAACAAAT CTGCATGTTG TGCACGTGTA CCCTAGAACT 180

TAAAGTATAA TTAAA 195

SEQ ID NO:6040

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07166

SEQUENCE DESCRIPTION:

GATCAGGCCC CACCTTGTGT CTACCCCAT CCCNGCTGTG AACGTGACAN TGAATAAAGT 60

CGGGGAAACG CGAAA 75

SEQ ID NO:6041

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07167

SEQUENCE DESCRIPTION:

GATCTGAATT GAGGAACTTG TAGTTTTTGC TCTCCCACTT CTTGGAAACC CCTATCTACT 60

TTCTATGTA TTTGACTACT TGAGGTAGCT TATACAAGTA GAATCATACA AATGTATTGT 120

TTTGTGACTA GCTTACTTCA NTTACAATAA GTCCTCAAGT TCTNCCATGT TGCTGTGTGT 180

GTCAAAATTN CCTTCCTNGC TAAGGCTGAA TAATATTNCA TNGTATATAT ATGNCNTTNA 240

TCCAGTCATT CATCAATGAN TACNTGTTTT TNGTGTGTGG TGTGGAANC CTNCTGGGGA 300

CATGGTNATA TTTTN 315

SEQ ID NO:6042

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07169

SEQUENCE DESCRIPTION:

GATCTAAGCT GATTTAAATC TAAAAACTGG ATAAGAAGCT GTGGCTTGTA ATTAAAAATA 60  
GACCTTTATT CACTAGAAA 79

5 SEQ ID NO:6043  
SEQUENCE LENGTH:189  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS07170  
SEQUENCE DESCRIPTION:  
GATCAGGTAT TTAAAGGACA TCTGACAGTG CCTGGCACGG GATAGGTGCT CCATAAATGC 60  
CTGTAGCTAT AATTATTACT GTNCCACTAG CTGTTTACTT AAGTAACATT GAATTTCCAC 120  
15 AGANTGCATT TCGAATCAGG TGGACTATGA TTATACTGAT TNTNAAAATA GNGAGCTGCA 180  
TCTGTAAA 189

SEQ ID NO:6044  
SEQUENCE LENGTH:151  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS07171  
SEQUENCE DESCRIPTION:  
GATCTGGAGT GGAAGGGGAA TTCATTTGTT CATTGTCTAT CCTTTTGTAT TGATTGAATT 60  
25 TTTNATATAT ATATGTAAAT TTNCACAATA AAATTTTTTN CCAAATAAA ATAAACAAA 120  
GGGGCTTTTT GCAACCCAAT TCCTATCTAA A 151

SEQ ID NO:6045  
SEQUENCE LENGTH:178  
30 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07173  
SEQUENCE DESCRIPTION:  
35 GATCATAGCA CTNTATCATC TTAAAAGTTA ATAATAGATT ACTTGTAACA CAGGCTCACT 60  
ATGNGAGAAT TCATCAAGCT GTATGTACAT TTATTGTGCT CTCATTGTA TGTATAANTC 120  
AATAAATTGA AACAGTAAAC GAAAAGGTAA TTNTAGANAN CCTACAGTGA TNCTTGNN 178

40 SEQ ID NO:6046  
SEQUENCE LENGTH:380  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07174  
45 SEQUENCE DESCRIPTION:  
GATCCGTCAC AGACTAAGGA GATGGCAGGC ATTGACAGCT TCACTCCATG AAGGCCATCT 60  
CTGTTTCTNT CCTCCGCTTA ACCAAGCTGT TGTGGTTTTT NAGCATAGTG TTGTATGTTT 120  
CATTGCTAGC TGTCCGTGCTG TTAAACACAG TGTGTATTTT TTTNCTAAA TGTACATAAT 180  
TAGAAAAGAA GATAACAATA GGANGCTATG TGTATCTCCT GTGTAAAGNA GTGGCTTCAC 240  
50 TGGAAAATG GTGTGGCTAG CATTTCCTT TGAGTCATGA TGACAGATGG TGTGAAAACC 300

55



ATCTAAGTTT GCTTTTGACC ATCACCTCCC AGTAGCAATT NTGCTTTCAT AATCCNTTTT 360  
AGCANTCCAG GCCTCTTTGN 380

5 SEQ ID NO:6047  
SEQUENCE LENGTH:72  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS07175  
SEQUENCE DESCRIPTION:  
GATCGTAATG TAAAATTCTT TTACCATGTC AAGAAATTAT TAAAAATACA GGTACTTTGA 60  
CCTCTTTCTA AA 72

15 SEQ ID NO:6048  
SEQUENCE LENGTH:226  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20 CLONE:HUMGS07178  
SEQUENCE DESCRIPTION:  
GATCCTGAAA AGATAGGGCT ATTGTCCCCT GCCTCCTTGG TCACTGCCTC TNGCTGCACG 60  
GNCTCCTNAG CCCACCCCCT TGGGGCACAA CCTGCCACTG CCACAGTAGC TCAACCAAGC 120  
AGTTGTGCTG AGAATGGCAC CTGGNGAGAG CTTCTGTGT GCCAGNTTTT GTTCTGAGTG 180  
25 CTGTACATGT ATTANNTCCT NTA CTGCTNG CCACATTGTA CCNNTN 226

30 SEQ ID NO:6049  
SEQUENCE LENGTH:225  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS07179  
SEQUENCE DESCRIPTION:  
GATCCCCGTA CCACAGTGCC AGCCATGCC TTCCCCTGGG CTACCATGT CCCTTTCCTC 60  
35 ACCCAGTTGG TAGAGGAGTC AGGAGGTGGG AGGCCGTGGG CTTTGGTTTT ATAATGTAAC 120  
CACTGTGGGG GTGGGGGAGG ATGGTGAACC ATGTATTNA GTGAAATATT TAATATATTT 180  
AANTATCANT AAANTCAAAC TCTTTGTAAA ANANANNAG NANGN 225

40 SEQ ID NO:6050  
SEQUENCE LENGTH:332  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS07180  
SEQUENCE DESCRIPTION:  
45 GATCATCCTG GGCAGCAAAG TCATACACTC TTGAGGGAAG AGAGAGACCT TCTCATATTG 60  
TTTTATATTG TTTTATACTC AGTACCTGTT TTAAGAAAAA AACAAGGAAG TGAAATCAA 120  
GACAGGCAGC CCGGCACCAG GCCTGANACC AGCCCTGGGC CTGCNTGGCC TAAACCTAGT 180  
AGTTAAAATT CAACTTACGA CTTAGANCCT GATGTTATCC GTAGATTCCA AGCNTTGTAT 240  
50 AAAANATTTG TGANACTCCC TGTGTGTTC TGTGCCAGTG CATGNNACCC CTGTACATA 300

55

TCCCCTAGAT TGCTCANTCA NTCNCGGTTT GN

332

SEQ ID NO:6051

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07181

SEQUENCE DESCRIPTION:

GATCACAGGC CTTTGGAGCA CTTTACTCT CTGAGAAGAA CTGGAGCTAG AGATGTAAAA 60  
TGGACAGTCT TGATGGGGTT GAGAACCTTC TGGGGAGCCA GATGACCCTC TCTTTGCACA 120  
ATAGATAAAA GTCTTTATAT GANTATATAT AANTTTNTT NTTTTCCCT TCCTGTGGGA 180  
TTTCTGGAGA ATGAGAATTA TCCAAATNCT CAGTCTACCT GNGATAGTAA ATNCATGGCT 240  
TATGCTTCTG GTCCTTAAA 259

SEQ ID NO:6052

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07182

SEQUENCE DESCRIPTION:

GATCGNACCA CTGCACTCCA GCCTGGAAGA CCAAACGAGA CTCTGTATCA AAAAATAATA 60  
ATAATTAATA AAGTTTACT GGAAAAAGA AA 92

SEQ ID NO:6053

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07183

SEQUENCE DESCRIPTION:

GATCAGCTAC AATGCCCTGT GTTAAATTNT TAAAAGTTT CCCTTTTCTT TTTTGCCAAT 60  
AAAGTTGTAA ATAAAGACCA TCATACATTA AA 92

SEQ ID NO:6054

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07185

SEQUENCE DESCRIPTION:

GATCCCTTCC CGCCACACGA TGCTCCGTTT TCTTCCGTTG TGAATNCCGC GTCCTGTCCT 60  
GGTGACAGGA GAACAATNTT GGTGAACGTC GCAAA 95

SEQ ID NO:6055

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07186

SEQUENCE DESCRIPTION:

GATCTCCTTC TCACTGCATT CACTCGGTTC CCATAGCCCA AGTCATATTG TNTCTCTCCT 60  
 5 GGACAGTAAT AACCTTTTNT TGGGCTCCCT GCTTCCAACC TTGCCTTCTG TAGTGTACTT 120  
 TCCAAATAGA AGCCAGAGTG ATACCTTATA TTTAA 155

SEQ ID NO:6056

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07187

SEQUENCE DESCRIPTION:

GATCAGGAGG CCCACTTGGG TTTATAGTAT AGCCCTTCCT CCACTCCAC CAGACTTGCT 60  
 15 CATTTTCCGA GTTTTAACT AGACTACACT CTATTGAGTT TAATTTTNTC CTCTAGGATT 120  
 TATTTCTGTT GTCCTAAA 138

SEQ ID NO:6057

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07188

SEQUENCE DESCRIPTION:

GATCTGAAAA CCAAGTGGTG ACCTAGGGAG GGAACAAGCN CTGTGCAGCA TTGATGAAAC 60  
 25 TTTAAAGATG AAGTCCTGGT CCGGGCACGG TGGCTCACTT CTNTAATTCC AACACTTTGG 120  
 GAGGCCGAGG CAGGAAGATG GCTTCANCCC ACGACAAA 158

SEQ ID NO:6058

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07192

SEQUENCE DESCRIPTION:

GATCTNTGGC CCACTCCGCA TAAATCAGGT GCATAATGTA GCTGCCCGGG CTCTATACT 60  
 35 GCAACATTTCG CAAGGCAATT AGCTTGAAAA CTGAATTGAT GTACATTGAT TTTTAAATA 120  
 AAGTTATTGT AATATATTCA CTCGTTATAA A 151

SEQ ID NO:6059

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07193

SEQUENCE DESCRIPTION:

GATCTATACC CTAAGCAGAT AGCAAAGAAG ATAATGGAGG AGCAATTGGT CATGGCCTTG 60  
 45 GTTTCCTCA AAACAACGCT GCAGATTTNT CTGCACAAAC ATCTCCACTT TTGGGGGAAA 120  
 50 GGTGGGTNGA TTCCAGTTCC CTGGACTACC TTCAGGAGGC ACGAGAGCTG GGAGAAGAGG 180

CAAAGCTACA GGTTTACTTG GGAGCCAGCT GAGAAGAGAG CAGACTCACA GGTGCTGGTN 240  
 CTTGGTTTTN GCCAGGCTCC TCCGAGCACC TCATGCATGT CCCAGCCCT GGGCCCTAGC 300  
 CCTTTCNGN CCTNCNGTCT NCAGTGCCAG NACGGAANTN CCTTGNACCA NNGGNTNTTN 360  
 GN 362

SEQ ID NO:6060

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07194

SEQUENCE DESCRIPTION:

GATCCATCAT NATGTAAAN TTCACAATAT GGTTCAAATG TAACANTGCA GAATTGAATA 60  
 TGGAGGCATG CATAACCTTC CTCTTAGAAA ATGGCAGGTN TTGTAATTTC AAATTTTNT 120  
 GCAATTAGAT TAANTCATAA TGCAACAAA 149

SEQ ID NO:6061

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07195

SEQUENCE DESCRIPTION:

GATCTTGCTT TAACTTTCAA CACTTAGAAA ATCTACAAAC ATTCAGACCT GTCTGGGTTG 60  
 GTATTGCCAC CCATGACATT TAACATGTTG TGATGCTTGA AAACACAGGA GTAGAGAAAN 120  
 TCGATGANGA TTGTATTTN NCACCTTAAC TCCACATTGC TTTATTGGNT AATTNATANN 180  
 CTNN 184

SEQ ID NO:6062

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07196

SEQUENCE DESCRIPTION:

GATCAGTAGT CTCTATTCAA ACTTTNAAAA TGTCGTGGTA TTGTAACAAT ATATTTAATG 60  
 AAAGANGGTT ACAGACTCCC CTGAAGAACC AGCTTTCCTA CGCTTTTNAT TTNCTAACT 120  
 TGTCTAACCT GATTTNAAAA TGACTIONT TCCAGACTAA AAACATGCTT CANCCCTGTT 180  
 TCANGACATT NTGCTN 196

SEQ ID NO:6063

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07199

SEQUENCE DESCRIPTION:

GATCCAACT CTACATCCAG AGATTATGAA AAATTCTTAT AGAATTTTGT AACAAAGTATT 60  
 TACATGTTGG GTGAAAGANA TTTCATAGTC GTTGGAGTGC CATGAAATTA ATACTTGCAA 120

TTCAGATTGC GGTAGTTTAC ACTTTTCCTG TATGTTTCAA ATCAGGTGTG TACCATTGT 180  
NCTGAGANCA CCACAGANTG ATTTATCCAA AGTCCATTGA TTTNATACG TGTTTTGGTT 240  
TGTNACCAAN TTATNGTNAT TCNTNGCACA TTTTGGNAA TTNATTGTAT AGGNN 295

SEQ ID NO:6064  
SEQUENCE LENGTH:312  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07200  
SEQUENCE DESCRIPTION:

GATCTTCGCT GATTNNNTCC ATCAATNACC CGGAGCATCC ACTNACGCTA GAGGAGTTGA 60  
ACGTAGTAGA GCAGGTGCGG GTTCAGGTTA GCGACCCCGA GAGTACAGTG GCTGTGGCTT 120  
TCACACCAAC CATTCCGCAC TGCAGCATGG CCACCCTTAT TGGTCTGTCC ATCAAGGTCA 180  
AGCTTCTGCG CTCCTTCTCT CAGCGTTNNN NNGATGGACG TGCACATTAC TCCGGGGACC 240  
CATGCCTCAG AGCATGCAGT GAACAAGCAN CTTTGCAGNT AAGGNGCGGG TGGCAGCTGC 300  
CCTNGNGAGC AN 312

SEQ ID NO:6065  
SEQUENCE LENGTH:108  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07201  
SEQUENCE DESCRIPTION:

GATCAGTGCT CTTCAAGGTG TCAAGATTAT CAAAGACATA AAAGANTGGN TGANCTGCCA 60  
TAGATTGGNG GAGACAATGC AATGTGAAAT CCTGANTTTG ACCCTGAN 108

SEQ ID NO:6066  
SEQUENCE LENGTH:103  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07202  
SEQUENCE DESCRIPTION:

GATCTTTAGT CCGAGTATGN GAAATTCAAG CAACTTTGCG AGANAAAGGA ATACTATTTT 60  
TNAGNCAACA AATTAAGGAA CTTGAAAAGC TAAAAANTCA GAN 103

SEQ ID NO:6067  
SEQUENCE LENGTH:127  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07204  
SEQUENCE DESCRIPTION:

GATCANNGAA ACTAAACATT ACACCTTCTG GNCTTTNATT TATGAAGTGG CACAGAATCT 60  
AACTTTNCAC TGAATATCTT TCCATTCACA TCTCCTCTGC CTTAGTCACA ATGGCAACAG 120  
TACAGNN 127

SEQ ID NO:6068

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07206

SEQUENCE DESCRIPTION:

GATCTCCCAA GNAAGCACAA ATAGTTTTTT TCGCTAACTT AGTTATGAGT GAAGCCTCTG 60

TNCACCTATA ACTNGCCAGT TTCATTGGTG GAATAAGTCC CCTTACTCAT GATTCANCAA 120

TATNCCTATA TTANAN 136

SEQ ID NO:6069

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07209

SEQUENCE DESCRIPTION:

GATCAGAGAA GGTTTTGTTC GTCCTTTTAA TCTTTACTTC TTTGAATTGT GAAAGTAATA 60

CTACATATTC ATAATAAATT CAAATAATAC AGAAGTATAT TATGTAAA 108

SEQ ID NO:6070

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07210

SEQUENCE DESCRIPTION:

GATCCGTGCT GTCCAATCCG GTAGCCACAC ACGGCTCTCG GGCACCGCAC AGTGGCTAGT 60

CTGAAACCTG ACATGCTCTA AGTGTAATAAT ACATGGTGGA TTTTNAAGAC TTGAACCAA 120

SEQ ID NO:6071

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07211

SEQUENCE DESCRIPTION:

GATCCTGGCC CTCCACCTNC CTCCAGGCCA CGAAATGGGA ATNCCAGCAC TAAGCCAGGC 60

ACCGGGCAGA AGCTGGGCCT TCCGCCTCCN TTGGATGGGG TCAAGAGGCC ANGCCTGGNA 120

CATTTTGGNG TGTCTGGCT ACCAGCTCTC ACCTACANCC ACGCACCTCT NTAN 174

SEQ ID NO:6072

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07212

SEQUENCE DESCRIPTION:

GATCTAGATA TNAGGTTTT CTCCTTCATT CTCAGCTGTC GAAGAAATCA AAGTAGCATA 60

TGCACAAGGT TAAAAACCAC ATATACAAAT ACTATAGAAC AGCTTATANT GAAAACCTTG 120  
 CCTGCCCTTA TANAANNTGT GATTATCTTC TTCTGTTAAT GTCAGTAANN GATGGTTTGT 180  
 CCTAAA 186

SEQ ID NO:6073  
 SEQUENCE LENGTH:229  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07213  
 SEQUENCE DESCRIPTION:

GATCTGAGAG ATGATACATG ATACCAGATG AAAAGAAGGA GAAGTGTGTA CCATATGTTT 60  
 TNAGCAGAGG NCCCTCCAAC TTATGGCATC AGGGGCAGAA AGTCACAGCT TATCCCAGGC 120  
 ACCCTGGCAG GTTCTCAGAG CCTGCCTCCT CCCTGTTTAT ATGCGTACAG CCTGGTAACC 180  
 CCCAGGCATG CAANTATACA GTCTGTAACA ACAGGNNNTT NNTNNNTTN 229

SEQ ID NO:6074  
 SEQUENCE LENGTH:50  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07214  
 SEQUENCE DESCRIPTION:

GATCTTAAAA CTGAATAAAA ATATTTAATA AAACITTGAA ATATTTTAAA 50

SEQ ID NO:6075  
 SEQUENCE LENGTH:297  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07215  
 SEQUENCE DESCRIPTION:

GATCCATTCT ATCCATCCGT TATGTGGCTT TGCCATCCCA GCTTGGAGTG TCTTTACAAA 60  
 GATAATAACA GTTGTCTTCT TTGCTCTCGT TTTGGATGCA TAGACTGAAA AATTAATAACA 120  
 AATAACTTGT AAAATGGCTT GTNAAAAAAT ACAATTACCT CTAATTAGTA GTACGCGTAA 180  
 NTNTTTTACA GAATGANAGG CGTGCTTTNN ATTTCTTTAC TGCATTACAT TGGTGGCGAA 240  
 AGANGTCTGT ATGANANTCA GTNCTTNTGC TGACACAAGN TCCATTGGT NACANAN 297

SEQ ID NO:6076  
 SEQUENCE LENGTH:191  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07216  
 SEQUENCE DESCRIPTION:

GATCCTCAAT CAGTGGGTGG AGGATAACAG GGTAGATTCA CTTGTTTGCA CTTNTACAGT 60  
 TGTAAGCTGCG AGTCCAGAAG TCCTCTAGAG CATGTTTACT GGCAGTGAAGT TGGTGAGACA 120  
 GTTGTGGAGT ATCCATTCT GATGAGTACA GAAAAAAGAA GAAAAAGAAA NGANGAGAAA 180  
 AANTTANGAA A 191

SEQ ID NO:6077

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07217

SEQUENCE DESCRIPTION:

GATCCGAGCG TCGTGAAGCTC ACCTGAACTT TGGAAGGTTG GCACTGGGGG GCCGCATCCC 60  
CCTGGGAAAT NACTGAACGC GGGGTTTCAN TGGGTCCC GC CTGGGTCTAA GGACCCAGTT 120  
TCTTCTGTNA GCACGGGCAG TGGGAGGCCG GTGGAAAGGC GCAGGGGCCC ACCTACGCGT 180  
CTCACATCTT CAGGGGCGCA TTTCTACAAT AAAAAGCTCAC CCAATTAGAC CTAAA 235

SEQ ID NO:6078

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07218

SEQUENCE DESCRIPTION:

GATCTATTGG ACCAAACCTT CTGCACACTC GGCCAGTTCC CTCTCCAATG TCCGGTGCCA 60  
TCTTTCCTGA CCTTTGTTTC TTTCTGTTCA GGAACCATCA GTCCCCCTGT AATAAAGGTG 120  
GTAGATTTC A TTGAGGTTTT AGATTGAAAC TTTGAATAAA TCAAAAATAC TCATTCTTAA 180  
A 181

SEQ ID NO:6079

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07219

SEQUENCE DESCRIPTION:

GATCTATCAT TACAAAATNA ATTGAATAAT AAAATAGTTT GGTAGAAACT TAAA 54

SEQ ID NO:6080

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07220

SEQUENCE DESCRIPTION:

GATCCAGAGT TGAAGACCCT TCAGCTGGCT CTGCCTGCCA GTGCCACANA GTGCCATGGC 60  
CCAGGAAGAC AGGTTTTNTT CCATCTAGGC CAGGCCATCC AGTGGCCATC CTCCGTGTCC 120  
TCCCGCCTCC TCCTGGTGTG ACTTCTGAAA ACCAAGAATT TGTTCTGTG GACTTTTTCT 180  
GTGCTATGGA CCATTGTCCT CTCACCCACT CAATAAATCT TGAAA 225

SEQ ID NO:6081

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid



TOPOLOGY:linear

CLONE:HUMGS07221

SEQUENCE DESCRIPTION:

5 GATCTCTNCT AACNNTAGTA AATAAACT AAAGTGGTGG GCTTTGATAA TGCATTTNGT 60  
GGATACAAAA TCATCGNCTC ATCACTTTCT AGAATGAAAG GCTGGGAGGC ATTGCTCACC 120  
TTTTGCGTGA AGAAAAGACC TGTCCTTAG AGCCAGTTT TNCTTAAGGG GAGGACAGAC 180  
CGTCGTCACC CAGTGGACCN CGTTGGATGG NTGGATGCAG TNCATNCTTT AGAAGCACCG 240  
10 CATACCTGCT TGTACAGGT NCAGNGTAAG TGGTCTTNGC TNCTGTGGGA N 291

SEQ ID NO:6082

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS07222

SEQUENCE DESCRIPTION:

20 GATCTNCCCT AGCCCTCTNT TCCAGAAGAT GCCCTCCAAT CCTTTCCACC CNATTCCCTA 60  
ACTNTNGGGA CTCGTTTGG AAGTTTTCTG TGGGCTTGGC CTTGGTN 107

SEQ ID NO:6083

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS07223

SEQUENCE DESCRIPTION:

30 GATCTAGTTT TCCAAGTAAC ATTTGTGGT GACAGAAGCC TAAAAAAG CTAAATCAG 60  
GAAAGAAAAG GAAAAATACG ANTTGAAAAT TAAGGAAATG TTAGTAAANT AGATGAGTGT 120  
TAANCTAGAT TGTNTTCATT NCTAGATAAN NTGTATAACG CTCTCTGTNC TAN 173

SEQ ID NO:6084

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS07224

SEQUENCE DESCRIPTION:

40 GATCACCTGC GTGTCCCATC TACAGACCTG CGGCTTCATA AAACNTCTNA TTTCTCTTCA 60  
GCTTTGAAAA GGGTTACCCT GGGCACTGGC CTAGAGCCTC ACCTCCTAAT AGACTTAGCC 120  
CCATGAGTTT GCCATGTTGA GCAGGACTAT TTCTGGCACT TGCAAGTCCC ATGATTTCTT 180  
CGGTAATTCT GAGGGTGGGG GGAGGGACAT GAAATCATCT TAGCTTAGCT TTCTGTCTGT 240  
GAAATGTCTA TATAGTGAT TGTGTGTTT AACAAATGNT TTACACTGAC TGTGCTGTA 300  
45 AAAGNGAATN TGGGAATAAA GTTATTTN 328

SEQ ID NO:6085

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

55

EP 0 679 716 A1

CLONE:HUMGS07225

SEQUENCE DESCRIPTION:

5 GATCTCAGCT ATTTAAATAC AAACCTTGAAA AAAATATTTT TCCAGGGTAC CATAAATATG 60  
ATTAANTNNN TAAAAAATTT AGTGTCACCT GATGAAAATA TAACTAGACC AATAGTAAAA 120  
TNCAGGTGTA TCTTANTTCC CTGANGTCCT CATTTN 156

SEQ ID NO:6086

10 SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07226

SEQUENCE DESCRIPTION:

15 GATCCTGGGC TGCTGGTGCT ACCTGCGGCT GCAGCGCATC ANCCAGTCGG AGGACGAGGA 60  
GAGCATCGTG GGGGATGGGG AGACCAAGGA ACCCTTCCTG CTGGTGCACT ATTCGGCCAA 120  
GGGACCGTGC GTGGAGAGAA AGGCCAAGCT GATGACTCCC AACGGCCCGN AAGTCCACGG 180  
CTGAGCCAGG ATTCAAGGNT CCTNGTCCTA TTTNCAGCCG GCCAANNGGC GCTNGNAGGG 240  
20 GNAAANCCAT ACGGTTGCGC TNNTGTCTGA GAGGAN 276

SEQ ID NO:6087

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS07227

SEQUENCE DESCRIPTION:

30 GATCTTGCCA CATCTGGCAC GGAGACGACA CAGTAATNCT GAAAAAGCCT CTATGTAGTC 60  
CTGTTAGTNT CTTAAAGAAC CTAAGAAGCTN GGACCAGTAA AATCCACAGA AATTCACTCT 120  
TGCCTTTAAG AACTTTTGAA AACTGTTTAA A 151

SEQ ID NO:6088

SEQUENCE LENGTH:373

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07228

SEQUENCE DESCRIPTION:

40 GATCCAATGG ATTTAAACAG AAGCNCTTTG CCAGGCTTGC CAGCAAGAAG GCAGTGGAGG 60  
AACTTGCCCTA CAAATGGAGT GTTGAGGATA TGTAACCTTC CTNAGGCTGT GGGGGTGGCT 120  
GGNCTGTGGT AGTGGGCATA GGCAGCGAGA TATCCAGTGG TAACAGTTGT CTGTGCTAAT 180  
AATTGGAGCC CACACAGNCC AGCAGCTTGT TGAATGCCAG TTTTGACCAC AGAAGGTTTA 240  
TTCGAGGCCT NATGTTTGA CTGAGGTACC TGTACTTCTT NGGGTGTTGA CAGCACCAGG 300  
45 TGTTGCTGGN TTTGAGAGGG AGCGTTGATT TCTCNTTAC CAGGGNTTNT TCTTTGGTTA 360  
GGGTGTTTCT TCN 373

SEQ ID NO:6089

SEQUENCE LENGTH:174

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07229

SEQUENCE DESCRIPTION:

5 GATCAGNAGA GGCCANGCTC CNCCCCACCC CAAACAGCAT GAACTTCCCA AGGCTCCATC 60  
CCTTTCTCCC AGTGCACAGG CTGGTCACTT TCTCCGGGTA CCCCCTTGGG TACCTTGGCT 120  
GTCTCAGTTC TATTTAACCA TTTCCCACT TTTGAGCATT TACTCACAGT TAAA 174

SEQ ID NO:6090

10 SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07230

15 SEQUENCE DESCRIPTION:

GATCTCAGAT TTTTTTGA GTTAACATGC CTGACACAGA CATCCTTCC TCTCACAAGC 60  
TGTGTGACTT AGTAGATAAA ATACTGCCTT CTGCCTTTGG GACCATGATT AAAAACAAG 120  
ACAAAAACCA AAAGTCATTA AA 142

20 SEQ ID NO:6091

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS07231

SEQUENCE DESCRIPTION:

GATCACTGGA CATCAAAGAT TCATTGCACT TATGAACAAG GAACCTTCTT TTCAATTTCT 60  
GTGTAATTTG CAAGGCTGTA CAATGTGTGC TGATGCAAGC CTTTTTCAGT TCAAGAGAAT 120  
AAATGTTTAC AANTATAAA 139

30 SEQ ID NO:6092

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS07232

SEQUENCE DESCRIPTION:

40 GATCTATAAA TCAAGAAAAT CCATTGTCAT AACCATTTTT AAAAGTCAAA AATTAAGACA 60  
TCCTTAATTA AAANGTTTCA AATCTAGACA CTAAATGTGT GTGANTGTAC AAAGAAAACA 120  
ANCCATTGCT TATNCTGTTA TATACTAGTG NNCCTTTTAN TTTTGCTTGC TGTTTTAAAC 180  
TTGGACAGTT TGAGGACTTT NGTTGGANCT TCGTATTGTA NGANCTGTTN 230

45 SEQ ID NO:6093

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07235

SEQUENCE DESCRIPTION:

50 GATCGAGGAC TATTCNGTG CTATTCATTC CTCCATTGCT AAACAGATNA AAAGCGACGG 60

55

TTNCTNCACT AACAGCAGCT GGGAAAGANG TTATGCTTGT TGN

103

SEQ ID NO:6094

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07238

SEQUENCE DESCRIPTION:

GATCCCAAGG ACCTGGAGCC ACGGGCTGCC AACTGCACTC GGGTACTGGT GTGGCATACT 60

CGGACAGAGA AGCCCAAGAT GAAGCAGGAG GAGCAGCTGC AGCGGCAGGG CCGGGGCTCA 120

GACCCAGCAA TTGAGGTGTG ATGGCGGCC CACCCCACT ACCACCTCTT TTCAGGCACA 180

GACCTTGTGG GACTGGGNCC AGGCCTNCCC AGGATTGTGG GTTTTCCAA AGTCCTTGAC 240

CNTTTN

246

SEQ ID NO:6095

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07241

SEQUENCE DESCRIPTION:

GATCCACCAG CCTCAGCCTC CCAGAGTGCT GGGATTACAG GCGTGAATGT AATNNTTTT 60

AAAAAGAAAA ACATGGNTGT AAAGAAAGTA AAGCTTCGTT TTGAACAGTT ATGATGGTAA 120

CACANCTCAA NGGTGCAACT AANGCAGTGC TGCANCCN

158

SEQ ID NO:6096

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07243

SEQUENCE DESCRIPTION:

GATCTGTGAC ACTNACATGG CTGTGGTGTG CATACTGTGT AGTTACATAG CCCTTCCAAT 60

TCTGGGTCCA TTTGCACTAG CAAATTAAAA TATGCTTTGA TTCATACTTA AA 112

SEQ ID NO:6097

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07244

SEQUENCE DESCRIPTION:

GATCCCAAAC NACTCACTCC TTAAATTCAC ACTTTGCCAC TTAAGTCCAG TGTGGATGAC 60

AGAGCGAGAC CCTGCCTCAA A

81

SEQ ID NO:6098

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07245

SEQUENCE DESCRIPTION:

5 GATCAACCTC AACACCTGGC NTCTCANGCC TATATACCGA CATATNCAGC AAACCCTNAT 60  
GNAGGCTACA AAGTACGCGC AAGTACCCAC GTAAGTACG TTAN 104

SEQ ID NO:6099

SEQUENCE LENGTH:54

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07246

SEQUENCE DESCRIPTION:

15 GATCTTTTCT AAATATTATT ACTTGTAAT AAAGTCTATT TTGNTCCCGT GAAA 54

SEQ ID NO:6100

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS07249

SEQUENCE DESCRIPTION:

25 GATCTAAATA TGAAAAGTAT GTCCTGCTGA ATTTTCCTGT GNATTGGTGA GCGGACAGAC 60  
TACCTGTAAA CCATGACCTC CTTGCCAAAC GTTAGTTTTA TNAGNTCACT NGTAACCTTT 120  
GAGAATNNTC TGN 133

SEQ ID NO:6101

SEQUENCE LENGTH:104

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07250

SEQUENCE DESCRIPTION:

35 GATCGTNCCA CTNACCTCCA GCCTGGGGGN NAGAGCAAGA CCGTGTCTCA AAAACAATTN 60  
AGTCTGAAAC ACAATTGTCC TGAATCTGTC TGACTATAAC TCTN 104

SEQ ID NO:6102

SEQUENCE LENGTH:126

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07251

SEQUENCE DESCRIPTION:

45 GATCTCAAAA AAGAAGGAAT TTCTCCTNTN TNTCTTGCAG TTAATGTAAG ANTACTTTAA 60  
ATCTCTAANC TTCTGAAGTG TTAGAGGTAG AGATGGTCTA GTAAAGATGT GGTAGTAATG 120  
TNTTAN 126

SEQ ID NO:6103

50 SEQUENCE LENGTH:179

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07253

SEQUENCE DESCRIPTION:

GATCAAGCCA TCGGAGCTGC TAGAGTTCTG TCTGGACTTT CCAGAGACCA AGTNTTCCCT 60  
TTTGCTGCCT CTAAGAGGCC TGTGCCTGCA GACATGTGAG ACAGCAGGTC TGATGGGGGT 120  
GACAAGCTTT NTTTTTTTNN CCNAAAGAAN TTNCAAATTC AATTCCAGAT TGNTTTTNN 179

SEQ ID NO:6104

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07257

SEQUENCE DESCRIPTION:

GATCAAATTT CANTGGCTTT NGACAGAAAA GAAGGCTCTG GATTTAAGCG GGTGGTCACC 60  
TGTNAGACCA GGTCTACCTT GGGACTGTNA TTAACTGAA TCAGTTATTT CCTTGAAATT 120  
TCACAGTAGT GGGTGGGCCT GTTTTAAGGN TCTGACAGAT ACCACGAAAC ATGAAGCACG 180  
TGGAATAACA AGACCCCGG GGTCTTTCTG AGTGCAAGGC TGAAATGGGN CAAGGGCTCC 240  
TCACGGGGNG TGGAGGGNNG CCGGGAGNCT TNCNTGGTTG TTNCNTTTT TGN 293

SEQ ID NO:6105

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07259

SEQUENCE DESCRIPTION:

GATCCCGTNC GCGCGCTGC CCGAGAGGAA CAATGACAGC TTTGCAGTTC TCCNGGAGTN 60  
CGCTGAGGAG CAGCTGCAAG CCGACCANGT NTTCAATTAC TTCCACAAGN 110

SEQ ID NO:6106

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07261

SEQUENCE DESCRIPTION:

GATCTAGTAC TCCTTGATGA AGAATCGGGG CCTGTAACT TACCTCCAGC ACTAAAACAT 60  
CCTCANGANT TACTATAATG TGTCCAAAAT ATCACTGCAT ACAATATCTG NNATTTGAAG 120  
TGAAAAACTG ACTTTNGTAT AGTATAAAC ACAGGCTTTC ACAANTTTTG GTNTNGCTGG 180  
NTN 183

SEQ ID NO:6107

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07263

## SEQUENCE DESCRIPTION:

GATCCTGANG ATGATGATGA TGATGATGAT GAAGAATAAA TGGAAATCAAA ATGCTAGCTT 60  
NATTTGACAT NAATAAGTAA AATAAGTCAT CATGTNTTCA ACNCTGTAGT TCAGCTGTTT 120  
ACATTGAATA ATNTN 135

SEQ ID NO:6108

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07264

## SEQUENCE DESCRIPTION:

GATCCTTTCC AGTTTAAGCA GCCAATCAGA CCNCTTCACA TTTCTAAAAA AATGACCTAA 60  
CTAAAGCACC AGAGCTCGGA GANTTCCAGG GAAGCCAGAT ACCGAGGCGC AAATTTTTTA 120  
AAAAATAAGA GTCAGAAATA AAAATAAANG GTNTCTGTTG GTCAAGATTT AAA 173

SEQ ID NO:6109

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07265

## SEQUENCE DESCRIPTION:

GATCAATTGA AATCAACTGT GTTTTGTNTT CTCTATGTCA AAGTTTAGTT TTATATTGAG 60  
AATGTAACT TATTGCTTTG TATCTNGGGA AAAAACTTT GTAAATAAGN TATAAAGTTT 120  
CTTTGAGACA GTAAAATTAT GATTNCTTGA AA 152

SEQ ID NO:6110

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07266

## SEQUENCE DESCRIPTION:

GATCTGCTCA CCTCGGCCTC CCAAAGCCTC AGCCTCTTAC AGTGTTGGGA TTACAGGCGT 60  
GAGACACTGT GACCCGGGAC GATTTTCAAT CACAGTTTTT TGNTACGAGT GGAAAATGCG 120  
TATTTATAAG AATGAAGTAG TACAGACATG ANTNTGTAGA AATCTCTATA ATCCTGCCAT 180  
CCAAGGTTGG TACCTGTAA TGTGTATATC AGGGATGTGC AATCTTTTGG CCTNCCTGTG 240  
CCACACTTNG AAGAAGAAGA ATCGNCTTGG GCCACGGATA NANTNNACT AACACTAGCA 300  
ATACCTGGTG NGCTGAAANA GNNAGTTAAT TCNCNTN 337

SEQ ID NO:6111

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07267

## SEQUENCE DESCRIPTION:

GATCCTGTTA ATNAAACCAC AGACACCATA TATCCTTCTG CATCCTTTGG CCAATAAAAAG 60

TTGCTGGAGA ACCAAA

76

SEQ ID NO:6112

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07268

SEQUENCE DESCRIPTION:

GATCAAGGAG AGTCACAGCC TTATTAAAAG TTTATTAAAC AATANTATAA AANTTTTAAA 60  
 CCTACTTGAT NTTCCATAAC AAAGCTGATT TAAGCAAAC TGCATTTTTC NCAGGAGAAA 120  
 TAATCATATT CGTAATTTC AANGTTGTAT AAAANTATTT NCTATTGTNG TTCAAN 176

SEQ ID NO:6113

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07269

SEQUENCE DESCRIPTION:

GATCGACACG TGGGGGCGCC TGAGCGAAGA TAACCGTAAT AAATAGTAAC CTAACGGTCC 60  
 AAA 63

SEQ ID NO:6114

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07270

SEQUENCE DESCRIPTION:

GATCAGNCCT CGCGCAGTGG CTCAAGGCTG TAATCTCAGC ATTTTGGGAG NCCGAGTGAG 60  
 ACCTTGTCTT AAA 73

SEQ ID NO:6115

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07272

SEQUENCE DESCRIPTION:

GATCTTAAAT ATTCTAAAGT TTGTATTGTG ACTTCCAGTA ATGTAAACTA TATGAGGCTA 60  
 ATCCTCTTTT CCTCCTTTT GTTTGTTAAC CTCATTGGG ATAAGTGTAA CTAGTATTAT 120  
 TTTATTTATG TAATAAAAAAT ATATGTGAAA TAAAGTGTTA CTGGTAAAGG ACTTGTAAC 180  
 ATGATAANTA TTAGCAAGTT GCATACAGAN TTAANAGNGN GGNGNGNANG GNGTGNGGTN 240  
 TGN 243

SEQ ID NO:6116

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid



TOPOLOGY:linear

CLONE:HUMGS07274

SEQUENCE DESCRIPTION:

5 GATCAGAAGT TCAAGGGACC GTGAAAGCCC TCAGAGTCAG CACCTAGTTT CAGACCAAGC 60  
 ACCCTTTTCGA ATCCCTGGAT GGCTGAGGGG GCTGAGGCCG GCTCTGACTG GGCAGCTCAG 120  
 CNCCTCCCCC AGAGCCCAGG GTCTTGCACA CCCCTNCCTG TAACCAAGGA ACACTCTGAA 180  
 ATAAAGGTGA ATGGCTAAA 199

10 SEQ ID NO:6117

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS07275

SEQUENCE DESCRIPTION:

GATCAAAATA CTAATAAATT ACTCACAGAC TCAGTGTATT TTTNCTTGA GTAAAAGTCC 60  
 AGGATGGGTA ATAGAATACC TGCTGTTGGC TTTTGAAAA ATTGGTACTG TATGTAGCAA 120  
 AATAATGTGA AACCCATATG CATGGATATT CTTAACAATT TGAAGAAATC GTCACAGCTT 180  
 20 TCCTGGGTTG TTGAGCCTCT AAGATGGTCT TTTCTCTGA TGTGATAATA AAGTGTTTAT 240  
 TCTGANCTCT AAAAAAANN NANNGNGGNG NNTGNNGTGG NGN 283

SEQ ID NO:6118

25 SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07276

SEQUENCE DESCRIPTION:

30 GATCACAGTT TTACAAATCT TAGTTTTAAA TAAATTATTT CAGTGTGCTG TTAGTCCTCT 60  
 ACAGTCATTT TGGTTTAAAA AGTGACTATT TATTTATGGT AGNATATCAA TAATTTATTA 120  
 ATGTTAAAAA ATACTGTGTA TGACATTACA AACCAGANCA GTTCCTGGGG GAGAGGNTTC 180  
 TNATTGATTG GCAGTTCTGA GAGGGCAAGA NGANTGGNAC TTTATNCTTC AAAAGGNGGT 240  
 35 TTTGGTTTTN CCAGGTACTG CTTATGTNAA TCGTTTATTT TTNTTTCATC AAAGCCTGGC 300  
 ANGTNTATGC NTTCCAN 317

SEQ ID NO:6119

SEQUENCE LENGTH:360

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07277

SEQUENCE DESCRIPTION:

45 GATCGACGAG CTGCTGCAGG AGTTCGAGGA GAAGAGTGGC CGCACCTTTC TGCACACCGT 60  
 CTGCTTCTAC TGAGCCCAGC GCCCGCATGG AGCCGCCTCT GGAGCTTCCT GTTGTTTATA 120  
 CTTTTTCCTT CCTGACATTT GTTTTTACTT ACAGGTGTTT TGCTGGTGAC GGTAGCATTAA 180  
 CCCAAATAAA CTGTGCATAT GAAATGGGAG AGGAGATGCC AAAACGCCAG ATGAAAAGCAA 240  
 TCAAGTTTCT TCTTTTCCAC TTTTACTTAT GAGCGGGATA TTGATTACAN GGNNTTTCCT 300  
 50 CTTTAACCAA AAAGGAAAGA CANGGTTTG TGTGCACTTC CCGNCATACC TGTGTCTTTN 360

55

EP 0 679 716 A1

SEQ ID NO:6120

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07278

SEQUENCE DESCRIPTION:

GATCGGGAAG ACTGAGTAGG GAAGGCAGGG CTGCCNAGAA GTCTCANAGG CACCTCACGC 60  
CAGCCATCGC GGAGAGCTCA GAGGGCCGTC CCCACCCTGC CTCCTCCCTG CTGCTTTGCA 120  
TTCACTTCCT TGGCCAGAGT CAGGGGACAG GGAGAGAGCT CCACACTGTA ACCACTGGGT 180  
CTGGGNTCCA TCCTGCGCCC AAAGACATCC ACCCAGACCT CATTATTTCT TGCTCTATCA 240  
TTCTGTTTCA NTAAAGACAT TTGGAATAAA CGNGCATATC ATAGCCTGGA AA 292

SEQ ID NO:6121

SEQUENCE LENGTH:30

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07279

SEQUENCE DESCRIPTION:

GATCCAATAA ATNTCCTTTT TTTGCTTAAA 30

SEQ ID NO:6122

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07280

SEQUENCE DESCRIPTION:

GATCGGGAGA GGGAGGAGAG GCAGTCTCTT GACAAAATAA AGTATTTTTA TTCATTTGTG 60  
TTTATTAAAT GAAAAANCAA TCCCATGGTG TCCCTGTTGT GTGGTGGACC TAATGNCTGT 120  
TGAAATAAAG TTCTGTGTTT TCCCTGAAA 149

SEQ ID NO:6123

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07281

SEQUENCE DESCRIPTION:

GATCCACCAA TGGAATTAGA TGGGTAGAGT TGGGTTCTTG AGTTTTACCA CCACTTTGTT 60  
CCCACTGAAT TTTGTAACTT GCTGTGTTTG CATCCTCTGT TCCTATTCTG CCCTTGCTCT 120  
GTGTCATCTC AGTCATTGTA CTTAGAAAGT GCCCTTCAAA AGGGGCCTGT TCACTGCTGC 180  
ACTTTTCAAT GAATTAAAAA TTATTTCTGT NCTAAA 216

SEQ ID NO:6124

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07282

SEQUENCE DESCRIPTION:

5 GATCTCATCA ACCCTTTGAA ATGTTCTGGG CAGCACAGCT CCTTGGTCTG CATGGTTGGT 60  
 GTAAGTATAA TCANGTAGTG AAATTGTATG GTATATACCT ATATGCCANC AGGTACACC 120  
 CGTATGTGCA GAATTTGCTA NTATAACCAT TTCAATAAAA ACCTATTGAA AAAGCTGAAA 180  
 AAANNANAAA NGNAGGAGGN GNGGN 205

10 SEQ ID NO:6125

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS07283

SEQUENCE DESCRIPTION:

20 GATCTTTGCC AGGGGTCAAA GCGTCGGGAA GCTTGGGGTC CTTCATCCTG ACGTTATCAC 60  
 CAAATTTNAG CTGACCATGC CCTGCTCCTC CTTAGAAATC AATATTGGAC CCTTTTGTG 120  
 AAGATTGGTC TCTGTGGTGT GATTCTCTNC CCAGGTGTCC CTTTCTCCTC CCCTAGTGTC 180  
 CTTAAGTCCT CCTCCACAGG GAACATCTAT TTGGGCTTTG ATGTTTAATA AAGTAGAAAG 240  
 CACTGGNAAA AAAAGAAANN NGNNNTGTGT NTGTTNNNN 279

25 SEQ ID NO:6126

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07284

SEQUENCE DESCRIPTION:

30 GATCCTAAGG AACATAAAGT TAATTAAAAA CTTACACCTA ATTATGTAAA TNGCCTTGTT 60  
 AAAGACATGT GATTTGTATT TNAGATGCTT GTTTCCTATT AAAATACAGA CATTTCTACC 120  
 CTCAGTTTCT AAATGTAGAC TATTTGTTGG CTAGTACTTG ATAGATTCCT TGTAAGANAA 180  
 ANTGCTGGGT AATGTNCCTG GTAACANGCC TGTNANTATN TNANGN 226

35 SEQ ID NO:6127

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS07285

SEQUENCE DESCRIPTION:

45 GATCCCATTT AGCCCCTGAA CATAATACCA TCTGCAGTAT TATAAAAGTC ATTTAGAAGG 60  
 TCAGGGGGAT AATCTAGAGG CAGGATTTTG GACATTGTGA AGGAAATGTG CTCCTTCTCA 120  
 GCTCACTTCA ATAACATTTT NCTGAGACTG AAGTTTTTTA GACAAGANTA AGANAACCTT 180  
 GCTTTNTTCA GTTATCACAT GTGANAGCTT TTGCTTTTGG TTAGGAAANG GTGTGGNTGA 240  
 CTCTACTGCG TGGNTGGTTA CATTTTGCTT TCCGTGNAAT TGCTCNGGAA ATGNTCNGGA 300  
 CATNCCNTTT NCCATTTGTG TGTCAGTGCG TATGGTNAN 339

50 SEQ ID NO:6128

55

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07286

SEQUENCE DESCRIPTION:

GATCTCCTAG GACCTAGTGG ACATCTGGNA TTAATTTAAT CTCAGGAAAA ACAAGANATN 60  
AACCCAGAGA GAGTCTGGGT TCTGGAATTC AGCGTANTAC CTCCAGACCG TGGTGTCTGG 120  
CCTCCATTTT TGTCTGTNAT TCAGCTCTGA CTTACAGCTG CAGTCACCTT TNCTATAAGG 180  
CACCTGGGTA GAAGGGTGGG TGGGCTTCAC ATCAAATTTT TTNCTTCCTT TAGGGTGGGG 240  
NATTGGNTTG GCTNTNTTTT GTNGTGGNN 269

SEQ ID NO:6129

SEQUENCE LENGTH:47

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07287

SEQUENCE DESCRIPTION:

GATCTGTCCT CCAAATCCTC TATTAAACCT GATAGCTTGA GCACAAA 47

SEQ ID NO:6130

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07288

SEQUENCE DESCRIPTION:

GATCAGCCCT TCTCAGCCTC CCAAAGTGCT GGGATTACAG NTGTGAGCCA CTGTGCCCGG 60  
TTCTGTGGCC TTTTCTAACA TTATCCAAGN NGCCCTAAGG TTCCTTATGA CAGGTTTGGG 120  
GATTGGGAAA GTTCAATTTT ATTGTACCGC CAATGAAAAG GTGCTATATT TTTTCTTGA 180  
ACCTNAAGGG CAGAGGCTGA ATTAATCATA TTCCTCAGCT CATTCCACAT TATCATGGCA 240  
AAGCTCTCTT TTGCTTATT TATTTATTCT CTNNTATCTT CATACTTAAT CTCATTCCAT 300  
TCTCTGNCAAT GGGCAACCAT NNAATNGNN 330

SEQ ID NO:6131

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07289

SEQUENCE DESCRIPTION:

GATCTTACAT GAGCATAATC ATCCTTATAC TTCATGAGGG GATTATNAGT ACAATCCCCA 60  
TTTACTGTG TTTGAGTTAA AAACCAAACA TCCCTGTAAT TTAATTTGAA GATTCTTTAA 120  
CAGATTGCAG CAAAGTTCAT TATAAACTG TTATGGTGTC TTCAAAGNCT TGATAAAANT 180  
AACACTGNGA GAGANTTGGT CCATTTGTAT GCTGTATTTC TATTACTTGC CAAANGGAAT 240  
GGGGNTAGGA TTAACCTTGT TTCCATTCTC TTCNCATGGG TATCCATCCC CATGTTTANC 300  
TGNCACNCT GGGGGGCTCN GTTGTGTGCT GTN 333

5 SEQ ID NO:6132  
 SEQUENCE LENGTH:21  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07290  
 SEQUENCE DESCRIPTION:  
 GATCATAAAT AAATGTTTAA A 21

10 SEQ ID NO:6133  
 SEQUENCE LENGTH:331  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 15 CLONE:HUMGS07291  
 SEQUENCE DESCRIPTION:  
 GATCATTTTC AAAAATTGCA TTGGGGCCTT CGTTATTTAC CATAGTATTT NCACTTTTCAT 60  
 AGTTTGTGCA CCTTTTGTGA CTGTGAACAG TTCAACCAGT GACCGACTTC TCTCTCATGC 120  
 20 TGTTTACCCC ACACACAATT TCCCACTCAA TTCTGAAAAA AAGAACCTGT TAATAGGTTG 180  
 GAAAGCTGTG TACTCTATTC ATATATTGTC CTTTCATGCT AGTGGAGAGT GGTGTCATTA 240  
 GCATCTNAAT TTTAGAGTTG TGNAATGATT TTNCCAATTA GGAATTGANT GTGTATTTNT 300  
 NTCCTGTTTA ATAAGNNGNG CAAATNTGNT N 331

25 SEQ ID NO:6134  
 SEQUENCE LENGTH:40  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07292  
 30 SEQUENCE DESCRIPTION:  
 GATCTTAAAA CAAAATGAAA TAAACGTGAA AAGGAGCAAA 40

35 SEQ ID NO:6135  
 SEQUENCE LENGTH:53  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07293  
 SEQUENCE DESCRIPTION:  
 40 GATCGTGAAT AGTAAGTATC ACTTCCATAA ATAGAAAGTG TCAGAAAAAT AAA 53

45 SEQ ID NO:6136  
 SEQUENCE LENGTH:336  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07294  
 SEQUENCE DESCRIPTION:  
 50 GATCTTGAAA GAGGTAAAT AAACCTTCAC TGCTCCACTC CAGGTGAATC CGCCCACTCC 60  
 CACTGACCTA GTAGAATTTG TAATTAATA CTTACCTTCT ATTTCTGAAA TCAGTTGTGA 120

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ACTGTTGCCT TATGTTGAGA GGTTTAAGAA CCTCAGTGAA TTCATTTTTT AAAATCTGCT 180  
ATTCTGAGAA GCATTGAATG AATTCTTAAC AAGAAGNCTC ATCTGTAGCT GTTTGCTGAC 240  
TCCTATGAGC CCATAAGGGT TCTGTGCTTA GCATTAACAA ANTAAGGTTT ATAGGGTAAA 300  
AGCCAATGTA TTANTTTTTT TTTGCATGGG GGGCNN 336

SEQ ID NO:6137

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07295

SEQUENCE DESCRIPTION:

GATCTAGGAC ACTCATATCC AGGGTGATTC TCTTCATAAG GAGGCATGGG CTGAGTCTCC 60  
ATTTATAGGG GCTGTCCCA TAGAGACTTC AAGCCACACC TTTCTAGGGA TTCAGGTTGC 120  
ACATTACCTG ATTCTACAG TTGATTTGAG CCTGCAAGAC TGTAACCCA TCCCATTATC 180  
ATGTTTCTT CCTCATTTAC CTACATTTAT CATTAAACCT TTGTGATTCA GCAAA 235

SEQ ID NO:6138

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07296

SEQUENCE DESCRIPTION:

GATCCAGGAT GACTGTACAT CTCAGATAAA GGAGGCTCAG CGCTGGAAGG ACAGCTGGAA 60  
GCAGTCCCTG CACACTATCC AGGGCCTGTA TGTGTGACCC TCCGCCCCAC CATGAATAAA 120  
CACTTTCTTA TACAGACTCA AA 142

SEQ ID NO:6139

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07297

SEQUENCE DESCRIPTION:

GATCCGCCAA GCAGGGCAGT ATCTGGGTTA CAGCCACAGC AGGAAGAACC ACTGGAGAGA 60  
CACTCAGAAG GACTTCCCTG ACATCTGCAC CAAGGAGAGT CTGGACAAAG CTACTGAAAC 120  
TCCTCCACCT GCTTCTAAAA TGCCAGAAG CCAACTGGAC CNGTTTGGTA TTTNGAAGTA 180  
GGNGGNTGGN GGCTTTAACC NCCAAAGGGT TCCTGAAGCC CNGGAACTTG GANTNTGGAG 240  
GGGGTTNNGG CCTTANTTGA GGGTTGGTGG GTTTCNN 277

SEQ ID NO:6140

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07298

SEQUENCE DESCRIPTION:

GATCAGAAAA CATTGATTTA TATTTAAAAA TAGGATATTG GAGCCATTGT CTTAGATAAT 60

TNNCAAGGCA AGANCAAGCC TGCAATAAAT AATGAGACTT TGACATTCCT TGGCGAAGAA 120  
GATGTCTCCT GCCCTAATAT GACTGTCACT CAGCAATTC ANTTTTNTGT TTAGTTGATT 180  
TANAANGGGA GGATAANTTG TCCTGANAAG TTTTTTTGTT TCCTTAACAT TTCANNGTTT 240  
TCNCTGN 247

SEQ ID NO:6141

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07299

SEQUENCE DESCRIPTION:

GATCCCTGAT GGGATGCCTG AAACCCAAAA TACTCTTAAG TCTTGTATTC TAGGGCCTTC 60  
TAAGGCCAAAA NATTGAGAGA CCAAAAAAGA GAAAATATGT TTAGTAAAGA AAATATTTNC 120  
TTTGACTAGT TATGATGGTC ATATAGGGGA GANAAGGCAA ATTTTGGNAA TGTAAGATGG 180  
GGACANTTAA TGTNTATNCN CTGTCCAANT TCAANAGGTA CAACNGAN 228

SEQ ID NO:6142

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07300

SEQUENCE DESCRIPTION:

GATCCACCTG TCTCTTGAAA ATATAAAAAG ACAAACAGG TTTGCCTTGG CATCAGAGAG 60  
CACAAAGATT AAAAGTTACT TTAAATTTGC CAATATTTTG GGAGANCAAT AAANCTACAT 120  
TTTTCCCTCT TCCATACTGG TAGATGCGAA ATTNATCTGT GCATGANAGG GTCACCTCTG 180  
TNATCGTGCA ACAGNTTTGG TATTANNCCT TNNCTGTGGT TTNCCAN 228

SEQ ID NO:6143

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07301

SEQUENCE DESCRIPTION:

GATCCTCTGA TATACAATTA GAGATATTTT AATATAGNCC CCAAGCATTC TGTGCATAAA 60  
AGTTAACATT AGGCTGTGGT GCAGTAACCA TTAAATGTCG AGGCTCTATT TCGGAAATAC 120  
ACTACAAATG TTAAAGTACG TGGCTGTCCT CTAAAGNCAC TAGTAGAGCA AAGCCTTAAT 180  
CATATCANCT TAATTCTGTT ACACAATATG TGTTTTTNAA TATACTANCC ATTTCTNATG 240  
GAANGGTCTT GTGGGGNGCC CNTCCTCTCG CCANGCCATC ACAGGCTCTG CATAACGN 299

SEQ ID NO:6144

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07302

SEQUENCE DESCRIPTION:

GATCGGGTGC TAGGACAACT GCAGTCCAAT CCACCAGCTC TCCNTGCCCC TGTGTCTTAT 60  
TTCAGACATG AGAATAACTG TACAGTGTA ACTTATAAAG CGTTTTTAAT GGTGTAGAT 120  
TGGAATAAAA GTATGTCATA TGAACAGCTA AA 152

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SEQ ID NO:6145  
SEQUENCE LENGTH:131  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07303  
SEQUENCE DESCRIPTION:

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GATCCACCT GCTCAGGCCG TACACCTTAT GGGGAGCCAT TAAGGGGNC CATCTAGGCA 60  
TTCTGGNTAC AGCCAGTGC TCATCCAGC GTATGCTCCN CTCTNTAGNG CAGCCTAAAG 120  
NGTCAGCCAC N 131

SEQ ID NO:6146  
SEQUENCE LENGTH:154  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07304  
SEQUENCE DESCRIPTION:

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GATCTTCAGA GAAATAAAAC TTGAGTGCAG TAGTTTATTT GGC GTTTGGC TCCAGGATGC 60  
AGGNGTGGGA AAGATGGTAG AGAGCCAGAA GAAAANTCAA TAGAACGGTA TTACGGCGNN 120  
TGGNTATATA ATNCTTCCCN GAATTGTCTG ACTN 154

SEQ ID NO:6147  
SEQUENCE LENGTH:251  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07305  
SEQUENCE DESCRIPTION:

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GATCCAGTGC TATTCTGTCA CCAACCTAAG AATCCCAATT GCACCTTCTG TTTCTGACAG 60  
TCACAGGTGA CAGCTGNNGN TCTATAATAC AGACTGGTGT CTTAGAGGTA GGAATAATAC 120  
ATGATTATNA AGCATCACCC TGCTAATACA TAATAATGTC TTTTATATT ATAAGNGATT 180  
GAGTTTAGTT CATTNCAATA CATTTGTACN TGTA AAAANT GCAANGTNGA CCTNNGTAAT 240  
CNTTTAATCG N 251

SEQ ID NO:6148  
SEQUENCE LENGTH:213  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07306  
SEQUENCE DESCRIPTION:

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GATCTCGGAG ACTCNGTCCA TTCTAAGATA CCATGTTTCC ATGACCCTAC ACACAATAGC 60  
TACACAGGTG GAGCAACATG AGTCTGAGNA GCTTTGCACA AAAGANGCTT GTTTCCACA 120  
AATGNANCTG GGGTGGTTAA CTTCTAATTG TACCCTGTCT TAGCGTTCAG ATGCATTGGT 180

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TCCTTCCCCA ATGTGACCAT CTNNNNATTC NAN

213

SEQ ID NO:6149

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07307

SEQUENCE DESCRIPTION:

GATCAAGATG AATNTAATGT ATAATCAGAA TCCTAGGTAA GTAAACAAAA AAAGGGTTTT 60  
 TTTNAGAATC AAACCTTTGG GGATTGGGTG GTAAAGGGAA ATATTNTNT NCN 113

SEQ ID NO:6150

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07308

SEQUENCE DESCRIPTION:

GATCTGTGCA TCTGGCCAGC ACTGTGGTGA CATCCTTAGG AATCCATGGG GAGAGAGAAA 60  
 GCATTGAGGA GTTAGTGGGT CACGTTTGAC AAGGGCCAAT AAAGAAATAT GCAAAGACAA 120  
 AAANCAAGAA GNACATTGTC ATATTNCTA CCTTTTGTTT ATATAAATTT ATNTCANTGA 180  
 TTTTCGCTTN TGTTAATNTG CAATGTATAT NNTATGCTAA CNTTTNCN 228

SEQ ID NO:6151

SEQUENCE LENGTH:42

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07309

SEQUENCE DESCRIPTION:

GATCACAATT GTGGACATTA AAACAGAAAC TGTTCACACA AA 42

SEQ ID NO:6152

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07311

SEQUENCE DESCRIPTION:

GATCCAGCTT ATNCTTTAAT TTTCAAGTCC ATTCTTGGGG CTGGTGGGGA GGCAGGAGAA 60  
 TACCCCTCCC TAAGCCCTTA GTGTGTGCCG AGCTTGCTTT GTNATGTTGG CAGGGGAGGG 120  
 GAGACCTGGG TGGTGACTGA GTTCCCTTTA TCAAACCCTT CAATGGGCAC AAAATTGAGT 180  
 GCTTGATTTT AGGTTTTTATT TTTTATGAA TGTCCAAATC TGTGTTTCCC CCTGCCATCC 240  
 CAGACTNTGT GGCCAGTTNA AAAGTGTCTG GNNTGTGTTC ANCTCTNCCC TAANATNCTG 300  
 GAGNAGGGGT N 311

SEQ ID NO:6153

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07312

SEQUENCE DESCRIPTION:

GATCTNNGTG GGTAGCCTCA AGCTGGAGAC ATTGTCTGNC CTCACTGCCC ACTGGGTAGA 60  
 GACACCTGGA TGACATTCA GTACCCGCTG GCAGCTCCTC CCACTCATCC AGAGACGGCC 120  
 GGTGGGCAGG CGGGGAGAGC AGCTTTCCTT CCCTGGNGAG AACCGTCTTT ACCTCAGCTC 180  
 CTAGGGNCTC CAGCCAACAA AGCTNCAGCA CGGTGACTNG GTGATGGGNG ACCAATNNCA 240  
 GAAGTAAANN GACTGTAGAC CNATATTCCN 270

SEQ ID NO:6154

SEQUENCE LENGTH:40

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07313

SEQUENCE DESCRIPTION:

GATCAAATTC TAAAATAAAG TTGCCTGTTG TGACTTTAAA 40

SEQ ID NO:6155

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07315

SEQUENCE DESCRIPTION:

GATCTATACT TAACATATTT AAAATAGTGA TGATTGAAAT AACTGCAAGG TATAGATGNA 60  
 ACTGAAGGNT TTCACATTCC TTTTTTGTTC ATCATTGGA ATTTNCTGTA TTTANCTGNC 120  
 TAGAGANCAN 130

SEQ ID NO:6156

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07316

SEQUENCE DESCRIPTION:

GATCATATCA CTCAATGTGG CCATTAATAT TTCTGGAGAA GACACAAACC TATTTATAAT 60  
 ACTTTTNAAA AATCCGAAGT GATAATAAGA NTGTTTTTAC ATTGAAAGTA ATACTTAAGT 120  
 GTTTACATAA CATTCTGTAT GCACTCAAGA AAATAAAGTT TTGTTAATAC AAA 173

SEQ ID NO:6157

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07317

SEQUENCE DESCRIPTION:

GATCTCAGTT ACAGTTTTTT TTTCTTTTTT AATTCATTA TTTTGGGTTT TTGGTTTTTG 60

CAGTCCTATT TATCTGCAGT CGTATTAAGT CCTATTGCTA GAATAGGTTA CTNNANGAAA 120  
 GATTATATTC TGAAAGAAAA ATAACGACA TTATATATAA CCAATTAATT TAANGTATTG 180  
 CCATTTAAAT TACACACTGN GAGCATGTCC TATGCAGACA ATAGATTTTN CCTGTNCAAN 240  
 NNNTTNTN 248

SEQ ID NO:6158  
 SEQUENCE LENGTH:187  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07318

SEQUENCE DESCRIPTION:  
 GATCCAGCAG CGCAGGCAGG AGCTGGAGCA GTCGCTGGTT GTNCGCAACA CCTAGGAGCC 60  
 CAAAAATAAG CAGCACGACG GAACTTTCAG CCGTGTCCCG GGGCCAGCA TTTNCCCCG 120  
 GGCTCCAGCA TCACTCCTCT GCCACCTTGG GGTGTGGGGC TGGATTAAAA GTCATTCATC 180  
 TGACAAA 187

SEQ ID NO:6159  
 SEQUENCE LENGTH:21  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07319  
 SEQUENCE DESCRIPTION:  
 GATCATAAAT CCCTGTCTAA A 21

SEQ ID NO:6160  
 SEQUENCE LENGTH:122  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07320  
 SEQUENCE DESCRIPTION:  
 GATCAAACGT GCTTAAGAGC TAACTCGTGA CACTATGCAG TATTGTTTGA AGACCTGTTG 60  
 TTCAACCTCT GTCTCTTTAT GTTAACTGGA TTTCTGCATT AAATGACTGC CCCCTTGTTA 120  
 AA 122

SEQ ID NO:6161  
 SEQUENCE LENGTH:125  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07321  
 SEQUENCE DESCRIPTION:  
 GATCTCTGAC TCATTGTGGC ATATGAGGTG TAAAATNTTG TCAAAAAAGA ATCTGGTGTT 60  
 TAAACCAAAA TCACACTATG GTGGCATTAA ACCGTTCACT TTTATTCTAA ACNNNANCCA 120  
 NCGCN 125

SEQ ID NO:6162

SEQUENCE LENGTH:41  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07322  
 SEQUENCE DESCRIPTION:  
 GATCTGTCCA CGACATGGAA AATAAACTGG ATTTTCAGAA A 41

SEQ ID NO:6163  
 SEQUENCE LENGTH:137  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07323  
 SEQUENCE DESCRIPTION:  
 GATCCTATAC GTGAAGGAAC ATATTTAATT TCCTCNCTTT ATATTCCTG GTTAAATAT 60  
 CGTCATTATA GTTAGCAATT TGGAACTCTGG CTTACATTGG TTGATACAAA TAANTAATAG 120  
 ANTANNGCAA NATCAGN 137

SEQ ID NO:6164  
 SEQUENCE LENGTH:88  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07324  
 SEQUENCE DESCRIPTION:  
 GATCTTTTTT CTATGCGTAA TCAGACATAC ATATATACTG CAGTGTATCT CACGTATTAA 60  
 TTTTAAAAAA TCTTTTGTTC TACTTAAA 88

SEQ ID NO:6165  
 SEQUENCE LENGTH:274  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07325  
 SEQUENCE DESCRIPTION:  
 GATCTCTGTA TTTGTNTTTC AACTAACAAC TAATTTNAAA TGTATTGTAT CTTTAATNAC 60  
 CTGTNCTCTT AGATTGTNTT TTGCTAGTAA CCCTTACTCA GCTTCTGCCT TTGGGGCTTG 120  
 GACTAATATT GCTTGTATGG AACTACAGTA CTGTGACTAA ACATGGAGCT CAATGCAGCT 180  
 ACTGCTTACA ACTGCTTAAA CTTTGTAGTG TGGACTTCAT TTTTCTCTGT AATAACANCT 240  
 TATTAAATCC TNGGTGGTAT GCGGTCCTG GAAA 274

SEQ ID NO:6166  
 SEQUENCE LENGTH:310  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07326  
 SEQUENCE DESCRIPTION:  
 GATCATGTTT AGAAAGGGAC TCATTTGGTC CCACTTTGTA ACATGGGAAG AGTAGAAGAG 60

AAAATTAAAT GTGGAAATCA TAAATGCTTT TCTAACAGGG TTATGCTATT CTGTAACACT 120  
 AAATGCTCTG CTTTTCTCTT AAAAGATTAA GTTTTATTAA TTTTGCATA CATTTCTCTA 180  
 TTTGANTATA TCTTAACCAT TTTATGTTCC AAATTCGTTT TTTGTCCAAG ACATTCTATC 240  
 AGANTTTTNC TTGCCTCTAT AAATCTGAAA ANTGGGTTCT AGAATGTCCC ACTTGCTGTC 300  
 TCTNAGAGTN 310

SEQ ID NO:6167

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07327

SEQUENCE DESCRIPTION:

GATCCGCCCA CCTCAGCCTC CCAAAGNGCT GGGATNACAG GCATGAGCCA CTGCACCTGG 60  
 CCTTAACCCC TCTTTAGATT GGAAAAAATA NTTACAATT TAAAAATAGC TTAGTGTTGA 120  
 ACCCTTTGGT AAATAAAGA CCCTTTTATA ATGCACATAT TCCCAACANG GTTAATATAT 180  
 TTNGTGAGAT TAAACAAGGC TTGTATATGC TTGACCTTTC TTAANNTATG TCCATGTCAT 240  
 ACTATTATGA NTGTACATTT TTATGAGTCA TNANTATTNT TTTCAAAANG CGCTNCAGGC 300  
 CCNTGAN 307

SEQ ID NO:6168

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07328

SEQUENCE DESCRIPTION:

GATCAGAAAA TGTGTGACCT TTTTAAAGTT AAATTGTTAA AAAATTTTAA CTATTAANCA 60  
 TTTTAAATAT TAAA 74

SEQ ID NO:6169

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07329

SEQUENCE DESCRIPTION:

GATCTCAGAT GCTAGAAATA GTAGACAAAG ATGTTATTTC CCAGTGCAAA TAAAGAAATA 60  
 AAGATAGCAA A 71

SEQ ID NO:6170

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07330

SEQUENCE DESCRIPTION:

GATCTCAATG TGCAAACCTC TTGGACTCCA GACCCCTGTC TGGTTGGCAC TCCCAGCAGT 60  
 GTGTGGTTTC ATCAGGAAAT CCTTGCAGCA GGGGTTTAGA TGGTTCCTTC AGGAGGTGGG 120

NAGCCTCCAT AGCATTGAAG GCCAGCCTGC ATCTCGCGGT GTGTGTCCAC TTCTCCNCTC 180  
ACTTTCCCT CACCCATCCC TTAAAGTGA TTGGCTGTNA GGNGCACAGA GGGTGGCAAT 240  
TCCATCTGTN ATGGGNTCAG AAGGCATTNG CCGCCATTNT TGATTNACA TAAAACTGA 300  
TGNAAN 306

SEQ ID NO:6171

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07331

SEQUENCE DESCRIPTION:

GATCTGTCTG TTGTTGGAAT TGAGATATTA AAATCCCCTA CTATTATAGC GTTCCTCCAG 60  
TCAAA 65

SEQ ID NO:6172

SEQUENCE LENGTH:33

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07332

SEQUENCE DESCRIPTION:

GATCTTCCAG CACCAAATTT AGATGGCCTC AAA 33

SEQ ID NO:6173

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07333

SEQUENCE DESCRIPTION:

GATCAAATGT GTGAGAAAAT CAATGGGTTT TAAAGACTAT TCTATGTCAA CTATAACATT 60  
TAATTTGGGG ATTTCTGTCC CTTATAATGT CTACCTCATT TTGGATGGAA TCCTTGAGGC 120  
CTGGTTTATT TTCCTTTNCC TTNCTACACA TCGCTGCTCA GAGTGATGAA TGGAGTTGTG 180  
TTTTGAATAA AATATCTATG CATCCNTTGT TGAGCAAA 218

SEQ ID NO:6174

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07334

SEQUENCE DESCRIPTION:

GATCATGTTT TAACTAACTT CATTTTGTG CTGAATCATA ATNNATGCTC TAATGACCTT 60  
TTCTTTCCTA TCCCAACCCT GTGTAATCTG CTCTATTTAG GGCTAATTGT TCCTTGCTT 120  
GTATGTATGT AATGTGTCCT NGTNTTCTC CTCCTATTN NTNCTATAA AACTCCATCC 180  
NNTTTN 186

SEQ ID NO:6175

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07335

SEQUENCE DESCRIPTION:

GATCCATTCA ACTTGTGTGT ATCAGTAGTT AATTNCTTTG TATTGGTCAG CATTCCATTA 60  
TTTGGAATTT ATACAGTATG TTTATCCATT CACCTGTTGA AGGACATTGT TTCCAATGCT 120  
TATTACTAAT AAAGCTGTGA TGAACATTCA AA 152

SEQ ID NO:6176

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07336

SEQUENCE DESCRIPTION:

GATCTGTATT TAATGAGGAG GAGCCGAGGC CCCAGCTTCA TCCAGCTTCA ACCAATGCCT 60  
GGACCTGTCC ACCTGANAGG CCCCTGGGGC TCCCAGCTG CTGGCCAGAC CCTGGCGCTG 120  
CCACAGTCCT GGCCTGCCC AAGGCCATAC CTGNCTAGCC CTTGGNTCC ATCCTGTGGA 180  
TGCCCACTCA CCCCTNAGAC TCCTNCTGNC CATGCTGTGG NCGGACTTGT AAGCAN 236

SEQ ID NO:6177

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07337

SEQUENCE DESCRIPTION:

GATCATGCCT GTGTTTACCC TCTAAGCTGA AGCTGCTCAT CAACGGTGAG ATGGCAAAAA 60  
GGTGGGTCCA GAAGAGGGGA AAAGAAGGGA GTCTGTGAAA ACAAATGCT GAAGANTCTG 120  
CATCAAATAA ACCCTTCCTT CCTTCAAA 148

SEQ ID NO:6178

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07338

SEQUENCE DESCRIPTION:

GATCTCCTTA TTGACCACAG ATTATTCCTC TGTTTCAGCAC TCCTTATTCT TATCCCTGTT 60  
ACAATTCTTA TTATGGTGCA CAAGCTCCAT AAATATTTAT AAAACTGATA TTAATTGANT 120  
AAAATATTGT CTAGAGGTCT CAGTCATTCT TCAAA 155

SEQ ID NO:6179

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07339

## SEQUENCE DESCRIPTION:

GATCATCTAG ACATAATTNC TGAAGATGAA CTTTGGACC AACTTCTAAG TCACACAGCA 60  
 TCATTATCAG ATTTATTACA CAACGNCCTT TTNGTTTNA CTCTATTCT GAGGAAAAAG 120  
 CCTTCCCGAA ATCCGTAATG ANTTTNTCCA TGGTAACCCC TCTCCTGTTT TNACACAGNA 180  
 AAGTTTCTCT NGA CTGTN 198

SEQ ID NO:6180

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07340

## SEQUENCE DESCRIPTION:

GATCGCTGGT TTCCTCTGCA GCGCGAGGGC TCCGGCGACC AGAGGATTCT NCCCGGAAGG 60  
 CATTCTGCC GCGCTCCNG GGGCACCCCT CAATTGTGTA CTACGTCCTT GTTTAGTGTG 120  
 TATCCGTGCC CACGTAGATG ATGTCTGTAA CGNAGTTTGT TTTGAAATAT GAGNATATGC 180  
 GGCTTAAA 188

SEQ ID NO:6181

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07341

## SEQUENCE DESCRIPTION:

GATCAGTTTA TTATTGATAC ATCACTCCAT TAATGTAAAG TCATAGGTCA TTATTGCATA 60  
 TCAGTAATCT CTTGGACTTT GTTAAATATT TTNCTGTGGT AATATAGNGA AGAATTAAG 120  
 CAAGAANNTC TGAAA 135

SEQ ID NO:6182

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07342

## SEQUENCE DESCRIPTION:

GATCAGTTTT CCNAGTCTTT GGGAAACGGG TTGTGTTTTT TNCCCTTTC CGTGTTGGAT 60  
 TTCCGGTCCC GGCTGACACC TCCCTTCGTG TGTGCGNCCC TCCCACCCC TGCCTTTGTN 120  
 TCGGTGCCCT GTGTCCGTTT TCTNATGTGG GGATGTTGT GCTGCAGACA AAAAGAACA 180  
 NAAAAANTTT TAAATACCA CAAAGATGGN ANAAAANGAC AAAANN 226

SEQ ID NO:6183

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07343

## SEQUENCE DESCRIPTION:

GATCGTCACA TGCCGGGGAG CAATGTGGAT-GGCCTGGGGA-CTCCTGGGTT TTCTCCCTCC 60



CGACTCCCTA ATAAACCCCG TGAACCTTGG AGCCAAA

97

SEQ ID NO:6184

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07344

SEQUENCE DESCRIPTION:

GATCACCTTN AGTNCTNAGC AGGGACTAGG CTTGCAGGTA ANATAATGGG CCAGGGCACC 60  
CAGTCCAGAA GGAGCAATGG CACCTGGGCA GTGCCAGGCC TTAAAGCCCG CTGCTCCTTT 120  
NCGGTAGAGG AGAGGCCCAT CACTGGTGTG GTGGGGTGGG CTCTCCCTTA GGCTTGGGCA 180  
AGGCAGCCAC CTGCCCTTNC TCTCCCTTAG TGTTCCCTGG CCTCCCTGCC ATCAGGTTGC 240  
TGGGAGTGGA GATGGAGGGA TTATTGAGCA GAAAATNAGT TGGATGGAGN TAAACAGNTC 300  
CCATCCCTGG GTAATGGATT N 321

SEQ ID NO:6185

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07345

SEQUENCE DESCRIPTION:

GATCAGCTTG GAAGCTTAAA GTCCAATCCT TACTTCGAGT TTGTTTTGAA AGCAAATTAT 60  
GAATATNATG TTCAGGGACA AATATAACTT TTNCTAAAAA TGGCCATTGT TTATGAAATC 120  
TGTATAAGTG TGTCTTATA CAAATTTNAG GCCATAAACA AGTGTAAGTT TGTACAATTT 180  
CATAACATGT ATAGCTGAGT TTTTATACTT TATATGTAGG AAGCTAATAT AAAATAGTTA 240  
TGTAAGTGTG ATTTTGGTTT TCAGTTATGT GACTTGTTTT TNCCACCNGA AA 292

SEQ ID NO:6186

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07346

SEQUENCE DESCRIPTION:

GATCCATAAC AGAGATNCAN AGAGGCACCG TGGAGTTCCA GGGTCATCGG TCAGCGAGGA 60  
ACAAGGAGGG AAAGGTGTCT TCCTGCCCCCT TGATGCTCAA CTAAGCATCT GTTCCCTAGA 120  
AATACATGTG TCCAGGNNGN NTCCATGGGC TTTNN 155

SEQ ID NO:6187

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07348

SEQUENCE DESCRIPTION:

GATCTTNAGT TGTTTTAATT TTTTTTTTCT GCATCTGAAT CTGCATGATT TCCAAACCCT 60  
GTACCATCTG AATTTTGCAT TTNAGCACTT GCACTATTAC TCAGCAGCAG TAACATGGTA 120

ACACTTAAAA TGGTACTCGG GGACCTCCAA AGACTAACT GNCANGCCTT CAAGGNGCCC 180  
AGGGGTACGT TANCCTGTCA ACGGCATGGT TTAATCCCTT CTTTACACTT GTGTAAATTT 240  
CAGTTACTGG TCATAGNNGG CTTTCAATGT TCGGTGGCCT NTTATTANCN TGTTTATGGG 300  
N 301

SEQ ID NO:6188

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07349

SEQUENCE DESCRIPTION:

GATCTTTATC AATATTCTGG ATTAGACAAC AAATNACCTT TCTGGGTGTT TCTTGTAAC 60  
TATACTCCTG TTTGAATGTT AAACCTTTGTT GCTAAAGTTT AATTTAAGA TGTTTGAATG 120  
TNCAGTTTAT GTATTGANC TACAATAAAC CAACCCTTTT NATATATCTG TNTNGTATAT 180  
GATTATNGTN ACTTAATTNT NAN 203

SEQ ID NO:6189

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07350

SEQUENCE DESCRIPTION:

GATCAAAGCA GGTGGGGCTT TGGGATGTGA AGTGGGTTCT NACGCGGGGC CCCACAGACC 60  
TGTCTCCGCG TGANTGCCTG CAGGCCCTG CGTCATTCTT CAGCTGCGTG CGAGGCCTCT 120  
GGCTTGAGGA GCCTCCCCGC TGTGCACAGT TCTCTCTTGG CCAGGGCAGG GCTTGGGGCA 180  
GCACCAGGCT GGGGCAGAGG AGGAAAGCAA GAGGACAGAC CTCCAGAAGA GCAGCGGAGG 240  
GCGGGTGAGG ATTCCCCAT ATACCAGTGT GTGTTTCTCT ACCCATGAGG AATAAAACCA 300  
TGCAGCAGCA TGCAAA 316

SEQ ID NO:6190

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07351

SEQUENCE DESCRIPTION:

GATCCCCAGN ACTGCAGCCG AGCCCCGGGC TTCCTTTCTT ACCATTCTGT ATGCTTCCAA 60  
GGTGTGACCA TTCAAACATA CNNTATTATT AAGATTATTA ATAAAGATT CTTTCTTCAA 120  
ACCAGGAAA 129

SEQ ID NO:6191

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07352

SEQUENCE DESCRIPTION:

GATCAGAATC AGAAAACAGG TAAACCTCAC TCACACATTT GGACTCATTT GAACAAAAAT 60  
CTAGGCCAAA ATACTGAAAA GCCTATGTGT TTTTAAATT GGAAGTATAT GTAAGGTAA 120  
TGCATTAGT GAACGTGACT AACAAAGACT AATGTGCACA TTAACAGNTG TNCTTTTAA 180  
GGTTTATGG GAGGCTGTGC ATTGCTCAA AGCTGTTGG AACGCCTTCT GACCAGTTGC 240  
CTTCAGAACT AGTTTGNCT GTCANTNAA AANCCAGTGN NTTTACTCNN GGN 293

SEQ ID NO:6192

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07353

SEQUENCE DESCRIPTION:

GATCTGCATG TGTGACACTG ATTCTTTGGA AATAAAGAGT GGAAGCTGCA AA 52

SEQ ID NO:6193

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07354

SEQUENCE DESCRIPTION:

GATCTAAATT TAAAAATAG GAATGAATCT NTAATTGCA GCTTGTGGAG AGTATAAAC 60  
ATTTTGAGCA CAATATGCAG CACATAACTT TTCAGATTGT GTTGCATAG AAAAGGTAA 120  
AATCAATTCT TTCAGTACT GTATTGTCA TTTCTGTAA AGGTCTTCCT ACATTGAGA 180  
CGAGACCCTT TAACATAGGC TGCCTTAGTA ACAAATAAA ACAGATGTGT CATAAA 236

SEQ ID NO:6194

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07355

SEQUENCE DESCRIPTION:

GATCTAGAGG GNCGATTTC AGCCAGGGCT GCTAGACGGA GGCCTACTCT TCCATCTTC 60  
CTGATGGCAG GATGGCCTGG CCAGGGCTG GAAGACAGAG ACCTCCTGCC TCCGCCTCAG 120  
TAAGACGACA AGGAAAGGCA AATGCCCAAG GAAAGAAAA GGAAGGCTCT TCTCCCAGA 180  
GTTCCCCATG CAGACATGAG TCGTGCTCA GTTCAGANTC ACTCCGAGA ACTCATCCCT 240  
AATGCTGCAG ATTTGGGCTG GAACAGATTC AACTGTCTG TN 282

SEQ ID NO:6195

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07356

SEQUENCE DESCRIPTION:

GATCTTCATC TCTGTTTGC TCCACTTGTA TTCTCTTTC AGTAACTGGA TTAATGCTTT 60  
GAGCCCAAAA TGAGATATAT TTNTAATTAC TGTAGATTAC ATGTTGTTTG GCTGGGAATA 120

CAATACAATA AACTTTATTT TGCATAATGC ATTTCAAA

158

SEQ ID NO:6196

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07357

SEQUENCE DESCRIPTION:

GATCTGGATT ACTATGTAAA TTCACAGNAG TACCGCTAAT ATAATTTTGG TTGCNTGTAT 60  
 TANCATCATC TGGTCTGNAA ATGTGGGTTT TTATTGGCA CATTANATA AAN 113

SEQ ID NO:6197

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07358

SEQUENCE DESCRIPTION:

GATCTGGAGC CACAGTCTGT NTATCTTCCA GTTCATCTCA GTCCTCGAGA AAGGCCCTNT 60  
 AAATATGTAA CTTTCCATT TNCCTTTAAC CATGGGTTGT GTGAGCCAGA AAGAGCTTTG 120  
 AGAAAGATGG CTGCTTCCAC CAGGGNGGAG GCTTCTNGGT CTGCATGATG ATGGGGCCCG 180  
 TTTCTGGCCA NAGGGTGGCT CTGGGAGCAG TTGTNCTGCG GGCTTGCTGG GGGCGAACTC 240  
 TAACTGTTGC AGAAACAGNG CTTNATGGCT TGCTNNGGGT ACTTAGCTGG AATATTTTAA 300  
 AGTGTCAAGT AAATGTGATN TNN 323

SEQ ID NO:6198

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07359

SEQUENCE DESCRIPTION:

GATCTGTATG TACTTTTAGT TGTATTAATA AAGTGACAGT GAGTGTCAAA 50

SEQ ID NO:6199

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07360

SEQUENCE DESCRIPTION:

GATCACCAG TCTTAAGGTT TCAAAAAC TC TTTGACATTA GATTCACAA CTGCACAATT 60  
 GANCTTATTG GCCTGTAAC TATTTNCTAA ATGCTCAGTG CTATTTATAT ACTACAGTAN 120  
 TTNCCTGTTA AGNNGGCAGT TGTAAGNN 149

SEQ ID NO:6200

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07361

SEQUENCE DESCRIPTION:

5 GATCGGACTG GAACTGTTTCG GCTGCNACCA GAAATTNATT TTCCTGAGTA AATTGCCGAG 60  
AATTAAGAAT GAAGAGGGCC ATTTGCATCT CCTTAAATTA TTCAGTTACC TGCTTTATTG 120  
CTCCATGTGG AAAACTTAAA ATTGTTAAGT TGTGCATTAC TGTATTNNAN CTTGTTGCTT 180  
AGTTTCTNCA TGTATTNNTN CAGTAATGGC TGANAGTGTT AACTGTNCCA TACTTTTNGC 240  
10 ACAATGTNCT GCATAAGGTT ACCTGTGTAC AGAGTTTAC TTAGNTTAN CTAAAAATATT 300  
GCCTGGGTTT AGTNTTNATT TCCATTNTN 329

SEQ ID NO:6201

SEQUENCE LENGTH:150

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07362

SEQUENCE DESCRIPTION:

20 GATCTAGGAT GTGGNTGTGG AGTACTTAGC ATCGGAACTG CAATNTNAGG AGCAGGGTTG 60  
TGTGTTGGAT TTAACATAGA TGAAGACGCA TTGGAAATAT TTAATAGGAN TNCAGAAGAG 120  
TTTGANTTAA CAAATATTGN CATGGTTCAN 150

SEQ ID NO:6202

SEQUENCE LENGTH:142

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07363

SEQUENCE DESCRIPTION:

30 GATCCAGGCG CCTGGGCAGA GCACCTGCTG TCTGCCCTGC ACTTTGAAGG GTTGTCTGTG 60  
GGATTGAAAT NAACCAACTG CCGGCTGAGC GGAGGCTCCC TGGGAGTNAC AAGTTCCGTA 120  
TTAAAATGCT TTCAGTGGNA AA 142

SEQ ID NO:6203

SEQUENCE LENGTH:294

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07364

SEQUENCE DESCRIPTION:

40 GATCTATAAA ATTCAGTTT TAAAAAATGT GTTAAGGCTT TGTTTTTGGC CTAACAGGTG 60  
GTCTATAAAG AAGNAAGTTG TATGAGGTAA TGAGAAGGCT GTGTATCCTG ATGTTGTCTGA 120  
GGAGTGTCT CTATACCTTC ATTGAAATA ATTGTNTTTT TACTGCCCTC TAGTCTTCTG 180  
45 TTTCCTTACT AATATNCTCT CTTGTNTTAT TACAGAAAGT GGNGTATTGC AATATCCTAC 240  
TATAATTGTN TTGCNCTCTT TGTGTTNATC CCAGTNTNNG TNAGTNTANG CTTN 294

SEQ ID NO:6204

SEQUENCE LENGTH:306

50 SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS07365

SEQUENCE DESCRIPTION:

5 GATCCCAGCC CGGCCTTTGT GGGACTAAGG TGGCGCTGAG TGGGAGAGCA GCAGGCGATG 60  
CGCGAAAGGC GGGACTTGGA GGTCTGTGG GTTCCTGTGG ATAACCTCAA GGAGCACGGN 120  
ACCTGGGACA TGACTGCCCC CAGCATTCTT TCTGGCGGCA GACAGNGTTT GTNAGTTCGC 180  
CAACATCCTG CTTTCATGNG AACAGTTTGC TGTTTGCTNA CAGAGCCTCC AGTNGTATAC 240  
10 TGAGTTGGTC ACGACCNTNA TTNCTTCGNN CCTACAAACA TNTCCCACTT TTCGNTTNTN 300  
TGGTTN 306

SEQ ID NO:6205

SEQUENCE LENGTH:146

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07366

SEQUENCE DESCRIPTION:

20 GATCTTCAGT AAATATTTTG AAATGAATTC ATTTATGGAA GAATCAAANC TAGGTCAGAT 60  
TGTCCAAACC AGACTAAGAA ACTGCATAGG GTNTTTTATG AGGTNTTTAA TGACTCATCA 120  
GCNCCATTAT ANCTGANATT NCTACN 146

SEQ ID NO:6206

SEQUENCE LENGTH:298

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07367

SEQUENCE DESCRIPTION:

30 GATCTCACTG CCCAGGCTGG TCTTGAATC CTGGCCTCAA GCACTCCTCC TGCCTCACCC 60  
TCCCCAAGCG CTGAGATATA GACCTGAGCC ACAGCGCCTT GCCAGTTGTT TTATGTTCTT 120  
TATCCTTTTA CCTGCTTGCC TTCTGTAACC TGGGTTGCAT TAAATTTACT CCTACTNGTG 180  
AGTAAATGTG AACCATAGCA ATAAATTTAG TCTATCCCCA GAACCTTCAG TAGCAAGGAC 240  
35 CNATATTNCT ACGGTATTTG TNTGTGTCCA NANANAAATA AAATTACCTT NAAAAANN 298

SEQ ID NO:6207

SEQUENCE LENGTH:28

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07368

SEQUENCE DESCRIPTION:

GATCATTAAG GATAAACATA TTTTAA 28

SEQ ID NO:6208

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS07369

## SEQUENCE DESCRIPTION:

GATCCTGTTG GCAANGGGAA TGTAGAGCTT CCAGGGTGCA TTGCCCACTG TTCTCATTGC 60  
 ATCCCAGTCC TCCAAGTCAG TCTAGCCTTA CTGTACACTT GACAAGTGCT TACTCAGCAA 120  
 GTCCCAGACC CACGNCCTNT TATCTCCNAA GACTGGNTTT GGCCATGNCC TTCCTCATCA 180  
 GGCCTATGCG CANNANTATN TAGGN 205

SEQ ID NO:6209

SEQUENCE LENGTH:302

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07370

## SEQUENCE DESCRIPTION:

GATCCATTTA ATATGTTATC CCCACTAATT AATTTTCGTA TATNATTTCC AATATTTGGA 60  
 AAGCTCTTTA TAGCCATTG GTATTTCCCTA TTACCCACCT CCTATTTTAA ATATTTATCA 120  
 GTCTAAACTT GTGCAGTGTA GTAAACATGC AAGTTGTTAT GCTTGAGCTG TATTACCATA 180  
 AGTNGCNTTT TANGTAACT GGTGNNTTGT GGCCATAGAT GTTTTTGCTT TTTGTTTGAT 240  
 TTTNTNTTNC AGGCTAACTG TTNGNGGTAT ACATNTATTT NTCTGTTGTA CAGATTTGAA 300  
 NN 302

SEQ ID NO:6210

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07371

## SEQUENCE DESCRIPTION:

GATCCCCAC ACCAGCGCCC AAGAAAGGAC CAGCGTTGCA CAGCCCGGTA GAAAGGGTTT 60  
 ATTTATGCGC AACGGTTCAC ACAAGCCTTC CTGAAATTCC ACTTTACAGT AAATAAAGCT 120  
 GTGCGTTTCC CCTTCCCATG CACAACTGCG TATCAATCTA CAACTGTCAT TTAAGTGTGA 180  
 AAAAATAGNG CGTCTCCCCT TTTGTCATCG TTCTGGTAAC ATTTGGCGTA GCATCTGACA 240  
 GCACGGAGNT GCTCACTCCT GGACCGGTTA TTTGGTTAAA ACCCAAATG TTAGGTCGGA 300  
 N 301

SEQ ID NO:6211

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07372

## SEQUENCE DESCRIPTION:

GATCCATTTA ACTATTCATC AGAGGTGCTG TAATTTTAAA TTGTCTCTTG TCTCCTTCAG 60  
 TTAATTTTCA GAATTAAGAAA CATACCATGG GNAAGAAAAA CNCNAANCAN N 111

SEQ ID NO:6212

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07373

SEQUENCE DESCRIPTION:

5 GATCCTGGAA ATNAGATGGG CCTTACTCTG TCGACTAAAT GAATAGCTAT TTTCTTGTCA 60  
 TTTTITAAAG TGCAACTCTT GCTTCATGCT GCTTAAGTTA CCAGATGAAT GCTGNGAAAT 120  
 AAGTAATCAC AGNCATTTTA ATACCATTTC ATTGCTGTTT TACGCGTGTT CATTACTTAA 180  
 CAAAAAATTA TCTTTTAGCT TTAAAA 206

SEQ ID NO:6213

10 SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07374

15 SEQUENCE DESCRIPTION:

GATCTAGCCT GCCCTGCCTG CCTGCCCTGG GCGATGAGGT ACGGTGGGGA AGGTGCCTAT 60  
 TTTAGAGAAC TTTGTCACAG TATTAAAGTT CCCAGAACAA A 101

SEQ ID NO:6214

20 SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07375

25 SEQUENCE DESCRIPTION:

GATCTAGAAT GTAACATAAT TGCTTATAAA TGTCAGAGCA TTTTNAAG GTACAGTATA 60  
 TGGGGATTGT NTCGTTTTTC CTAGCAGGGG AACCTTAGTT AATANTAAAA TACTACTTAT 120  
 TTGAGTTACT GNTACAGNTT CATTAAAGGC TTGTGTGCAA ATGTGGTCTC ANTCTTTTTT 180  
 CCCTCCATGA TTTTCCTATG TGCTTCCTCT GGCATTCACT GNGGTTTTGG TAAANTAANT 240  
 30 TGCCNNTTAA NN 252

SEQ ID NO:6215

35 SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07376

SEQUENCE DESCRIPTION:

40 GATCAGGAGT ACCTCCCTCA AGAGTCGAGG GNGGTAGATT TCTACACGCA GAGGAGGTGC 60  
 TGA CTCTCA GGGCACGCCA GCAGTNGNNT GTTGCTTTN TAAGGGAGGG CCACTAAGAA 120  
 AGTTAGTGGA TTGCAAAGTT GGTTGCCTGG TGGNAGTTAG ANCAGACCAA CATTATATGC 180  
 CATAACTTTA NGAGTTCCAT AGGTGGCGGC GCAGTTCTTN CGNATCAATG TNAACCTTG 240  
 NGGGGGGTGT TCATTN 257

SEQ ID NO:6216

45 SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS07377.



## SEQUENCE DESCRIPTION:

GATCAGACAT AAACCTAGCA TCTTAATGGA AGAAAAATGA GGGGAACCTC AATTATGATT 60  
TATTAAAGAC AATTTCTATT ACACCCTCCT TTATGACAAG TGACATTTTA GATGTAAAAG 120  
TAAANCTTT ACCATGCCTT TTTTTTTTTT NGTGGGCCTA CCTTNGGGGC NTNAANCCCN 180  
GGGGNNCCN 189

SEQ ID NO:6217

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07378

## SEQUENCE DESCRIPTION:

GATCTCGCAA TGTCTGCCTT AATATTTTAC AATTAAACCT TTCATATTTA TTATAATTTG 60  
GTAATATTCA TTAATTTTCC TGTCTTTTAA AAGTCTTGAT AGATTTGTCA AAGTATATGT 120  
NCTTTTCCCT ATGCTGGTTT AGAAGTNCGA NATATCACTT CTAATAGTAA TTATGCTCAA 180  
NTAGGTACAC ATATACATAC ATNTTCTCT CNCNCTTTAT ATACTTNTGT GCAATTGGCA 240  
CTTTTGACGT ATGTCATANN NNTGTCATNC CN 272

SEQ ID NO:6218

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07379

## SEQUENCE DESCRIPTION:

GATCCTCGGC CTCCCAAGT GCTGGGATTA TAGGCATGAG CCACCGTGCC CAGNCTAATT 60  
TCTAATTAAT TAAA 74

SEQ ID NO:6219

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07380

## SEQUENCE DESCRIPTION:

GATCTCGTCT GCTCACCTTA GCTTTCTGCC TTGGCAGCAC GGGCTGCGGA AGAAAGCACG 60  
CTGGGCCAGG AGGCAGGGGT GCCCAAGCCA CAGGGAGCCC CTGGGAAGC CTGCTCCATT 120  
CTTCTGGTGA CCTTGGCGCT CCTTCACTCA TCTCCCTGC CCCCTCAGGA ACTGGTGGCC 180  
CAGCTTCCAC ACCNNCACCT CCCAGTCTCT AGNCTATCCA TCTGTCTGTG TATGGCCTGG 240  
AGTCACTNCT TCCTCANGCC CCCAGGGNAA NGTGTGCTCA AAATAAAAAC CAGNGGNCTG 300  
AAA 303

SEQ ID NO:6220

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07381

## SEQUENCE DESCRIPTION:

GATCCCCTTT CCCACATCCG TGCTGTGTCA TTGTTGCTCT GCTTCCTTTC AATGTGTCAG 60  
TGCCTGGGGG GAGGGGAGGA GCACCCCTC AGCCCCCTG AACCTGACCA AAAGCCATGG 120  
CTGTTGCTCC NNNCTTTGTA TGATGCAAT GCTGAAATGT ACAAATCAA CCATGACAAC 180  
AANGAAAAAG GCCTTGTA GCAAA 205

SEQ ID NO:6221

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07382

## SEQUENCE DESCRIPTION:

GATCATAAAA ATGAAGGAAA ATGCCCAAGC ATATCCCCAA CCCCTCACCC CACAACCACC 60  
ACCACCACAC ATAANCAAGT TGCTGACATA NNAGGGGGAC CTTTTNANN 110

SEQ ID NO:6222

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07383

## SEQUENCE DESCRIPTION:

GATCGCATCT CATTGTTAAC TCTTTACTGA TATGTTTGT AATACAGAAG TGAAATGTGG 60  
ACATAAAATA GTTACGCTAT TTGGTTAATG GTACTAGACA ACATGTAATT AATGACATTC 120  
AAAAATTTAT GGCTAGTGAT ATATATAANG TAAAATTTTC TTTGCAGTAA AATATGCCCT 180  
TNATTATNGN CGGGNGGCTA TANGGNCCA ACAGTTTGTG TGAAANTAGC TCCNAATCAT 240  
ATCTNTNN 248

SEQ ID NO:6223

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07384

## SEQUENCE DESCRIPTION:

GATCCCTTTA CACTCTTCAA AAGTGNGAAC CCCAAAGAGT TTTCATGTAT GTGGGTAAAA 60  
TCTATTGATA TTTTCTGTGA GAATTTAAAA ATTATGTAA AANAATAAGA NGATGACTA 120  
TTTTNCAAAA CAANANATGA GNTGN 145

SEQ ID NO:6224

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07385

## SEQUENCE DESCRIPTION:

GATCTGCTTG GTGAAGAGTT CAGGAAAGTA TATCAACAAA GGNGTGAANT TTGTGAAGAG 60  
AAATNNTATC ATCAAAATTG GGTAAGCAT AGNTTTTTTG TATGTTACCA CTAGATGTCA 120

GCATANCTN

129

SEQ ID NO:6225

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07386

SEQUENCE DESCRIPTION:

GATCAGAAAA CATTGATTTA TATTTTAAAA TAGGATATTG GAGCCATTGT CTTAGATAAT 60  
 TTTCAAGGCA AGANCAAGCC TGCAATAAAT ANTGAGNCTT TGACATTCCT TGGCGCGGAC 120  
 GATGTCTCCT GCCCTANTAT GACTGTCACT CAGCAATTC AATTTTATGN NTACTTGATT 180  
 TAAANCGGGA GGCTANACTT GNTCTGAAAN GN 212

SEQ ID NO:6226

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07387

SEQUENCE DESCRIPTION:

GATCTTACTG AAGATGATGT TCCAGCAGCA GCGACTTAGC CCCAGGAGCC CAGTTTCAAT 60  
 GGCCTTGCTG TGTGGTGTTC CAAGTGCATT TAAAATGTGT GACACAGNAA CGGCACACTC 120  
 TTNCACATGC TTTTGNAGTA TTATAANNCA CTTTATTACA AATTGTCTT NGCTATTAGC 180  
 AAATANAACT GATTATCATT CTTTATTAAC CCACCTNGGC CTTTNNAAN CCTCN 235

SEQ ID NO:6227

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07388

SEQUENCE DESCRIPTION:

GATCTCACTC TTNCCAAGC TGGAGTGCCG TGGCAAATC ACAGCTCACT GCAGCCTTGA 60  
 CCTCCTAGGC TCAAGCAATC CTCCTACCTC AGCCTCCCAA GTTGCTGGGC CTGTAGGTGG 120  
 ACACCANCAAT GCCCTGTTGA TTTTNAATTT TTTTATATAG AGTTGAGGTC TCGGTATGTT 180  
 GCCAACCTAG TCTCAAATC CTNGGCTCAC GGCTGTAATC CCCAGCTCTC AGGGAGGNTA 240  
 AGCGGCGGNN GGNTAGCTTA AGCCNAGGAN TNCGAAGNCC TGNCTTNGGN 290

SEQ ID NO:6228

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07389

SEQUENCE DESCRIPTION:

GATCCATGGG GCCCAGGNCT AGAGGGCATC CGAGGGGCTG GGCCTTGGCC ACAGCCTCTT 60  
 GGATGATGTC CTTGCTCCAC CACGCAGGCC CTTGCTTCTC CCATCAACGA GTCTTGGCCC 120  
 AGGGGACACT GACCCTCCCN CAGGGAGGAG AGAGGAGTTC CTTNCCTTTA AACGAGGGCT 180

TCCACGACCT CTAAGGGGTG GCGNGGAAGG GAGGAGGATG AGAAGATGNA GATTAAATAA 240  
AGGTATGTN 249

5

SEQ ID NO:6229  
SEQUENCE LENGTH:125  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS07390

SEQUENCE DESCRIPTION:

GATCTATCTC AGGGCTTGTT GTAAGAATGA AATGAAGTAT AAAGCCATGT AGAGCTTGTA 60  
GAATATGCCT GGCACTTTGT AAGACCTTAA TANNTGTAA CTATCTAANC ACANAACAA 120  
CCNCN 125

15

SEQ ID NO:6230  
SEQUENCE LENGTH:71  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS07391

SEQUENCE DESCRIPTION:

GATCCTAGTG CTCCTGTCTG GTCAGGGCCT ATCTTTATGT GTTCGTAA CTTTAAACAA 60  
TGAGNATTAA A 71

25

SEQ ID NO:6231  
SEQUENCE LENGTH:182  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS07392

SEQUENCE DESCRIPTION:

GATCTGAAAA GTTATTAAGT TCAACTCCAC AGAGGTTTCCT AGGAGAATGT TAACAGTCCA 60  
GACCTTTTTC ACTACATCAA CCACGGATGA TTGGCATATA AAATCCTACT TAACCTTTAC 120  
ATAACTGCAA TACCAGGAAA CAAATATGTC AATAAAAGGA AACATCATT CATTTTTGGA 180  
AA 182

35

SEQ ID NO:6232  
SEQUENCE LENGTH:233  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40

CLONE:HUMGS07393

SEQUENCE DESCRIPTION:

GATCCAAAAA ACCATTCAGG CCAAGTNACC CTGACATGTG ACATCTACCT CCCGACCTAC 60  
CACCCCACTG GCTGGTTCCA GAACGTCTCT CACCTAGACC TTGCCTCCCC TCCTCTCCTG 120  
CCCAGCTCTG ACCCTGATGN TTAATAAACG CAGCGACGTG AGGGTCCTGC TTATCCCTGG 180  
TNNGGNNNCA GNTCNATCCT TGCATCANTG GGGAGGACGT GATGNGTGAG GAN 233

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SEQ ID NO:6233

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SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07394

SEQUENCE DESCRIPTION:

GATCAGCCTG TGCCACACTT CGCTCTTGAG GAGCTCAACG GTCTGGCAGG GCAGCAGGAG 60

GCTTTCTGGG CTCTGGNCTC CACGGATGCG TGGGCAGNGG AATGTGGGCT ATGTAGTCAT 120

AATAANTTAG GNCACAGAAA AAAAAAANAA AAAANNCN 158

SEQ ID NO:6234

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07395

SEQUENCE DESCRIPTION:

GATCTCTTTT CATTTGTCAA CCTTTTCAGT AAAGCCCTCT GTTACATCAA A 51

SEQ ID NO:6235

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07396

SEQUENCE DESCRIPTION:

GATCAGCGAG AAGGACAAGA AGAANNTTCT GGACAAGTGT CAAGAGGTCA TCTCGTGGCT 60

GGACGCCAAC ACCTTGCCG NGAAGGACGA GTTTACGCAC AAGAGGAAGG AGCTGGAGCA 120

GGTGTGTAAC CCCATCATCA GCGGACTGTA CCAGGGTGCC GNTGGTCCCG GGCCTGGCGG 180

CTTCGGGGCT CAGGGTCCCA AGGGNGGGTC TGGGTCAGNC CCTNCCATTG AAGGAGGTGG 240

NTTAGGGGNC TTGTTCCTT TNGTATGTTT GTCTTTGNGN 280

SEQ ID NO:6236

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07397

SEQUENCE DESCRIPTION:

GATCTAAATA CTGTGTTAAA ATATAGAAAA ACGGAGACTC TNATAAGGTT TTNACCTCT 60

ACACTTGAAA GTGAGCTCTT ACAAGAAACT AATCAGTGTT TCGTTATTCC ATATCAGTGG 120

CTTTTACTGT CAACGNTTGT GTAAGCTNAC TTATCTGGCA AACTTTTCTT TTCCAGAANT 180

ACTATCTATN TTACTNTNN 199

SEQ ID NO:6237

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07398

## SEQUENCE DESCRIPTION:

GATCCACCCA CCTCGGCCTC CCAGAGTGCT GGAATTACAG NCGTGAGCAC CGCGCCTGGC 60  
 CAAGNAAAAA TTATTAGAAC AAGTGAGGCA TCACACTCCT CTGCCATTCA GTCAAAAGTA 120  
 NGCACCAATT TATTAACACA AACATTACAT AATACATGAT ACAGGCGCAA TCTCGCTACT 180  
 GCTAGCACTA CGNNAATGTT GTTCTTGAC TATAACATTA AACTGTAAA TACTGACAGT 240  
 GAAATGCACC NATANNGGNN ACCTGTCATC ACNGGGNNN 279

SEQ ID NO:6238

SEQUENCE LENGTH:21

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07399

SEQUENCE DESCRIPTION:

GATCCAAAAA CTAACCTCAA A 21

SEQ ID NO:6239

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07400

SEQUENCE DESCRIPTION:

GATCCAAGTA CTCTCTCTCC TAAAGACACC ACCTTCCTGC CAGCTGTTTG CCCTTAGGCC 60  
 AGTACACAGA ATTAAAGTGG GGGAGATGGC AGACGCTTTC TGGGACCTGC CCAAGATATG 120  
 TATTCTCTGA CACTCTTATT TGGTCATAAA ACAATAAATG GTGTCAATTT CAAA 174

SEQ ID NO:6240

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07401

SEQUENCE DESCRIPTION:

GATCTTGAAG AGACCGCTGG CAGCACCAGT ATTCCCAAGA GGAAGAAGTC TACACCCAAG 60  
 GAGGAAACAG TTAATGACCC TGAGGAAACA GGCCACAGAN GTGGCTCCAA GAAAAAGAGG 120  
 AAATTCTCCA AAGAGGAGCC GGTCAGCAGT GGGCCTGAAG CGGCGGTTGG CAAGAGCANC 180  
 TCCAAGAAGA TGCAANAGTT CCATAAAGCA TCCCNAGGAN GNTTAAGAAT GCAAATGGAC 240  
 CATTCTCTTG GNNGGTTNGG NCATACCCAT NAGCCCNAGG TGACATTTCC CNTN 294

SEQ ID NO:6241

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07402

SEQUENCE DESCRIPTION:

GATCTCGCCC TTACCCCGGG GTCTGGTGTA TGCTGTGCTT TCCTCAGCAG TATGGCTCTG 60  
 ACATCTCTTA GATGTCCCAA CTTTCAGCTGT TGGGAGATGG TGATATTTTC AACCCCTACTT 120

CCTAAACATC TGTCTGGGGT TCCTTTAGTC TTGAATGTCT TATGCTCAAT TATTTGGTGT 180  
TGAGCCTCTC TTCCACAAGC GTCCTCCAT GTTTGGNTAG CAGTTGAAGN GGTGTGTGGG 240  
TGGGCTNTTG GGNGTGAGGA TGGAGTNTTA AGTGCCNACT NNCNCTNNN ACCNN 295

SEQ ID NO:6242

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07403

SEQUENCE DESCRIPTION:

GATCTAATCC CTTCAAGGAA GTGATAACAC TGGGAGTGGT AACAAGAGGA GCAGGGAAGC 60  
AAGGGCCAGC CCCTGGTTCT CCATCCCNAT GTGTTNGAGG GTGGGACCAG NTGGACCTGG 120  
TCCAGGCCAG GCCTCATTCC TCCTGGNCCN GGCAGGGTCA GAGGGNGGAG GGGCNTGGTC 180  
CAGGNATGGG TCCNTTCCAN N 201

SEQ ID NO:6243

SEQUENCE LENGTH:26

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07404

SEQUENCE DESCRIPTION:

GATCTTGCCA GTTGATAAAA CGTAAA 26

SEQ ID NO:6244

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07405

SEQUENCE DESCRIPTION:

GATCGNTGCC TGGTTTGTCT TCTCTGTGTC CTGGAGCAAA GCCAGTTCCT AAAACTAAAA 60  
CTCCATTCTA GTCTTGGGAA GAAAAGTTTC TACTCAGAAC TGGGGAAGGA GTGGAACCTTA 120  
TGAATTGGGC CTCTAGGCTG TCTCTGTCCC CTCAGCTCCC CGACATGCAT TACTCTCTG 180  
CCGTGGGTCT GCAGTCGCTG CAACCTACCC TCTCTCTGCC TCAGCCTTAC ACCCAAGCAG 240  
TAGGTCTGTG CTCTCCCTGT CTCTAGGTCG NTGAGAGAGG TGCTTTTNTT CATAAAACCT 300  
TTGGGGTTTG GGATTTCCTC AGAN 324

SEQ ID NO:6245

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07406

SEQUENCE DESCRIPTION:

GATCCATTCC GGCGCCTTCC TCTCCAGTC ACCCAGAGGG CCCCAACCCC GGCGGNCCTT 60  
TCTTCCTCAA ATGTCCTCGG CTCTATACCG TGNCTGGGTC TTTTNTCTNT CTCTCTGCCT 120  
GGAAGATTCC TTCTTTNCCC TTTTGTCTTG CCCACTACTG TTTACCCTTC AAGTTTCAAG 180

GTCATGTCAC TGTCTNAGAG AGGTTTTCCT GTGNTNGACC TGTTTTTNAT CAGGAAGGCT 240  
TGCTNNTTTC CATNAN 256

5 SEQ ID NO:6246  
SEQUENCE LENGTH:37  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS07407  
SEQUENCE DESCRIPTION:  
GATCATTA AAA CCTGGCTTGA GTCTCTGTTC TGGCAAA 37

15 SEQ ID NO:6247  
SEQUENCE LENGTH:152  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07408  
20 SEQUENCE DESCRIPTION:  
GATCAAGNTT GNTCTTCTGT GATATATGGG ATATNATGTT TTAAAGACCA TCTTGGAATA 60  
CAATTAGAGA ACTTAGTATT TTGATGTACT AAGACCTATT TTAAGTTTAA TATTCTACTT 120  
TGCAAAANCT TTAATTAANG ATGTTATTAA AA 152

25 SEQ ID NO:6248  
SEQUENCE LENGTH:213  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07409  
30 SEQUENCE DESCRIPTION:  
GATCCTGCAT TAAGAAATTC AAAAATCAGT TAATCATCGT TACATGTTGT AAAAGTTGGA 60  
TACTGACAGT CTCTAATAGT TTATCATCCA ATNGCANGTA ACCTACAATT TTAGGCATAA 120  
ACGTTGATGT GTATAANCAAT GNATACAACG CTANTGGCTG GTCACAGTGT TTTCNCAAAC 180  
35 TACAGNTCAC ACCANGTNTT TCTCCTNTTC CTN 213

SEQ ID NO:6249  
SEQUENCE LENGTH:274  
SEQUENCE TYPE:nucleic acid  
40 TOPOLOGY:linear  
CLONE:HUMGS07410  
SEQUENCE DESCRIPTION:  
GATCTCCTCT TAAGCGGAAA AGAGATTGAC CTTCTAGCAG AGGCAAAGAA TGGAGTCTTC 60  
45 TGGGGGCAGC TGCAAAGCGT TCTCCCTAGG ACAGATGGAG CCTCCCTTC CTCATCTACT 120  
CTGTGGGTGG TTTCAGGGCC CACGAGTCAA CATNAGGAGT TGTGCTGGTG GTATGTGTGT 180  
TGGAGGCTGG GCTGGCTGAT TCACAGTGAC GAGGATGTCA CTAATANCAN GTATTGCGAN 240  
TGNTGATACC TAATAANAGN CTTTTTTTCC CAAA 274

50 SEQ ID NO:6250



SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07411

SEQUENCE DESCRIPTION:

GATCACCATG CTTGAATGTC CTCTACTGCT GATTCTAACA TCCGTGTCAG TTTTGGACCG 60  
GTTTCAGTAG ATGGATTTN CTCNNGNNA TGGGCCATAC TTCCTGCAT TCTTGCATG 120  
CCTCATAATC TTTGATTGGA TGCCAGACAT TGTAATTTT ACCTTGTTGG GTATTGGATA 180  
TTTTTGTATT CCTATAAATA TNCTTGNGCT TTGAAA 216

SEQ ID NO:6251

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07412

SEQUENCE DESCRIPTION:

GATCTAATTT TGTATGTGGG AATCTTGCCT TGCCCTGATT TCCAGACCCA TAGGCAGGCT 60  
TGCAGGCTGT AGCTGGGGAA GACCCACGC TTATNCTGGT GCCCTGAGCA AGCCCTCCTG 120  
CTCCACTATT AGGCAGAAGC ACCTGTTCTG CCACAGGAGG CGCTGTCTTT TGCTGGCAGA 180  
GCTCAGTTTC CCTTAAGGGG AAGTTCCTTA GGATTTAAGG CCTCATGACT ATCTCAAAC 240  
CCATGTTTGT TTGCCAATAA AGNAAATAAA TAACTGTAA AAAANNAANN AACNACCANN 300  
NAAAAACAC NAACANCAN 319

SEQ ID NO:6252

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07413

SEQUENCE DESCRIPTION:

GATCTACTGT TTGCATGTAA GAGACCAGGN TATGTAAGTC TTATATTTTA AGTGATACA 60  
TATTGTGTAT ATAACATATG GATATTAATA ATGGGGANTT GCACATTAA A 111

SEQ ID NO:6253

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07414

SEQUENCE DESCRIPTION:

GATCCCAGGA ACTGTGGGCA CCCATTTTNT GTGTCTCCA GCCNATTTC ACTCCTAGTT 60  
TGTCATGGNT ANTTTTTGT CTTCCCTGTG TGAGGGGNGC CATCAACN 108

SEQ ID NO:6254

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07415

SEQUENCE DESCRIPTION:

5 GATCACAACC ATCAGCATCA CGGCCACAGC AGCCAGTGTT GGGGCTGCTG GCATCCCCCA 60  
GGCGGGTCTG GTCACCATGG TCATTGTGCT TACGTCGGTC GGCTTGCCCA CGGAAGACAT 120  
CACGCTCATC ATTGCCGTGG ACTGGTTCCT TGACCGGCTT CGCACAATGA CCAACGTACT 180  
GGGGGACTCA ATTGGNGCGG CCGTCATNGA GCACTTGTCT CAGCGGGNGT GGAAGCTTCA 240  
10 GGAAGCTGAG CTTACCCTAC ACAGNCTGGG GAAACCCNTA CAAGTCCCTT AATGGNACAG 300  
GACGCAGGGG AGCATAN 317

SEQ ID NO:6255

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

15

TOPOLOGY:linear

CLONE:HUMGS07416

SEQUENCE DESCRIPTION:

20 GATCGAGACC ATCCTGGCTA ACACGGTGCT GGCGGAGATA AACTCCCTT GAAGCAGTGG 60  
AGTACAATCA AACATCTTGG CTGCTCCTGA AACCNGGTCC CACGNATTTC AGTCCGGCTA 120  
AGANCGAAGA GCTGGTAAAC CANTAANTG GGTGGAGGCC GAGAGCTCGG GGCCGCGAGC 180  
AAGCCTCCGA CGANNTGGTC CCCTGGACCN NCNGGTTN 218

SEQ ID NO:6256

25

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07417

SEQUENCE DESCRIPTION:

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GATCTNACTC ACAGAGGGAA GAACTTATAA TTCTTCACAG GTCACATAGA AGCATGANAA 60  
TTTGGGTTCA AGCAAGTAAA TTCTAAATCA GAATCCATAC ATAAAGTGTT TGCAATGTCC 120  
AGTTATATCT CCATGATATT TNCTTTGTGG AAGTTGATTG TCCTTCCTTA CAATAAATTG 180  
CTTGANTTGT CAAA 194

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SEQ ID NO:6257

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

40

TOPOLOGY:linear

CLONE:HUMGS07418

SEQUENCE DESCRIPTION:

45 GATCCTGTGT ATTTCCCTGA GTCTTCTAAC ATATGAAAAT TCATATCTAA ATCAACAAGT 60  
GACTGTAATC TGGTACTATA AATACTAAAT AAACACTTCT TCATAACACT GTACCAATTC 120  
AGCTTTTAAA TTTNATTACT TTGCTTTTCT GTCCTTTGCC AACTCTTAAC CTAGTTAATC 180  
CTAGTNCTGT TGACATTGGA CCAGGCTCAG TAAATAANCG AATGGATTTC CAGCCTTTTT 240  
TTCCCATCTG TNCCTGCTTT TANGTCCTCT GAATCTGCTT CTTTGCTTNC TGCTGCTTTA 300  
ATTTTANCAG TGNTTTTNGT CAAAACATAG GNTNCAGGGN CTNNN 345

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SEQ ID NO:6258

55

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07419

SEQUENCE DESCRIPTION:

GATCTGGGTT CTAGAGGGCA TGTGATGACT GTAAATGTTT ACTGGGTGGG TAGGGAGTGG 60  
TATCCAGTGT TCAAGTGCAG AAATCTTTGG CTTNGCTACC AGTTCCATAT GATGAGAAAT 120  
AAACGTTTCGC TGAGGTTTTG TTTCATAAAA AGANNNNNAA AANNTCN 167

SEQ ID NO:6259

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07420

SEQUENCE DESCRIPTION:

GATCCACACT TTAAAGAAA TTCCATAAAT GTATATTTTG TATTATGTAT TATTCCTGG 60  
TCCNAAGAAA ATATGTGAAT TCAGTTCTAA CTTNNGGANT GTACTGTTTG TTTTCANGTT 120  
CATTGNAAAN 130

SEQ ID NO:6260

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07421

SEQUENCE DESCRIPTION:

GATCCGAGAT GGCACCATTTG TACTCCAGCC TGGGCAACAA GAGCGAAACT CCGTCTCCAG 60  
ACAAACAAAC AAANCAANAA CAAGTGTCCT TATNNGNATG GGTGTGTTN 110

SEQ ID NO:6261

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07422

SEQUENCE DESCRIPTION:

GATCTGGCTG TCTAGAGGGA TTCTACGACT GCGTGCTGCC GCCTCCCCAA GAGGCATTCA 60  
GGTTATTGGA GAACTAATCT CATCTCAAGG GGCCAGNCAC CAAGTCCCCA AGCCTACAGA 120  
CCTCTTTCCG CCAGGCCCTG AAACCTGGCC CCGTGCCAGC AGGATGACAA GCCCCAGGGC 180  
GNTCCTGATG AATATGGCTT GGAGATGNTG TACAANTTTT TATTNCCCTN TGGNTTTTGA 240  
GGNATGAAAT GATTTGCACT TTTGAAAACC TGTTAACCGT AGGCCNCTTN GGNCANTGAN 300  
GNNTGGAAGN 310

SEQ ID NO:6262

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07423

## SEQUENCE DESCRIPTION:

GATCCACTCG GNCAACCCAA CAGTTTACC AACCACCCCG GGCTCGGAAC TAATAGGNAA 60  
AGTAGACTCT TTGTGAAGAA ACGAGCCANT NNCTGGAACA CCCTGGTGGA AACCTGTTGA 120  
CANGCCCTN 129

SEQ ID NO:6263

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07424

## SEQUENCE DESCRIPTION:

GATCACTTGA ATGTTAGGNT TCATAGNACT ATACTAATCT TCTCACAAAA GGTCTATAAA 60  
ATACAGTCGT TGAaaaaaat TTTGTATCAA ANTGGGGNGG CAAATTNGAA GCTTCTCCTT 120  
AANCTGTATT GATACTGACT TGAATTCTTT TCTANAN 157

SEQ ID NO:6264

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07425

## SEQUENCE DESCRIPTION:

GATCTCCTTC TTTAGCTCAA GGTGCTGCA ANTTGGAGCT GAGCTGTCAG TGGAACGNGT 60  
CCTGGAATN ATTAAGCAAG GCGTCGTTGC GCTGCCCAAN GACAGACTGA AGAAATTTCC 120  
AGANTTGAAA TTCAAATATG TGGAAGNGGA GCAGCCCGNG GNGTTTTTAT N 171

SEQ ID NO:6265

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07426

## SEQUENCE DESCRIPTION:

GATCCTACAT TTACAGACAG TTTTGTGATA ACCCTTTGCA TTGCAGCACC TAGTACAATT 60  
CCTTGGAAC AGCGTGGCTC AATAAATTTT TATTGAATGA ATAAATGTGG GCCCAGAAGC 120  
GTGCTAGANG AGTGCCTTTC TGGGCTACTN AAAAAANNA AANACNAAN AANN 174

SEQ ID NO:6266

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07427

## SEQUENCE DESCRIPTION:

GATCAAAGAC TCCCTGGAGC GAGAAAACAG TTA CTGCCAG AAGCAGAATG GAAGAGCCAA 60  
AAAGTACACA AAATGGACGC CATAANTTCT GAAATAAAAG TGTATGATGT GTTCTGAGTC 120  
AAA 123

SEQ ID NO:6267

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07429

SEQUENCE DESCRIPTION:

GATCTGGGCC TCAAAATACC ATAGTAGCTG CTTGATAAAA TTCTAAAAAT ATCTGGTTCT 60  
CTATTATGTA AACACTATTA CAGTCACCAG TGTGTGAAGA CTCTTGAGTC TGGTTCTCAT 120  
ATCAGAGTCA TCATTTTCT TCCNGTGGAA TAAANTGCCT TGTGGNCTC CAAA 174

SEQ ID NO:6268

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07430

SEQUENCE DESCRIPTION:

GATCTTTTCA CTGGCTGACT CTCCCATATC TGCAAGAGAT TCTGCAGGAA CTGGGTGTGC 60  
ACACGGTGTG GTAGCCAGTT CAGGTACTGN ATATTTAGGA TTTGGTGNCG TTCACTGTAT 120  
TGCTATATTT TTGTAGCTAA ATAAANTCTCA ATAANTTGTG AAA 163

SEQ ID NO:6269

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07431

SEQUENCE DESCRIPTION:

GATCTCCAGT ACTTTGTACA ATGTATAGTA TATTAAATAC ATTTATGTGT AATTTTGTGT 60  
GTATTTNTAT ATGGTATAAT TAAAATNATT ACATTTATGT GATTGTAAT CACAAAANGT 120  
ACTACTTACT ATATNCTGTA GNGTGTGTTG TGAATGTNTT TACCNGTGTG TGAGCATTAT 180  
GGNGTAGGGN TN 192

SEQ ID NO:6270

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07432

SEQUENCE DESCRIPTION:

GATCTTCTTT TGTAATGTTT TTCATGTTAC TGCCTAGGGC GGTGCTGAGC ACACAGCAAG 60  
TTTAATAAAC TTGACTGAAT TCAAA 85

SEQ ID NO:6271

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07433

SEQUENCE DESCRIPTION:

5 GATCCTAGTG AGGGATTGAT GAATGTTCTA AAGAAAATTT ATGAAGATGG AGACGATGAT 60  
 ATGAAGCGAA CCATTAATAA AGCCTGGGTG GAATCAAGAG AGAAGCAAGC CAAAGGAGAC 120  
 ACGGAATTTT GAGACTTTAA AGTCGTTTTG GGAACGTGTA TGTGATGTGG AAATACTGAT 180  
 GTTTCAGTA AGGGAATATT GGTGAGCTGC ATATATAAAT TTGACAGATA GCTATTTACA 240  
 TAGCCTTCTA AGTAAAGGCA ATGAATTCTC CATTTCCTAC TGGN 284

SEQ ID NO:6272

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS07434

SEQUENCE DESCRIPTION:

20 GATCAGTATT AACATCCAGG TTTTGATTGT TGTANTATGG TTACCTGGTA GATTACCTTT 60  
 GTATATAGGN AATAGACACT GGAATAGTAA GGNGTAGTGG GTCAAGATGT CTGCAACTTA 120  
 TTGTTTCAGAA TCACTCACAA NTGGGNAATC TGATATAAGG NCAAAANTGGG AGCACTGTGG 180  
 CCTNTTTTNN CAACTTTTGT GTACATCTGN N 211

SEQ ID NO:6273

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07435

SEQUENCE DESCRIPTION:

30 GATCTCATGA AGTCTTCCTT GGCCCAACCA GGCAGATGCC CCGGGCTCCA GTGGGGGGAG 60  
 GGGTCTGGGG TCTGGTCCGG GTTCCCNAAAT TTCTCTTNN CCCANATCNC TATTTCTACG 120  
 CAGTGCGNAT AAAATTTGGA NTCGACTAAA ACCCTTGGTG CCCNGAAAAN 170

SEQ ID NO:6274

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07436

SEQUENCE DESCRIPTION:

40 GATCTGCCCC CCTCGGCCTC CCAAAGTGCT GGGATTACAG ACGTGTGCCA CTGNGCTCGG 60  
 CCTCAGATTC CATATTTNAA CACCAGCTGA TTGAGAGAAG GGGAATNAGA AGAGCTGGAT 120  
 GAGTTTAAAT AACTTTNATT GTTCAGATTC CTGAACAGGN GTTGGGATAA TGGCCATCTT 180  
 TNCTTTCCTA TCCTTCCCCC CCTCACTGTG AAAAATAACA GTCCACCCCA AGTCATACAC 240  
 45 TGGACCCAGT GCCTGCGGGG ACAGGNCTGT GGGTTTCTTG GTCACACCTG TGTGGTGNT 300  
 N 301

SEQ ID NO:6275

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07437

SEQUENCE DESCRIPTION:

GATCCAAAA ACCATTTCNGG CCAAGNAACC CTGAAAANGNA ACATCTACCT CCCGACCTAC 60  
CACCCCACTG GCTGGTTCCA GAACGTCTCT NACCTAGACC TTGCCTCCCC TCCTCTCCTG 120  
CCCAGNTCTG ACCCTGATGC TTAATAAACG NAGCGACGTG AGGGTCCTGA TTCTCCCTGG 180  
TTTTNGGGGG GNTCCATN 198

SEQ ID NO:6276

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07438

SEQUENCE DESCRIPTION:

GATCTCTACT CAAAGATGTC TTGCAGTTTA TGAAGTGA TGTAACTTCA TGAATAACAT 60  
GATGACATCG TTATTAATA CATAAACTTT ATAAAGCTTA AA 102

SEQ ID NO:6277

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07439

SEQUENCE DESCRIPTION:

GATCTTAATA CCTAATTTCA TCATTCTGA AAATGTACTG TTTTAGAATG TATTACAATA 60  
TCAATGTGAA TATCTTGAAT CCTGTTACAA ATCCTGCACT GTATTAAACA TGTAATTA 120  
TTGTTTGTCT GATTAGCCAA TCTCACCACC CAAATGGGGA GGTATACATG TTTGANGAAC 180  
TGTGTAAGTC AGTAATTGAT TTGTNCTGAT GTTGTAAGTC ANTAGANGTG TTTTGAAGG 240  
NAGCATGGTG TGTGAGGCAG TGTCTGTCCT TTTGTGCCAG CTCTGTATGN TGTTGTNGG 300  
CCNTGTTTGT AGGCCTGN 318

SEQ ID NO:6278

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07440

SEQUENCE DESCRIPTION:

GATCTCGCCA ACAGCTAGCT GCTTAGGAGT ACCCCCACGA TACGCACAGC ACACCACTGT 60  
CCCTTCACTG CACTTTCTTC CTGCCTTAGG TAGTTGGGCT TGCCACCCCT AGTTTGCTTT 120  
TGTAAGTGGT TGGCAAGGTT AGAAGGCCTC GGCCTCTCTG TNATGCTGGG AAGTGCCTAC 180  
TCTCTGGGCC ACTGCTGCAG AGGCCGTGGC ACTTGTNATG GGTTTGAAG ACCCAGCCAT 240  
CTGCAGCAGA GGCAGCCTAT TCCCATTGCA AGGNGNGGAN TGAACGGAGT AATTATTCTA 300  
CTNTTCTTTT TACATAAATA N 321

SEQ ID NO:6279

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07441

SEQUENCE DESCRIPTION:

5 GATCCTGCAC GTCCGCAAGC CGGAGAAATA CCAGCTGCAC CTCCACGAGA GCTGCGTGCT 60  
GTCCCTGAAG TTTGCCTCCT GCGGACGGTG GTTTGTAAGC ACCGGGAAGG ACAACCTGCT 120  
CAACGCCTGG AGGACGCCGT ACGGGGCCAG CATTTCCAG TCCAAGGAGT CGTCCTCAGT 180  
10 CCTGAGTTGT GACATCTNCA GAAATAACAA ATACATTGTN ACAGGCTNGG GGGCCAAGNA 240  
GGGCACCGTG TATGNGNTNG TNTNCTTNGG CCATTNNCCC NTTCTGTNN 290

SEQ ID NO:6280

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07442

SEQUENCE DESCRIPTION:

20 GATCCAGTCT NTGGTATCAT GCTAGTNCTG ACAGGGCCTT GATAGTCTAG AGTTGGAAAA 60  
GATGGAAGC TTTTGTNAGN GTTTTAACAT TTNCTTGATG AAACAATAAA AAGAGGTAAG 120  
CTTTTNCCTN 130

SEQ ID NO:6281

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07443

SEQUENCE DESCRIPTION:

30 GATCCAGTTT TGTGTTGGAC CAAAAACCAG TATTGTACAA AGTATTAAGC ATATATTTTN 60  
ATATTTACTA AAATNGACTG TGGTGACTTT GGATAATAAG NAAAAATTTA ATATTAAANC 120  
CATGTTTATT ACAGTATAAT TAACATGTTA AACCATGGGG NTAAATGCCA TCANTAAAAA 180  
35 ATTATGNCAT NN 192

SEQ ID NO:6282

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07444

SEQUENCE DESCRIPTION:

40 GATCCACCCC CTGCCGCAA AACATTGCTC CTAATCCAC CGNCTGTCCC AAAACCTATG 60  
NGANCTAATG ATAATCCAC CACACTTTAC TGA CTNTNTT TCCAGACTCA GCCCGGCTGN 120  
45 ACCAN 125

SEQ ID NO:6283

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



# EP 0 679 716 A1

CLONE:HUMGS07445

SEQUENCE DESCRIPTION:

5 GATCTGAGTT GCAGCTCTGC ACCCTAAATC ACACCCTGGG CATTGTCTGG GCTGCAGGGC 60  
 TGCCAGGTTC TGTACTTGTG TCCAGCTATG GCCCTGGNTG CTGGAGCTGG AGGGTTTTCT 120  
 GTGCTCAGAC TGTAGCCTGT AGCTCTTGGC CTGTGTAGAG CCCCTCCTG TGCCCTCAGT 180  
 GGCTGTCGTT TGTAAACATN ATCAGGAAGA TGGGAAAGGT CAGGCAGNAT TTTCTGNCC 240  
 TACAAAGGN GGNNGAGAAA GGACACAGTA TTTTNAATGA NTTTACCATA TATCTTTGGN 300  
 10 N 301

SEQ ID NO:6284

SEQUENCE LENGTH:108

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07446

SEQUENCE DESCRIPTION:

20 GATCCTTGNT TTCTAAAAGC CAGTCCTNCC CTNCAGCTTT CCACAGTTTC TGTAATGTT 60  
 TAATACTTNT ACAGTCAATG GCAATTTTAA ATATATATAT ATAANATN 108

SEQ ID NO:6285

SEQUENCE LENGTH:159

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07447

SEQUENCE DESCRIPTION:

30 GATCTGGGGG AAAGGCTGCC AGGGCCAAGA GGCTCGTCTC ACTCCCTGCC CTGCCATTTC 60  
 CCGGAGTGGG AAGACCCTGA GCAAGCAGCA CTGCCTTCCT GAGCCCCNGT TTTCTCATCT 120  
 GTAAAGTGGG GGTAATAAAC AGTGATATAG GNGTGCAA 159

SEQ ID NO:6286

SEQUENCE LENGTH:125

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07448

SEQUENCE DESCRIPTION:

40 GATCACTGA CTCTTGTAAG CGGACCTATA CTCAAAAGGC TTTGGCACAC TGTCACGNTA 60  
 TTAGTATACA AATGTGCATT TGTGTTAAG TTAAANTGAG GTNTGCNGGG TAAACTGCNA 120  
 ANTAN 125

SEQ ID NO:6287

SEQUENCE LENGTH:63

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07449

SEQUENCE DESCRIPTION:

50 GATCTACAGT AATTTATTCT NTCTAAAAGT AAAGCATTTT CAAAACCTCAG TATTTAAACC 60

55

AAA

63

SEQ ID NO:6288

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07450

SEQUENCE DESCRIPTION:

GATCTTTTCC ACTGGNCTAC TACCTGACCA TAAACATGTC TGCATTGAA TTCTCTAAAC 60  
 CCTAAATCTG TGTCTATGAA AAATACAAAT GACTATTAAA TAAA 104

SEQ ID NO:6289

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07451

SEQUENCE DESCRIPTION:

GATCTACCCA CCTCGGCCTC CCAATGTGCT AGGNTTACAG GCATGAGCCA TGGCGNCCGG 60  
 NCAAGTTTCT ATTCTTAAAA TAAAGAGGTT ATACATCTAA NTTACAANTC GTGGCCAAAA 120  
 NGN 123

SEQ ID NO:6290

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07452

SEQUENCE DESCRIPTION:

GATCTGCCCC NCTCAACCTC CCAAAGTGCT GGGATTATAG GCGTGAGCAC CGCCCCCAGN 60  
 TGATTCCAGG CGAATTCTTC TCTGATGGGC GGGCGAGGGT GTGTTTCGTGT GATGGGTTGG 120  
 NGTGTGTGTG TCTNNGTACA CAGATGATGT GTTTTCCCTT CAGCTTCTTA CGTTTTCTGA 180  
 GCATCCGTTG TGCCTTAACA TTTTCTGNTT GTCCTTTGGG NCAAGCAGT ATTTTACTNA 240  
 TNCTTTGAAT GTTCTCATTC TATTNTATCA TGTGACTTAT TAAAANNAGN TTNTAN 296

SEQ ID NO:6291

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07453

SEQUENCE DESCRIPTION:

GATCTGATGG ATTAATAAGG GGTNTCCCN ATTGCTTGGC TCTATTCTC TCTTGTCTGC 60  
 TGCCATGTAA GATGTGCCTT TTGCCCTTCCA CCATGATTGT NAGGCCTCCC AGCCACATGG 120  
 AACTGTGAGN TCATTAAACC TCTTTTCTT CATAAATTAC CCAGTCTCGG GTATGTCTTT 180  
 ATCAGCAGTG TGCAAGNNGG GGNGNTACAC CACTNCTCTA ACTANNTN 228

SEQ ID NO:6292

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07454

SEQUENCE DESCRIPTION:

GATCCTGTGG TCAGAGGCCT CTTTGGCAGT GTNTTCTTAC CCTTAAGNAA GGTCATGAAA 60

TCCAGAAGGG GCAACCTTTN CAGGAGAGCT TTGGAGTCAT TTCTGTGTGA GNCACTATTG 120

CATAATCCTG NCAGNTTGCT TTTATATTTA AGGANTGATG TTACTTANCA ACTGAN 176

SEQ ID NO:6293

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07455

SEQUENCE DESCRIPTION:

GATCTGACTG CTGGCTATAG GATTTTGGAC TTAATGACTG AAATTGCAA TTGTCCTTTT 60

TCTTGGCATT ACAGATTTTG CCAAAATAAC TTTTGTATC AAATATTGAT GTGTGAAAGT 120

GAAGGAGCTA GTCTGCTGAA CCAGGAATAG TTTGAGATAT TGAAGTGTCA TTTTGNACA 180

TTTGAATACT TTGCAGGCTG GCTTTGTATA AACTTATCCT CNGGNNNCCT ATATGTTGTA 240

AATATNTAGN CCATAATTCC ATTATAANTA AANCCTATAA ACTATTCAA CNAANANCAA 300

ANAACANANN 310

SEQ ID NO:6294

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07456

SEQUENCE DESCRIPTION:

GATCCCAAAA AGTTTCCTTC TGCCCTTTTT CAATNCCTCC TTCCCGCCCN TCTGCTTTTG 60

TCATTATATA TTACTTTGCA TTTCTAGAA TTTCATATAA ATGGAATCAT ANAGTATCTA 120

CTCTTTGTTG TTGTCTGGCT TCTNTCACTC AGCATAATTA TTTTGAACT TATCTATGCT 180

GNTGTGGGTA TCAGTAGCTC ATTANCCNAT TGTTGCTGAG TAGTNTTNA TTGTATGANN 240

GTGCTACACG TTATNCGN 258

SEQ ID NO:6295

SEQUENCE LENGTH:31

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07457

SEQUENCE DESCRIPTION:

GATCTTAATA AATAATACCT TACTGCTTAA A 31

SEQ ID NO:6296

SEQUENCE LENGTH:38

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS07458

SEQUENCE DESCRIPTION:

5 GATCTATGTA CAATTTTAAT AAAATCCTGT CCATGAAA 38

SEQ ID NO:6297

SEQUENCE LENGTH:73

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07459

SEQUENCE DESCRIPTION:

15 GATCACCTAC TAAGANGTAC TTCCTACNTT TCATTCTTTC TTTATAAGAA TTAATTAANT 60  
TTTAATTGAC AAA 73

SEQ ID NO:6298

SEQUENCE LENGTH:311

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07460

SEQUENCE DESCRIPTION:

25 GATCCACCCA CCTTGGCTTC CCAAAGTGCT GGGATNACAG GCATGAGCCA CCGCACCCGG 60  
CCCTATCTCA AGCTTCTTAA CTGCACCTGC TAAATCCCTT TTGCCATGTA AGGTAACGTA 120  
CCAACGGTTT CAGAGNTTAG GNTGTGGNCA TTTTGGGGGG CTGTTTTTCT GACTGCAATA 180  
CCTGGTNTCC AGTGAATCCA TGTTTAGTGG AGGACAACAT TTGAGGCACT TACATGGATN 240  
CTAGGGGACA TNTATGTGAN TGTTAGGCAN AAAGTGCTGC CTNCANGNCA NGCAAATACC 300  
30 NATTNAATAT N 311

SEQ ID NO:6299

SEQUENCE LENGTH:115

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07461

SEQUENCE DESCRIPTION:

40 GATCAAAAAA TAACTATAAG TATCCTCAGC CAAGTAGCCC ATGCCGCTGC TCTGCCTACG 60  
GNGTACTCAT CTTTATTTCT TTACTTTCTT AATAAACTTG CTTTCAATGT ACAA 115

SEQ ID NO:6300

SEQUENCE LENGTH:310

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07462

SEQUENCE DESCRIPTION:

50 GATCCTACTG CCTCGTCCTC TCAGAGTGCT GGGATTACAG NNGTGAGCCA CCACAGNAAG 60  
NCACAAATAG CGATTTTATC TACTACCACC AGAAATCTTC TGACATACTG TTTTACCGCA 120  
TGAATATTG TTTTCTTTAT AAATTCCTTA ACAAATCTCT GTTGTATAGA ATACTGTTGG 180

55

TTAAATATA TCAGCAGCTA ATAGCTCATT TTAAATAGAT TCTGAAAGTT CAAGNATTTT 240  
AGGTTGGCCAG NCACCNNTAT ACTCTACANA ATCAGANANG GCTCATTCCT GNTTNCNAC 300  
ACAACAAAANN 310

SEQ ID NO:6301

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07463

SEQUENCE DESCRIPTION:

GATCAGGGAT GTCCAATCTT TTGGCTTCCC TGAGCCACAT TGGAAGAAGA ATTGTCTTGG 60  
GCCGCACATA AAATATGCTA ACACTGACGA TAGCTGATGA GCTTAAAAA AAAAAANTTG 120  
CANGAAAAAT CTCATGTTTT ANGAAGGTTT NCAGNTTGT GTTGGGCTGC ATTTAANGCT 180  
GTNCTGGGCT GCNTTGGNCC CGNGGGCTN 209

SEQ ID NO:6302

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07464

SEQUENCE DESCRIPTION:

GATCATAGCT CCTGGTAACT GTGGACTTGA TAGATTTNAG GTACCTAGTT CAGAACTCCC 60  
TAGTCACCAT CTCCAAGCCT GTCAACATCA CTGCATATTG GAGGAGATGA CAGTGGTAGG 120  
ACCCAAGGAA GAGATGTGTG NCTGANTAGT CGTCACCATA TCTCCAAGCT TCCNGGCAAC 180  
CAGTGGGAAA AGAAACATGC GAGNCTGTAG GAAGNNGGAA GCTCTTCCTT GGCANCTAGG 240  
AGGNNTTAGC CATTCTCTTC CTTATGCAAN GATTGAGGAN TGCAACAATA TAAAGNACGT 300  
GNAGTCCCA NN 312

SEQ ID NO:6303

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07465

SEQUENCE DESCRIPTION:

GATCCGCCCC CCTCAGCCTC CCAAAGTGTT GGGATTACAG GCGTGAGCAC CGCGCCTGAA 60  
NCTGAAGGTT ACTTTTCTTT TCAGTGGTTT GGGGCAGGGT GTTACACAGC TTAATAGATT 120  
AAGAAGAATA AAATGCTGAA TGCTAAA 147

SEQ ID NO:6304

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07466

SEQUENCE DESCRIPTION:

GATCATATTT CCTCAAAAAT AAGAGAAATA AGGTTTCATAA GGAAACTTGC TGGGATTGTG 60

EP 0 679 716 A1

GTTGTTTTGT TTTCTCAGCA GCACAAACAA AACCAGAATT TAGCCTTTAG GACTGCTGAG 120  
 TAAGCCAAAT TTAAATGACT ACTGCTTTGT NCATGGGTAA GCCATGTNCT TTTCAAATA 180  
 AGTGCCACTA AAANCCACAT AATGCTTTGG TTTCTATGTG GCTAATANNT ATTTNGTCCT 240  
 ATAGTTTATC TTATTTGTNA CTGATTTCN TCTCTGNAT GCCTCATATT ANT 294

SEQ ID NO:6305

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07467

SEQUENCE DESCRIPTION:

GATCCATTCG CCCAAGGGG ACAACGGGGT GTCAGGGGAG TNAGGGGTGG AGGTAGGGGC 60  
 CAAAGAGGCT TACACGATAT CCCATACCTT TAATGCCTTT GGCCTTCCAT TCTNACTTCT 120  
 CTNATGAGAT TATTGTCAAC CCTGCTTTCC CTGGTAGATA TTGCCAGGC CCAATGCTTT 180  
 AACCTTAAGC TGATATTTN CCTTTAGATG TCAATCTCGT TACCAGCAGC CTTTGACCC 240  
 AACTNCAGNG NTCTATATTT NCGTAGNGGN TTTTCNCCA TGTGCATGGA TNTN 294

SEQ ID NO:6306

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07468

SEQUENCE DESCRIPTION:

GATCCCAGAG GCTGAGGGTT GGGGAGAGGA AGCCATCATC TCATTACCTC TGTCAGTGCA 60  
 GGGGTGGCTN CTNCTTCCT TGTGCACTTG GGTCGCTGTG ATTGTAAATA AACGTGATT 120  
 CGTACCAA 129

SEQ ID NO:6307

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07469

SEQUENCE DESCRIPTION:

GATCTCTTTG TNATTTAAGA AGTGGCTGGA TTGGAACCTT TAATATGCTA ATNTGGAAAA 60  
 TTAATTACCT TTATGAAGGT GGTATTATAC AAATAAGCAC ACTAACCCT CGGAAGTTGT 120  
 TTTACCTACT TAAAAAGTTT TANTGGATTG CNCCTCTGTA ANCTATTCCT AANNTGTGTA 180  
 TGANATATTT NAN 193

SEQ ID NO:6308

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07470

SEQUENCE DESCRIPTION:

GATCTTTCTT CCTCTCCAGC CCACAAGTGG CTCTAGTGAG ACGAGCATTT AAGCTGCAGG 60

EP 0 679 716 A1

TGGTGGCACT CGGGTCTCAG AGCCACCAGA CGTGCAGGTG GGACAGTGGT TCCAGCTCCG 120  
GCTGCCTGTN AGCGTCCCTC CCAGGTGCTA GCCCTGGCAG GCACAGCCCT NCCCTCATGC 180  
CAGCAAAGGA AATGCTCTTG ATGAGAGGCT CGCTTTAAAG AAGCCCAAAG CGTGTGCTTA 240  
TCCAAGGGGT TCAGCTATTC CTGACTTCAC GGCTTGCATG TTTGATTTTG N 291

SEQ ID NO:6309

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07471

SEQUENCE DESCRIPTION:

GATCATATGT ATTTNTATGT TCTGTAAAGN ATTTGACTTA CTAGTTCTCA ATAAAATTTT 60  
ATTAGGACTA TAAAAAATAA AAAAAANTTT TAATAAA 97

SEQ ID NO:6310

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07472

SEQUENCE DESCRIPTION:

GATCTTATGT ACATACCCAT TTTAGCTTTC CCATGCATAC TTAAGTGCAC TTGCTTTATC 60  
TCCTTGGGCA TTCTTACTTA GGATTCAATA GAAACATGTA CAGGGTAAAC AATTTTTTAA 120  
AAATAAACT TCATGGAGTA TCTGAAA 147

SEQ ID NO:6311

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07473

SEQUENCE DESCRIPTION:

GATCACATTT TGAAATGCCT AAAAGACTTT ATTGTTCTAA TTATCCAGAT GTACCTTTGT 60  
AAAATAGCTC TTTTATGAAT TAGCTGATAA GGCTGTATGT TTCTGGANCA AATATTGGGN 120  
CACCTAAAC CTTCCGGTTT CCGGGGGCCN GGGAAATNGG AAATNAGGTT TCNAATNTTA 180  
AATNAGGNTN 190

SEQ ID NO:6312

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07474

SEQUENCE DESCRIPTION:

GATCTGGATT TTTGCCAATT CCTATGAAAA ATAATCCCCA GAAATAAACT ACTAAGGAAA 60  
ATAAA 65

SEQ ID NO:6313

EP 0 679 716 A1

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07475

SEQUENCE DESCRIPTION:

GATCCATTGG TGTTTGGTTT GGGGTGTTTT TTAAGTTTTT TCTTTTATAT CATCCAGAAA 60  
TAAAGACACG TACACTAAA 79

SEQ ID NO:6314

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07476

SEQUENCE DESCRIPTION:

GATCCAATAA CCCAGTTAGG TATTATAGAT TAGTATTTAA GTTTGCTGTA GATTGTGTGT 60  
GTGTGTGCTA AGTAAAAAGTN CCATGATTCA CAATTTTAGT ATTAACCCAT GTTGCAAAAG 120  
CTGTTACTGG CCAACAGATT GTNATGATGT GTACCATATA ACACAAGCNT TANCTNGGCA 180  
TTANCGTTTG TNAAGCCANN TNTN 204

SEQ ID NO:6315

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07477

SEQUENCE DESCRIPTION:

GATCTCATCT CTGAAAATAA AATACCCCGT TAAAATTCTG GCTTTTGTTC GTTAAGGTTA 60  
TTGAGAAGGT AATAGAAAAA GATATGATAC TACTTTNCTC TCTTGGATTT GTAAAANTAG 120  
TGGAATTTTC ATAAGGATTT TGTATTTTCT ATTGCTGTAT AACATTATTA ATACAAACTT 180  
ATTGCTTAA NANNCAAANN NNNN 204

SEQ ID NO:6316

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07478

SEQUENCE DESCRIPTION:

GATCACGAAG ATACATGTGT TTGACTGTTT AATTGAAAG TTTACATTTT TNATGCTTTG 60  
TGTTGGTGTG TAATTTTGT ACTCTTGCTG GCTAGTTTTT GTCAAATCTT TTTTGAATA 120  
TTGCTTAAAT GTNTTGATTT TATGATAGTG AAGCTTGTAT TCAGTGTTTT GCCAATNAAT 180  
ATTATATGCT TGAATAAANN GCAAAAGANA AGCTTAAA 218

SEQ ID NO:6317

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



EP 0 679 716 A1

CLONE:HUMGS07479

SEQUENCE DESCRIPTION:

5 GATCCCAGTG GGAACCTTCA TGCCTTATTN ATTTCTAATG GGTAAGGGG TTTTNTTACC 60  
 AAGCATCCCT GACCTCCTGG AGACACCACC TGCTTTCCGG GCGGCACTGT GATGGGAGCT 120  
 GGTGGCGACT GAGTCCTTCT GTACGTGCAA CTGGGAAACT TTTGTCCTTT GAGGCTAGGC 180  
 AGTCCCTGC CCTCCGTGTG TGTCTGTTAT CTGGGGGAGA GGAGTGTGGG AAGGNNTTGG 240  
 10 GGGAAGAGCT CCAGCCTGTN TTGNTCCCAA AGTTCTNNAG TGGGAAGACC NGGGTNACCT 300  
 TTTNAGGGTN TANGGTGNGG GGAANTTNTT TTTTN 335

SEQ ID NO:6318

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS07480

SEQUENCE DESCRIPTION:

20 GATCTGCGTG TCAAACGTGT CCATTTGTTT ATGTAAAGTG ATATTAAAAA AGATATAAAC 60  
 TATAACTGTC CGTTACTTTT GGCAAAAGAT ACAACCACAT AATGTATATA ATTCCTAGTT 120  
 TCCATATTTA TCCGCATGTA AAGGGCCGGT TTATCCATGT TACAGCTCTT CAATATTTAT 180  
 GGCTAGAAGA NCTCGTATGT ACACTTTAGT TTCCAGAACT GTTTGGTAAC CTTTCGTACC 240  
 TNATTAGAGG ATTCTNAAAT CTCAAA 266

25 SEQ ID NO:6319

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS07481

SEQUENCE DESCRIPTION:

35 GATCCACCCA NCTCGGCTTC CCAAAGTNCT GGGATTATAG GCGTGAGGCA CCGTGCCTTG 60  
 CCGATAAATG GATTTNAAGC TGAGTCTTTG AGGGAAGAGT AGGACCTGCA CTGAAACAAA 120  
 AAGACAATTT GTGGGGTTGG GNGAGGAAC CAGATGTAAA CAATGGAAAG NTTTTGGTGT 180  
 CACTTTGAGN NGGATTTTTT GGAAGGGTTT TGCAATGTCC ATTCTGTATC TTGGGTTANC 240  
 ACTAGTAAGT CAAATGGNGA ATAATTTGAG TGTCACTCNT TCCCTNCAGT TNGGAAAAAN 300  
 TTTTANCNG TTN 313

40 SEQ ID NO:6320

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS07483

SEQUENCE DESCRIPTION:

GATCTGTGCT TTNCCCCT TTGCCCACT GTCTAAGGTG GCTTTNAACT GGAACCCAAG 60  
 TGCAAATAAA GGTGGTATT CGCTCCTGAA AAAAAAAAAA AAAAAAAAAA AAAAAANAAA 120  
 AAAAAAANA AAATNAACNA AANN 144

50 SEQ ID NO:6321

55

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07484

SEQUENCE DESCRIPTION:

GATCCCTCCT CACTTGCCCT GCCACTTTGC ATGGTTTAT TCTTAACCTG GTCCCCCAGC 60  
 TGTNAAGTGT AGTGGCATCC ATTTCTAATG TATGCATTCA TCCAACAGAG TTATTTATTG 120  
 GCTGGAGATG GAAAATCACA CCACCTGACA GGCCTTCTGG GCCTCCAAAG CCCATCCTTG 180  
 GGGTTCCCCC TCCCTGTGTG AAATGTATTA TCACCAGCAG NCACTGCCGG GCCTCCCTCC 240  
 CGGGGGCACT GCCTGAGGGC GAGTGTGGGN NTAGCATTAG CTGCTTNTN CNNNCCTGGN 300  
 ACCNACTGTG GCCTGGAATN GNATAGTGGT NN 332

SEQ ID NO:6322

SEQUENCE LENGTH:376

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07485

SEQUENCE DESCRIPTION:

GATCTAATTA ATGTGAAGGA CTNGCCAGTC TGGGAAACCG CCTGCCACGT GGAAGAGCCA 60  
 AACCCGACTC TNTGCTGCCA CATGCCGTTT CCATGCCCGG CTGCTGGGCA CCTGGNAGAG 120  
 CTTCCAGAAT CCTCGCAGAC AGCCCAGAGC CTGCCGCTAC CCTCGGCCTG CCCACCACCA 180  
 AGCAAGCAGC AAGCAAGATG GGGTTCTCAT CAGTTCTTCC TTCCACAAT GTAGGACCTT 240  
 TCCTTTTACC TTNCAATGG GATAAAATAG TTCAGAGTTC ATTAGTCATA TTTCATTGGN 300  
 CACAAGGAAT TCAANGGTTT TTNANCAAT TTANCANTTC ACCCGTCTTA TGTNGTTTAA 360  
 NANTNANANC NANTCN 376

SEQ ID NO:6323

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07486

SEQUENCE DESCRIPTION:

GATCACAGAC ACCCAGTNCG TGGNCCCTGT CTTCACCCCA GCNAGCATCA TGTNAGTGGG 60  
 CCTCGTTCCC CCCGGAGAAT CCCAGCGGGG CCTCANAGAT GCATCTGGN 109

SEQ ID NO:6324

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07487

SEQUENCE DESCRIPTION:

GATCTTGGCT GCTTTTAACT AGAAGGTTGC TTTNATNAGC ATATTTATAC TGCTGAAGGA 60  
 TGAGTGTNAA TTAAATTAA CTTTGCCGTT TTGTAGAGAA AACTATTAC AAGATAAATN 120  
 CCAAGTCTTT NCACCTGTCA GGCATGCATA TNTNAN 156

EP 0 679 716 A1

SEQ ID NO:6325

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07488

SEQUENCE DESCRIPTION:

GATCCCAGTG AAGGGTTTTG TGTGTTTAGG CCTCATTTCT TTGTCTTTTT CCTACTCCGT 60  
 TCCTGGCATT TCCTGATTTC NAGTGTATAC TCTGTAGTCT CAGTTCGTGT TTGATTCCAT 120  
 TCCATGGAAA TAAAAAGTAT GTTGTACATA CTGCCGAAGA ATTGTCTTGC AAGTAAAGGC 180  
 TTCCCCCTTT ACTATAAGAC TATAANTAAA ACCTTATTN ATCCTTAAA 229

SEQ ID NO:6326

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07489

SEQUENCE DESCRIPTION:

GATCTTACAC ATTCTGTGTA TAAAGACCTT AACTCCACAG GACGGACATT TTAGAGTTTA 60  
 AATTATTAAG GCTATCATT CTTTAGTAAT GTCATATTG CAAACTTTTT NAGTTTTGGC 120  
 CTTTAATTTA AAANGCCTAA TTTTAANGTG CTGCCTGTNA GTAACCTTG ANTAANANCA 180  
 ANTTATNACN 190

SEQ ID NO:6327

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07490

SEQUENCE DESCRIPTION:

GATCTCAGCT CTTTNGGTGA CTGCATATGC AGTGGTGACC CAGCACAGTT TCCATCAATC 60  
 TCGTCAAAAG ACTTGAGGTT GTTGGGCACA GTATTTTACA TGACCACAGT TAAAAAGCTG 120  
 GGTATACACA ATTAACANCC AANGTGATAT GCATTTATAC CTTTCCCTTT ATGNCCAATT 180  
 TCTTTATAAA TATGGCTCAT CTGCTCATAA CTGTTAGNCC CACCCAAGTG TCATTAGTAA 240  
 CCTGAGTGTT TATGCTTGCA AACTGTATG TTGTTATTGT CTGATTTGAT NATATTCNGT 300  
 GNTGTTTAGN GAATGCNGTN GTGTTTNANT GNATCACAAA NAATTNCCCC ATTNN 355

SEQ ID NO:6328

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07491

SEQUENCE DESCRIPTION:

GATCATTTGA ATCTCAGTCT TCAGCCTGCA CTGATTTGTA GCCTGCACTG TCTTACTGAT 60  
 TTACAAACTG AAATCACTGA GAAATGTCTT TAGTTCAGTG AGAAGAAACC AGAACAATTG 120  
 TTCCTAGTGT TGTGTTGTTT TTTTAAAGCA AATTACTTAC TGATTTTNA TGGCAGGNGG 180  
 GNGAAAAAGT GTTACAACGG TTTCTAATGA AGTCCGGTAT TTANNTGGTA AATGACTAAT 240

GTGTTTAGTA GTGCCAAANT AAACCATTAN NTGNTTGTCC TTTGCCAAAN ANANNANN 298

5

SEQ ID NO:6329  
SEQUENCE LENGTH:225  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07492

10

SEQUENCE DESCRIPTION:

GATCACAAG AAAAAGCATT TTTAAAAAGT TGGCAAACGC TGAAACGCAC TGTGGTATGA 60  
GGCGCATTGC ATTTCCATAG CACTGAAGTA CCAGTTTCCA TTCCTGGGCT GNGATTGTTT 120  
TTCCCGTGGT TGTATTGTTT TGATTTAACG ACCACCAGNG TAACTGNTTT TTNTTTGTTT 180  
GTTTNCCTGGT GGGGTNNCCA CCAATTAAAA CTNNTANAAN CCCGN 225

15

SEQ ID NO:6330  
SEQUENCE LENGTH:229  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07493

20

SEQUENCE DESCRIPTION:

GATCGACTTC GATAAAATAC TTTTGCTTAA TCAAAATTAG AGTGTGTTTG TTGTCTGTGT 60  
AAAATAGAAT TAATGTATCT NGCTAGTAAG GGCACGTAGA GCATTTAGAG TTGTCTTTCA 120  
GCATTCAATC AGGCTGAGCT GAATGTAGTG ATGTTTACAT TGTTTACATT CTTGTACTG 180  
TCTTCCTGCT CAGACTCTAC TGCTTTTAAT AAAANTTNAT TTTTGTAAG 229

25

SEQ ID NO:6331  
SEQUENCE LENGTH:345  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07494

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SEQUENCE DESCRIPTION:

GATCTAAAGA CCCGATAGGT GCAGAACCCA TCTGGACACG GAGACCAGGA ATGGAGTTCC 60  
ATGGAGGCCT GGCTGGCACT GCACCCGGGC ATGAGGACAC ATCCAGTAAG AAGACCTGCC 120  
TCAAGAGGTG CACTGCGGTG ACCAGTGGAG GTNACTGGTT GGAGCCTGGA ATTGGAAGCA 180  
GATTCCAAGC TCTGGTGGAC AAACCTCTCCA GGCCTGGTGG GATTACAGC TGGGGCAGNC 240  
CTCATCCTGG CTGCNTGGCC ACAGNCCCNN GCTNTTTNCC ACTTGGTGGT AGGGCCGATG 300  
CCTTNTTTGG ANGAGNTGGG NTTNTTTTGG TCNCGACTGN GTANN 345

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SEQ ID NO:6332  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07495

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SEQUENCE DESCRIPTION:

GATCACAAG AAAANGCATT TTTAAAAAGT TGGCAAACGC TGAAACGCAC TGTGGTATGA 60  
AGGCATTGC ATTTCCATAG CACTCNAGTA CCAGTTTCCA TTCCTGGGCT GAGNTTGTGTT 120

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TTCCCGTGGT TGNATTGTNC TGATTTACAG TACNCCAGAG TAACTGNTTT TTTTTTGT 180  
 GTTTCTTGT GGAGTTAACA CCANNTAAAA NTTGTAAAN 219

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SEQ ID NO:6333  
 SEQUENCE LENGTH:60  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07496  
 SEQUENCE DESCRIPTION:  
 GATCTATTTT TCAGCTTTCA CTTATGTGAG CCAATAAATT CCTTTTTTGT TGAAGGCAAA 60

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SEQ ID NO:6334  
 SEQUENCE LENGTH:154  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07497

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SEQUENCE DESCRIPTION:  
 GATCTACCCC CCCATCAACG TGCCCCCTCG ACTCCCGGTG CTGCGGAAGA ACTGAAGGTT 60  
 GCNATGCCTT ACTCTGACGG GAGCATCTGT ATTTTAATGT TAAAAGCCCA CAAAATAAAA 120  
 ATAAAAAGTA ACTGAGATGA ATTTAATAAA CAAA 154

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SEQ ID NO:6335  
 SEQUENCE LENGTH:91  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07498  
 SEQUENCE DESCRIPTION:  
 GATCTATGCT GTATGCACAG ATTGCATAAT GGCTTTTTTN CTTAACATTA TGTGATAAGC 60  
 ATTNCTGA ATAANCTTAT TTTAAATAA A 91

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SEQ ID NO:6336  
 SEQUENCE LENGTH:181  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07499  
 SEQUENCE DESCRIPTION:  
 GATCAGGTGT GGCCAATNAA ATTNAAGAGG AAGTCTACCT GGGNTTCTGG GAAAGCTTTT 60  
 CCAATAAAAG ACACAGGCAT GGCTAACACC TCCCTGGGCC TCTTCTCCT ACCTTGATTG 120  
 AGGGTGTGAT GCCTGGAGCC ACAGCAGCCA CTTTGNNNNC ATGACAAAAA GGCCAAGNGN 180  
 N 181

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SEQ ID NO:6337  
 SEQUENCE LENGTH:77  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07500

SEQUENCE DESCRIPTION:

5 GATCACCAAA ACCTGATGTT TTAAATNTGC TTTCTTTTGG AAATTTATGT TTTCAAATAA 60  
AATCTCCCTA AAGCAAA 77

SEQ ID NO:6338

SEQUENCE LENGTH:265

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07501

SEQUENCE DESCRIPTION:

15 GATCCTATGA GTGTAGTTAA TGACTGTTNG TAAGTCAGTA GAGTAAAATN CTGTGTCCAC 60  
GGGGTGTAC AGCCTCACCA TACCCTGTTG AGGTGTGAAA TGCCCCGTCA GAAATTAAAT 120  
ACAAACTTAA ATGTGCCTAT TGGTGTCTAA NCTTCATACA ATGTAAGGNC AGATTCCTTT 180  
TNGGNNTACT GGGTGTCTGC GCCAGGTTTG NTAGTTAGAC TAAAAANCTT GANATTCACT 240  
20 TTTTGGGGGG NGGGNTATAC TGANN 265

SEQ ID NO:6339

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS07502

SEQUENCE DESCRIPTION:

30 GATCTATTGG AAAACAACAT GGAATGGAAT TCTGGAAATN ATTATTCATT GAAGAATGCA 60  
GTGGCCAAGA AAATATCAAA TGTAGATTGT NAACGCTTGA GAATCATGGC TATGGTTTCT 120  
NATGTCCTGG TAACANGCTG TTATCTTTNN NGACATTTTN N 161

SEQ ID NO:6340

SEQUENCE LENGTH:272

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07503

SEQUENCE DESCRIPTION:

40 GATCTAGTTA TAAAATACAT GAAAAGGCTG ATGCAGCAAT CGGTGGAATC GGTTTGGAAAT 60  
ATGGCATTGG ANTTTATTCT TGACAATGTC CAGGTGGTTT TANAACAAAC TTATGGAAGC 120  
ACATTAAAAG TTACATAANT ATTACCAGAG AGCCTGATGC TCTCTGATAG CTGTGCCATA 180  
AGTNCTTGTG AGGTATTTNC AAAGTGCATG ATAGTAATGC TCGGNGTTTT TATAATTNNN 240  
45 NNTTCCTTTT AAAGCAAGTN TTTTGTACAT NN 272

SEQ ID NO:6341

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

CLONE:HUMGS07504

SEQUENCE DESCRIPTION:

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GATCAGTGTG GAAAAGCCTT CANTCAGAAA GGAAGCTTAA TTNTNCACAT CAGAGTCCAC 60  
ACAGGCCTGA AGCCCTATGC CTGTNCCCAG TGCAGGAAGA GTTCCACAC CAGGGGGAAT 120  
TGTATTCTGC ATGGCAAAAT CCACACAGGA GAGACACCCT ATCTNTNCGG CCAGTNTGGA 180  
AAAAGCTTCA CCCAGAGAGG GAGTCTGGCT GTGCACCAGC GAAGTCTTCA CAGAGGCTCA 240  
CCCTTTGACC ACTTTCCTGA AGAGAAGTTC TCTTTATGAA TTAAGGAGTA CAAAATCCTC 300  
TGAGNTTGAN GCAACCCTAT CCAAGTTTCT ANTGGGANTG GTTGN 345

SEQ ID NO:6342  
SEQUENCE LENGTH:212  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07505

SEQUENCE DESCRIPTION:  
GATCTGTCTG CCCATCTGGC CCAGGGGGTC CGAGAAGGGA AGCCTTGGGC AAGAGGNGAC 60  
CAGTTGCAAT ACTGTACTTC CTGGTCAGTG GCCAGAGGAT GCGTGCAATA GCAGAGGCCA 120  
GGTNACCCCT TCAGCCTTGG CCTCTGCCNC TCCATTGGCC CTCCCTNCCT GNTNCTNCNT 180  
GGTGTINGGTC AGTCCTTTTC TAAAGNTGTC CN 212

SEQ ID NO:6343  
SEQUENCE LENGTH:316  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07506

SEQUENCE DESCRIPTION:  
GATCTTCGTA TAATTGGCCA CTAATGTGAG AGTTCACTAC TAGGCAGAAA CTATTATGGA 60  
CAGTNAATA ATGACTTTAA TCTACCACG TGAGTTTNAT GCAGTCTTTC CTGTCTAGCC 120  
CTTGCCCTCN CCTGCCCATG TNATTGCGGT GCAGTAGTTT CTGTNGTATA ATAGTGTGGA 180  
CAGCAGCTCA GAAAAGGAGG GAATGCTACT GATAATTTGT AGATAATNNN NTTTANGACT 240  
TAGGGGAACC ATTGACCTTT GANATTTTNA TTAGAAAATN ATTTGTNCAG AATCAGACTC 300  
CATTATTTNC CATATN 316

SEQ ID NO:6344  
SEQUENCE LENGTH:184  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07507

SEQUENCE DESCRIPTION:  
GATCAAAAGG AATGATGTAT TTTAACGTG TTGGCCAAAG TCACTGGATA AAATGAGAAT 60  
TGTATATTN TAATTCATTT TGCAAAATNCA GAAAGTTGGT CCAGATATAT GTCACAGANC 120  
TTTNCACCTG TATACTACTC TTACAATGGA AAANNNTCCC GAAANCTGTA TACTTCTGAT 180  
TANN 184

SEQ ID NO:6345  
SEQUENCE LENGTH:361  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07508

SEQUENCE DESCRIPTION:

5 GATCAGACCA TGCAGGTAAG GTGAACCAGC TGCACGGACC AGGTTCCCGC AAAACATTGC 60  
CAGCTAGTGA GGCATAATTT GCTCAAAGTA TAGAAACAGC CCACCTGTGC CCACTTTGAC 120  
CATTGGTGAG GATAGATATA AAATCACTTC TTCCAACGAA GCCTAGGTGA AAATCTATTT 180  
ATAAATGGAC CACAACCTCTG GGGTGTCTGT TTTGTGCTGT GACTTCCTAA TTATTGCTAA 240  
10 AGAACTACTG TTTAGTTGGT AATGGTGTAA AATTACATTC AGCTCCTTCT TGTCATATAA 300  
ANAGGAATTT GGNGGGTGTC GGTTTAAANA TTTTATTNCA CCTGTACCAT TTNGTCACTC 360  
N 361

SEQ ID NO:6346

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07509

SEQUENCE DESCRIPTION:

15 GATCTGTTGT TATACCAATT GAATTAATTG AGTTNNTTGT TGGACATTG GGTGGTTNC 60  
AAGTCTTTGC TATTGTGAAT AGTCAATGGC AGTATTTNA ATGTTGGTCT ATTATTGTAC 120  
TAAATAGTTG TTTATATTGA GCTTGGGAAA GCTTTCGTGT CCAATAGAAA TAGCATATTA 180  
20 AAATAAATGC CACTGTATAT NAATGANAGT GTTGATTATA TACCCTAGAN ACTTAANCCT 240  
25 TAAGGNAGTT ATGTNTNAAT TNNCTN 266

SEQ ID NO:6347

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07510

SEQUENCE DESCRIPTION:

30 GATCAACTCC AGTTTCCAAT GTCTATGTGT CTATGTGTGT ATGTNCCATA CATATGTATT 60  
35 CACATGAAGA CCGGCATGGC CAAGTNCTGC TGGAGGAGCA CTCAAGTGTG ACGAGCAGGG 120  
CCACTGGACC CTGCAGGGCT GTGGTGTATA TAGTGCAGCT TTGGAGGTGG AACTCTATTT 180  
NAACACTTTT CTATGGAGCC TTCCGAGTCC CAGGTTTTNA CTTGAGGCTG TCTGTCTGGA 240  
TGGCGGTTTT NAGACCTCCA TTAACATCCC TACCCAGCAT TCTGTACTTC GGGGGGNCTT 300  
40 CTATCTTGTN ATAAAACTTN TTACCAAGTG GAACATCGGT TACCCACCTT TTGTN 355

SEQ ID NO:6348

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07511

SEQUENCE DESCRIPTION:

45 GATCGTCCTG CCTTTGTAAG GCAGATTTGG AGGGGAGGCC CAACAGCAAA GATGGAGAGG 60  
50 AAAAAGGGAG TGGAGCTTGT GGAACAGGAA GCCCCCCAGG GTCTGTCCAG GGCTGCTCAG 120  
CTCTTNAGGA TGTTGTGGAT GGTGAAGTGG TGATGGTGTG CTGGAGCAGC CCAGCACCTC 180



CACTGGGCCC AGAAGGTCTT GACTTCGGAC ACTTACCCCT GTTTCACAAG TGTTTATAAA 240  
GCTGTTTTTN CTTNGTTTT TCTCCTAAAT AATCCTTACT TGGTAGTTAT NAATCCTTCT 300  
TTGGGGGAGG GACAGGGGCT TTAAANCCTG GAGGAAAATT AATTTTNNAT TAANGGAN 358

SEQ ID NO:6349

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07512

SEQUENCE DESCRIPTION:

GATCATGGAA GCTCCGTGCC CCTTCTCCCA TTCCTTGCCC TAAGTATCGC CTCCATCTGG 60  
TTGTTTGTCT GTATCCTTTA TTAATAAACA AGTAAATNTA AGTAAA 106

SEQ ID NO:6350

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07513

SEQUENCE DESCRIPTION:

GATCAGTGCC AGAAGTCATT GTATTCAAAG AAGAATAAGC AAGAAAGAAA AGAAGGAAGG 60  
AAGAGAGGTA GACAGATACA AGATGAAATC CTGTCAAAAA ATGGAAGGAA ANCCAGAAAN 120  
TGAGAGTNNN CCANN 135

SEQ ID NO:6351

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07514

SEQUENCE DESCRIPTION:

GATCAGGAAC ATGGCAAGGA ACACCACACC ACTGCTTTTN AGCATTGTAC TGGAAGTNCT 60  
ATATAATGCA GTGTTAAAAA AAAAAGAAAT AAAATGCACA TAGATTTGAA AGGNTGAAAT 120  
ACAACTTTNT NCACAAGTAA CATGATTGTN TTTNTN 156

SEQ ID NO:6352

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07515

SEQUENCE DESCRIPTION:

GATCAAAAAG AACTATGAG TAACAAGCTA TAACATAGTT CACCACAATG GGACCCCCC 60  
CCCTTTTCCT NACCCTACAG TTAGTAATAT TNCAATTAAA NTANCTATAT TCTNCTATAT 120  
TTNCCTGTT AAAN 134

SEQ ID NO:6353

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07516

SEQUENCE DESCRIPTION:

GATCCACATA TCTCTAACAC CATTAATATG AATCATTGGA AATATTTTAC TTATTAACAA 60  
AGTCTCTTGT GTTAAGCTAC AGATAAAGCT TTTGTGGTAG TGTCAAA 107

SEQ ID NO:6354

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07517

SEQUENCE DESCRIPTION:

GATCCAGAGA CATGTGGCAG CAGGCATGGC TTCCCCTTGG CCTCTCTGTA CACTGCCCCA 60  
GGACTGTCAT TTTGGCATCT GCAAAGGAAT CACTTTAGAA AGCCAGCACC TGGTTGATGT 120  
GTATTCATAC TGACATTAGA TTGATGTGCA CTGCAGGGGN AANNGCGGTA GCTGNCACAG 180  
NAAAAGGATG TTTTGATAGG AATAATTTTC TAGTATGTCT TGAAACATGT TCATCTGGAA 240  
GTATTTTCTT CCAAAGTAAT GTAGCATGAT TTNCAAGGA TTGTAAACAT GCCTGGGATT 300  
GGGAAAGNTA GGCCTAANGT TGTGCCAAAC TATATCAATA AATTCCCTTN 350

SEQ ID NO:6355

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07518

SEQUENCE DESCRIPTION:

GATCCCACTT GCATGCACCC AGAATTTTAT ATTCCCCAGG AATATAGCAG AGGAATATTC 60  
TGGTATCATA TTTATCTTTC ACCATCTCAA AAATTACAGT TTAAAAAACT CAAATAAAAT 120  
TCATCACTAT AACCAAA 137

SEQ ID NO:6356

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07520

SEQUENCE DESCRIPTION:

GATCCAACCC TTGCTAGGTA TCATAGTTTA GGCCCATTTA CCTTCCCTG TACTGGCAGT 60  
TCAGCCGCTT ACATGCACTC ACCCTGTTTG TGGCTATTTT AAATTCATAT TATTAATAAA 120  
CAAAAAAACC CCAAA 135

SEQ ID NO:6357

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07521

## SEQUENCE DESCRIPTION:

GATCCTGTCT CAAAAAAAC ATAACCGACA TCCAGAAGTG AAATAAATTA GCCAGTGTCA 60  
 CAAAGTAAA 69

SEQ ID NO:6358

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07522

## SEQUENCE DESCRIPTION:

GATCTTAAAA NTACAAAATG TAGACAATTA ATATTCAGGT GCTTACTTTT GAGCCAATAT 60  
 GTAGCAGAGA AAAACTAATT NNTCTGTGGC AGTATTTTNA TTTTNGGCAT TTCCCAGGAA 120  
 TTAAGTGAAG ACTAAACTC ATATGTGANG TGTAATGATA CTANGGNAAG AGTCAGTAAA 180  
 ATTNCCATTT GGCTACCAAA 200

SEQ ID NO:6359

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07523

## SEQUENCE DESCRIPTION:

GATCTTGTA ATATATAAAT NTAAATAANA TTAAANCTGT AATTCCTTTN CCCTCCAAAG 60  
 GCTTTTNTGT ACATGGCGCT GCATTTGGCT ATTCCTTTG GAAATAAATA ATGTN 115

SEQ ID NO:6360

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07524

## SEQUENCE DESCRIPTION:

GATCTTCCCA CCATCACAAA TGAATTTAAA GATGAAAAGA AACTCAGTTG CTCATACAAC 60  
 TGCATTTTTT CTGTCTATTA TGGGAAACAT CAGACGTTCT GAGTAAGATA TATCTCATGG 120  
 CATTAGTTAA TATAACTNAT ATTGTTTAAAN TCATGGTATT ACATGCAATT NATATCAGAT 180  
 AAAAGCAGAA CACATTTTTG TNCTGCCTCT CTTAAATGCT GAATGTAGCT GTNATGTATA 240  
 ANTCCATTTA GTTTTATGTN CTAAAGGNCT ATTTGTGCAC TCCAGNTTTN CAGTAAANTA 300  
 GNATTCCTAG TAAANCNNN 319

SEQ ID NO:6361

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07525

## SEQUENCE DESCRIPTION:

GATCCTAATT TNNTCACGAA TCCCGATGGA ACCCTGTGCT GTTNANACAT CAGTGTGTAA 60  
 AACTCTCTGT GTCCCTGTTG GGCTGTCCAG ACAGTCTGGA CTCTTGTAAT TTTAANATTT 120

AATTAAAGGA AACAAACCAA A

141

SEQ ID NO:6362

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07526

SEQUENCE DESCRIPTION:

GATCTTTTGC TTAGACGTTA ACTTGATGCA TCATTGGAAA GNTGTTTCTC TCATCTCTGT 60  
CCTAAGGCTT GATAAAGTCA TTAAAATTGT NTTCTTTTGA CTAAG 105

SEQ ID NO:6363

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07527

SEQUENCE DESCRIPTION:

GATCTCAGGC CAGCCGTTTG TNCTCCTAGC AGGGTTGCTG TGCTGGCCAC ACGGAGAGGC 60  
CCTAGAGAGC CTCATGGATT GTAACATAAG AAGAAACGGT TCCTTTTTGT TTTTTTAAAA 120  
ATNATTTTAA AATACCGTTT TTAACACCGT TCTCTCGGTA CTTTTTTTAA GCTAAGTCAG 180  
CATTGTCTTC CAGTGTTAAA GGCATCCCTC ACCTCTGCAT TGACCTTACG NATCCATGCC 240  
AAGGAATGGG ATTTCCATCC CTGNGGCCAG TCAGTTAGGG TGTCATTGT NCCTATTTGA 300  
NTTTTAAATG NAATCTGATG NGGTGAGNTC AGGTTTANAA NTCTTCAAAN GNNGCGTTNA 360  
TTGTACCAGG NNTGNTATGG ATTAATCCNT GN 392

SEQ ID NO:6364

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07528

SEQUENCE DESCRIPTION:

GATCTCCATT CCTTGGGCTC CGCGTCCGAN TTCATGGTGC GCCGCTGTGC TGGGAGCTGC 60  
AGTGGGAATN TNTGGGACAC CTTGACCAAA GGGGAGCTTT GTNTCGTGTG TTTTGAAAAA 120  
GGCTTAATGA AGAGAATGTT GTTCATTCTT AGTAGTATAG TTTGCAATTC TTAATGGCAA 180  
ATAATAAGTT TCAGTAGAAA ACAA 205

SEQ ID NO:6365

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07529

SEQUENCE DESCRIPTION:

GATCCTTTTC TACCCACTTT CCTATGGAGG ATTCCAAGTN ACCACTTCTC TCACCGGCTT 60  
CTACCAGGGT CCAGGACTAA GGCCTTTTTN TCCATAGCCT CAACATTTTG GNAATCTTCC 120  
CTTAATCACC CTTGCTCCTC CTGGGTGCCT GGAAGATGGA CTGGCAGAGA CCTCTTTGTT 180

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GCGTTTTGTG CTTTGATGCC AGGAATGCCG CCTAGTTTAT GTCCCCGGTG GGGCACACAG 240  
CGGGGGGCGC CAGGTTTTCC TTGTNCCNCA GCTGCTCTGC CCNTTNCNN TTATTNCCTG 300  
ACTTCAGGNC TTGAAACNNT TCCNGTGGTG TAAATAAAAA ANN 343

SEQ ID NO:6366  
SEQUENCE LENGTH:332  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07530

SEQUENCE DESCRIPTION:  
GATCTGTACT TTGAAAACAC ATTGAGTCCC TTTAACCAGG AAGAACTCTT CTGGGCGACC 60  
GTCCACATGT TCCTTCCCT TCCTAATGAC GTGAAGTCTG AACTCTACAG AGCCTCTGTA 120  
CCTTCTCTTT AAAGGCAGCT CTGCTCACCA GGAATTGGCT ATAATNCTTT CCAACTCTCT 180  
CATCATTTTA ATAGCTATCA GCAAATGTAG AGGTGTAGGG GATTTTGTA CATCTGATGT 240  
ATGTAAAAAG ANATATTCAA GTTGAAGGC AGNCTAGAAC TGNCTGNGA GATGTTTGAT 300  
GTACACATTA AANNTAAGGA ATTTACATA AA 332

SEQ ID NO:6367  
SEQUENCE LENGTH:258  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07531

SEQUENCE DESCRIPTION:  
GATCAAGAAT GGCAAGAAAA TCACAGCCTT TGTACCCAAT GACGGTTGCT TGANCTTTAT 60  
TGAGGAAAAT NATGAAGTNC TGGTTGCTGG ATTTGGTCGC AAAGGTCATG CTGTTGGTGA 120  
TATTCCTGGA GTCCGCTTTA AGGTTGTCAA AGTAGCCAAT GTTCTCTTT TGGGCCTATA 180  
CAAAGGCAAG ANGGNAAGGC CNAGNTCACC ATCCCCTAAA TTTTAAAAG NAGTTTCACA 240  
AAGTNTGCA TATTNNN 258

SEQ ID NO:6368  
SEQUENCE LENGTH:148  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07532

SEQUENCE DESCRIPTION:  
GATCTGTACA TTATTGCATG TGGCAGTAGT GTATTNCAAT TTTGCATACT ATTCCATTTT 60  
AAGAATATAT TGCTGTTTAT CCTATTGATG GATATTTGTA TTTNTNATAC TTTTGTGTAA 120  
TAATAAAAAT ACTGCTGTAA ATATTAAT 148

SEQ ID NO:6369  
SEQUENCE LENGTH:344  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07533  
SEQUENCE DESCRIPTION:

GATCTGATTC AAAGATAACC ATTACCCATC TTTCCAAGGC CCATCTAAGT AGTACAGGTG 60  
 TTTTGTCTTT TAAAATTGAC AGTCCTCTTT GCATTAAGTC TGTAGGGGGG GAATACAATA 120  
 TAAATATTCT NCTGTGTAAA CGTAAGAATG TGCTGTAATC TCCAGTTCCT TTGGATACCT 180  
 CAGAATTCTA TTTATTGTAT ACACTTATAC TGTTTATNCA ATGTTTTGGG TCTTACTCTT 240  
 TTTGACGTAT TCTCATCAGT CTTCACTCTA GTTTGCAAGC NCTGAAGTTA TTGATTACGT 300  
 CTAATGTGCA ATNNGGCTTC TATTAANTGC TATTNATGG TTCN 344

SEQ ID NO:6370

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07534

SEQUENCE DESCRIPTION:

GATCTNTGTC ACACCCAAGC TGGTGGAGGA GCACCTCAAA AGTGCCCAANT ATANGAAACC 60  
 ACCCATCACA GTGGACTCCG TCTGCCTCAA GTGGGCACCC CCCAAGCACA AGCANGTCAA 120  
 GCTCTCCAAA GAAGTGAGCA GCCTGGCCCC TGCTGTGCGA CCTGAGCCTC CTGGCTNNGG 180  
 GNCTGTAAAT ATGTATAGAC CTGTTTTGTC ATTTTTTTAA TAAAGTCAGT TCTGGTGGCC 240  
 CTGNAGCTTT GGNAGGGNAA GGGGGAGGCC ANAAANANTA AANGGGGGGA AN 292

SEQ ID NO:6371

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07535

SEQUENCE DESCRIPTION:

GATCCACCTG CCTGGCCTC CCAGAGTGCT GGGATTACAG TCGTGANACC GCACCTGGCC 60  
 AATTTTAATA TTTTAACTGA AGATGTTTCA TATAATATTC AGCAATATAA AAATTACTAA 120  
 TGACTTTTTT GGTAAGAAA 139

SEQ ID NO:6372

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07536

SEQUENCE DESCRIPTION:

GATCCTAACC GNAGGCCCAT CAATTGCAAC ATAGAGATAC ACATGGAAAG AGGGTTTAAC 60  
 AGACCCTCTC TNGGACACAN CTGTTTCTCC TTTGAGCANT ANTTN 105

SEQ ID NO:6373

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07537

SEQUENCE DESCRIPTION:

GATCCAGACC AGCGTCTGGC CCAAGCCATT CANAGGTGGG GTCTGGGGNC TGGGGGTTTT 60

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GTNTCGTGAC ACTTTGTCTC AAGGAGATTC CACATAGGGA TTTNAATTAG GCTTTCTNCT 120  
TGCNAAGGCC TGTGGCATCT AANCCTGGCT N 151

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SEQ ID NO:6374  
SEQUENCE LENGTH:288  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS07538

SEQUENCE DESCRIPTION:

GATCTNAGGC AGATAAAGAA ACTTCAACTT ATTTNAGAGA GGAGGTAGGG GATGGGGAGG 60  
TCACAGAGAA CTCTGGGTTT CTNCAGTTTA CTATGCCACA GCACCATATT TCCGGGTATG 120  
AGTTCTGAGC CCCACAATGG CCATAAGCAC TTAACCACAG ACCTAGTGAC GTATGTATAA 180  
NATATACACT AGATTCCAAA GNCTTAGTAT ACAAAGACC ATAAATATC TTATTTGTAA 240  
TTGTTAANA CTGATTACAT GTTAANNTGN TAATNTTTN NNTATANN 288

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SEQ ID NO:6375  
SEQUENCE LENGTH:319  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07539

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SEQUENCE DESCRIPTION:

GATCCTCTAC CCCCGGAATG AGGACACACT TCAGGACCCA GCCCACTGG AGTNTGGCCA 60  
AGNATTCTCC CAGCAGGAAA ATGGCCATTN CATGGACACC AATGANTGCN TCCAGTTCCC 120  
ATTCGTNTGC CCTCGAGACA AGCCCGTATG TNTCAACACC TATGGAAGCT ACAGGTGCCG 180  
GACCAACAAG AAGTGCAGTC GGGGCTACGA GCCCAACGAG GNTGGCACAG CCTGCNTGGC 240  
TCAAGTGGCC TTTTAGGTG GGTATTCTTC AGCCGTCTCT AGAATCTTN AGCCTCTTN 300  
TNGGCCTCA NATCTTGN 319

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SEQ ID NO:6376  
SEQUENCE LENGTH:166  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07540

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SEQUENCE DESCRIPTION:

GATCTCTGTA TGNTCTGTGT GTTCTGTGT CCTGGAATTG GATGCGTGGG ACTCGTTCTG 60  
TCCGCGGAGT GCACTCTTTT TTNCAGTGTG GCCCACATAT CTTGTAAATN TTTGCTGAAG 120  
AGTTGTGTCT ATATATAGAG AAAATATATA TAANCAGAGA AATAAA 166

40

SEQ ID NO:6377  
SEQUENCE LENGTH:158  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07541

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SEQUENCE DESCRIPTION:

GATCCAATGC CCTAACTTT ACATAAGAGT TCCGGCAAGG CTGTGACTTC AACTTGTGTT 60

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EP 0 679 716 A1

GTAAGTCAA CCTGCAGAAT CAAATTTAGG GTTATGTTTT CAGTTGTATC AGTCTTACGG 120  
CTACAAGATA TTAAAGAGAT TCTTCCTGG TTATCAAA 158

5

SEQ ID NO:6378  
SEQUENCE LENGTH:323  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10

CLONE:HUMGS07543

SEQUENCE DESCRIPTION:

15

GATCTCACCT TGTGTGTCAT CATAGAATTC AACTGGACT AAAACCTTTT AAGTGTAAGG 60  
ATTGTGGAAA ATGTTTTAGT CGAAGCTCTC ACCTTTATTC ACATCAAAGA ACCCACAAGT 120  
GAGAGAAACC ATATGAGTGT CATGATTGTG GAAAATCTTT CAGCCAGAGT TCTGCCCTTA 180  
TTGTGCATCA GAGGATACAC ACTGGNGAGA AACCATATGA NTGCTGTCAG TGTGGGAAAG 240  
CCTTCATCCG GNAGGATTGN CCTCATTANG CACCNGNGAT TTCATGTTNG NGNAGAGGCC 300  
TATANTTGTA ATCAATGGTN ANN 323

20

SEQ ID NO:6379  
SEQUENCE LENGTH:318  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07544

25

SEQUENCE DESCRIPTION:

30

GATCCTTCTA ATCTCCTGGA CCCTCCAGGG CACTCTGGTC CCTATTCCCC AGCTCCTAGG 60  
CAGCTGAGCC GGGTCCCTTA GGGGAGGTGA CCAGGAGCTT TGGTGCAGGG AGCTCTTNGT 120  
GGGGCAAAGG GCTGGACCCC TGCCAGGTCT GTGGACATGG TTATATGCCC GGNNAGAGGG 180  
GGTACAGGGC CCCAGGGATG GCCCCCAATC CCACCTCTGT TTATTCTGTA AACTGCAACC 240  
TATAAATAAC CTTTAGCATT CCTATTTGTA ACAAATNG NNTTTNTGNA AATAAATTAT 300  
ATTCCTAGT CTAAAAAA 318

35

SEQ ID NO:6380  
SEQUENCE LENGTH:77  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07545

40

SEQUENCE DESCRIPTION:

GATCTTCTCT GCCTTTATTG TTTTGCCATT TCACTAAAAT ATGTTTAGAG ATATATAAAT 60  
NCTGCTTGA CTCTAAA 77

45

SEQ ID NO:6381  
SEQUENCE LENGTH:32  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07546

50

SEQUENCE DESCRIPTION:

GATCTCATTT TACAAGAGAA TCTCTCTGCA AA

32

55



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5 SEQ ID NO:6382  
 SEQUENCE LENGTH:83  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07547  
 SEQUENCE DESCRIPTION:  
 10 GATCTCTAAG TGTAGCTGTA AATTTTGGGG TTAATTTGGC TTATATTGGN CCTTTTAAAA 60  
 GNAATAAAGT TTTTAAATGC AAA 83

15 SEQ ID NO:6383  
 SEQUENCE LENGTH:74  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07548  
 SEQUENCE DESCRIPTION:  
 20 GATCTATAAA GAAACATAAG CTTAAAGTTG TTTATCACTG TGGTGTTAAT AAAACAGTAT 60  
 TTTCAAAAAA TAAA 74

25 SEQ ID NO:6384  
 SEQUENCE LENGTH:342  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07549  
 SEQUENCE DESCRIPTION:  
 30 GATCCAGACC TCTCTAATAT GAAGAATAAT GAGCCTTATN ACTATAAGTT TGTNAAATGG 60  
 ATGACTAAAC ATAAGAACT ATCAGCCATC CCCGTTTCAG CATTCTGTAA CTCAGAGACT 120  
 AAATCACAGT TTGAGAAGTT TGTNCGTTTT TCCTTCATTA AAAAAGACAG CACACTGGAT 180  
 GCTGCTGAAG AAATCATCAA GGCATGGNGT GTACAGAAGT CTTGATTTGT GCAGAATGGN 240  
 TTAATGTTTT TGTTAGATGA CCTAGTATGG NATTGTTACT TAGTGCTGCC ACCTGCTGGG 300  
 35 ATGTTAANNG ANTGTNGGAT GCGTGGCCTG GCGGTGNNNG CN 342

40 SEQ ID NO:6385  
 SEQUENCE LENGTH:118  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07550  
 SEQUENCE DESCRIPTION:  
 45 GATCCTGTGT TTTGAGTCCC AAAGGCCATG CCAAGGATTG GCTTTGGNTG GCTTTAATCA 60  
 CCAACCCATC AACATCAAGC CTCNCCAGG CCGGTTCAAA TAAATGTANT TAAATAAA 118

50 SEQ ID NO:6386  
 SEQUENCE LENGTH:277  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

55

CLONE:HUMGS07551

SEQUENCE DESCRIPTION:

GATCCAACAA ATTAACCATA TAAGCACAGA AAATAGAGAA ACACAGTTAT TGAATCTACT 60  
CTTGTCATTA ACATTTTCAA AAAACAAAAT GCATATTGTA ATATTTGGTA CATGACACTT 120  
GCATGTTGNT ATGCCTATAT NCTTGCAAAG NATTCAATGT GTACTTAGCG GCGNTTAAAN 180  
CTATGTCATG TACAACNTT ATAAGCNTT TTNCNGGGGT CCCATTGTC CTTTCATCTT 240  
CAGTAAAGTC TTTGTCAGG AANNGTTGTN TGGTTAN 277

SEQ ID NO:6387

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07552

SEQUENCE DESCRIPTION:

GATCCAGGGA TGGGAATGG AGTGGGTAGG AGGGGTAATG CGGTCATTGG AGTCGGGGGC 60  
TGGAACATTA TGAGTGCTCA ATAAATATAA ACTAATGAGA AA 102

SEQ ID NO:6388

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07553

SEQUENCE DESCRIPTION:

GATCCAGAGG TGGGTGCAGC TGAAAGTAAA CAGAAATGGAT TGCCAGTNAC ATGTATGCCT 60  
GCGCAGTTCC CTTTTNATT GCAGAAGCTG TGAGTTTTGT NCACAATTAG GTTCCTAGGA 120  
GCAAAAAACC TCAAGGATTG ATTTATTGTT TTCAACTCCA AGGCACACTG TTAATAAACG 180  
AGCAGGGTGT TTTCTCTCTT CCTNTCTAAT ATATGGAGTT TCGAAGAATA AAATATGTGN 240  
GCAATATTTA AATTCTCAGG AATTGNCTNA TACTCTTGNG GAATGGANTT CAGTTTTCAN 300  
TCANGNTTTA CATTTNTGGT GGCTTAANAA NCNTTGGN 338

SEQ ID NO:6389

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07554

SEQUENCE DESCRIPTION:

GATCAGTCTT TTGAAATTGG GATTCTAAAT TAGAATGAGA GGAGGAGCTG CTAAAGCATA 60  
AAAATGGTAG GGGTGATTTT GGTNTTTTAT CCTAGTGACC AATGTTGACC ATTAATTGTA 120  
CATTATAAAT AATGTTTTCN TCTGGGACTT TTGCACTTA ANGCTGGTAA TTNTNATCAT 180  
AGGGCTTCAA ATACAAAAGA NTTGTATGCG GTNTTCAGAA AATAAACATG CTCTTTGCAT 240  
ATAAA 245

SEQ ID NO:6390

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07555

SEQUENCE DESCRIPTION:

GATCTTNACG CGNCTGGGGG CGAAGATTTC GCCATGGATG AGGATGGGGA CGAGAGCATT 60  
 CACAACTGA AAGAAAAAGC GAAGAAACGG AAGGTTCCGG GCTTTGGNTC CGAAGAGGGG 120  
 TCCCGAGCGC GGATGNTGAG GNTTATNACA GCNTGGAGCA GGATGGCGAT GAACCCGGAC 180  
 CACAACGCTC TTTTGAAGGC TGGATTCTNT TTGTAAGTGG AGTCCATGAG GAAGCCACCG 240  
 AAGAAGNCAT ACACGTCAAA TTCGCAGANT ATGGGGAAAT TAAAAACATT CATCTCAACC 300  
 TNGNCAGGCG TTCCAGGNTA TCTGGAAGGG GGTNTNCTCT NGTCN 345

SEQ ID NO:6391

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07556

SEQUENCE DESCRIPTION:

GATCCCCTGC TGGTCTCTGG CAGTCTCCTT GATTTTGGGT ACCATGTATA TTTCCCCTT 60  
 TNACTTTAAC GCTTTCTAGG ATAGGGTAAG CACCCTTAAT TCAGGCACCG TCCATNAGCT 120  
 TCCTTTGCAA AGGCTACTTA TGGCCGGTCA CAATCCAGCA CTCAGACAGA GCCAAGGCAA 180  
 TATCCTCTTG CCCATGGCTA TNATGTCAGA CAGTGGATGG GCTCCAGCAA CAAGAGTCAA 240  
 AATAACTAAA GGCCTTTGCT CTCCTCTGAC ATTGAGGCCT GGGGCTTACA GTTTGGAATA 300  
 CAACATGTGA NGGTTTTTGN TNGTTGTTG TATTATTGNA GAN 343

SEQ ID NO:6392

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07557

SEQUENCE DESCRIPTION:

GATCAAAAAT TGTGGCCATC TTTGCAAATN ACTACCTNTA GCCTGTNAAA ATACATTTC 60  
 AAAAAATGTTA TGTGCAATGA AACTAAATT NAAGAGCAGT TACAGTGTGA CTCATCATG 120  
 TTAAAAAAN ATCGAAGAGC TAAAAAATAC GTCTAATTTA TGTAACCCNT TGGNATGTAT 180  
 TNNTN 185

SEQ ID NO:6393

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07558

SEQUENCE DESCRIPTION:

GATCATTTCT TGTAATGTTT TGAGAGTAAT GCATACAGAA ATATAATAAA NTGTGTTGAA 60  
 ACTGCAAA 68

SEQ ID NO:6394

SEQUENCE LENGTH:163

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07559

SEQUENCE DESCRIPTION:

GATCCCCATT GTGTATGANC TGAACAAGGA GCTGAAGCCC ACCAAGCCCA TGNAGTTCCT 60  
GGGTGATGAG GAAACGGTGC GGAAGGCCAT GGAGGCTGTG GCTGCCCAGG GCAAGGCCAA 120  
GTNAGGGGTG GGCTTGGGCA ATAAAGGCAC CTCCCCAAC AAA 163

SEQ ID NO:6395

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07560

SEQUENCE DESCRIPTION:

GATCAACTCC CACTCATCCT GCAGATTAA GCTTGGATGT CACCTCCCGA GGGACGCTGT 60  
GCCTGCCTCC CTCGTCAGAG CAGGTGTTGT CATCTACTCA CAGAATCTGG CTTCTTCCA 120  
CAAAGCACCC CCGTGAGCAT CTGTTTAAACA TTGTCTCTCC ACCTAGACTG TAAGGTCCGT 180  
GAAAGCAGGG ACCACACCCA TTTGTGCTCA CTTGGGACCT ACAGCCTCTA ATCCAGAGCC 240  
TGACACAAAC CTCAATAAAT ATTTAAGGAC TGAAA 275

SEQ ID NO:6396

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07561

SEQUENCE DESCRIPTION:

GATCCGGGAC CTTCANACCC AGGGAAAGGG TGAGGGAGAC TGGGGCCTGG TCTGCTTTCC 60  
CGGGCCTGAA AGCTTCCCCG AGGTTTGCAG GGTGAGGAG GAGGAACGGT GGGGGNNGGC 120  
AGTCACTGNN N 131

SEQ ID NO:6397

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07562

SEQUENCE DESCRIPTION:

GATCCATTTA AAACAAGCTG ATAGTGTTTC GTTAAGCAGT ACATCTTGTG CATGCAAAAA 60  
TGAATTCACC CCTCCACCT CTTTCTTCAA TTAATGGAAA ACTGTTAAGG GAAGCTGATA 120  
CAGAGAGACA ACTTGCTCCT TTCCATCAGC TTTATAATAA NCTGTTTAAAC GTGAGGTTTC 180  
AGTAGCTCCT TGGTTTTGCC TCTTTAAATT ATGACGTGCA CAAACCTTCT TTTCANTGCA 240  
ATGCATCTGG NAGTTTTGAT ACTTGTAAC TTTTTTTTTT TTNGGGGNNN ANTNTTTNNG 300  
GGNCCAGGGG TTTTTTTTNG GAACCCCTTG GGCNNTGGCC CNGGGGTACC CGGCNAGNN 359

SEQ ID NO:6398

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07563

SEQUENCE DESCRIPTION:

GATCTCTGAC GATACCTGTA TGTTCCTTATT GTGTAAATAA AATTNCTGGT ATGAAATNAA 60  
A 61

SEQ ID NO:6399

SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07564

SEQUENCE DESCRIPTION:

GATCCTGTGG GAAAGAGAAA GGCATCCCAG AAGTTTGACT TGTTTTNCTT TTAGAATCTG 60  
TCTCTGCAGG AAAGAAAAGT CATTTTAATA AAAACCAAAA TAATTATATA TAATTGTNGC 120  
CTTTCCTCC CCATCCTCTC CACTAAGCCA GCAACTAAAT GTATTCAGAA AACAAGTTAA 180  
TCAAGGAGGG CAGAAGAATT TTTTAAAC TGTAAGAAAN TGTCCTAAG TTTAGATTTA 240  
TTACCTGTCA TTTAGGGCAA AANTCCAGTG TCCCCAGCAC ATGGTGACCC AACTNTGTCT 300  
CACAGTTGCA AAGTGTGTTG GAAAATAAAG TTGCTTTGTG NACTTNGNGG GNAANNCNNT 360  
NANNNNN 367

SEQ ID NO:6400

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07565

SEQUENCE DESCRIPTION:

GATCAGGAAC CAAAAAGAAG AATGTACTTC ATCTGGTTGG GCTGGATTCC CTCTNATAAG 60  
CCTCCCCAGT TGAAGTAAAG ATGAGGCTAG GCTCTAGCAA GTTGAAGTCA AACCAGCTCC 120  
TTCAAGAAGC TTTGAGCAGA ATGAAGTGGG GAGGACCCAG CTTCCAGCCC AGGAAGCCCC 180  
CTGTACCTGG AGCCATCTGG GATAAGACTT TGACCCATGA CTCCCATATC CACAGCCTGT 240  
CCATCCTAGC CCATCCCAGT TTATCCTGTA TCATTTGAGC TGGGNTTCCA CATCCTCTGA 300  
GTTGGTAGTC CCATNTCAAG TCNTTNAATA AANGNCTNTT TGGANTATTT GANTTCACAT 360  
TAAAAAANA ANAAAGGCN 379

SEQ ID NO:6401

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07567

SEQUENCE DESCRIPTION:

GATCGGGGTA TGAAGTGTGC ACACGCAGCC CAACAACGGG CAGTGGTCTC TGTGCTCCTA 60  
GGCATCCAGC ACAGGTTCTG GCAGGGCACC CCTGCTGGGG TTGGGGGCTG GTCTGTGCAT 120  
AATCCTGGAC TGTGATGGGA ACAGCCCAGT GCAGTCTAAA CTTCAATTGT GTTGAAACTA 180  
CTTTAATAGA CAAAGTAATA AATCATGTTT ATCTATTGAT TTAAA 225

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SEQ ID NO:6402  
SEQUENCE LENGTH:60  
SEQUENCE TYPE:nucleic acid  
5 TOPOLOGY:linear  
CLONE:HUMGS07568  
SEQUENCE DESCRIPTION:  
GATCTTCAGT TGTATTTTNG TGAATATTTT AATACATCTT TTTCAATTTC TGAAAACAAA 60

10 SEQ ID NO:6403  
SEQUENCE LENGTH:176  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
15 CLONE:HUMGS07569  
SEQUENCE DESCRIPTION:  
GATCCGGTGC TACGGGAAAC ATTTTCCTAA GATGCCCATG AGAACAGACC AAGATGTGTA 60  
CAGCACTATG AGCATTAATA AACCTTCCAG AATCAATAAT CCGTGGCAAC ATATCTCTGT 120  
20 AAAANCAAAC ACTGTAAC TNCTAAATAAAT GTTTAGTCTT CCCTGTAACC TTCAAA 176

SEQ ID NO:6404  
SEQUENCE LENGTH:360  
SEQUENCE TYPE:nucleic acid  
25 TOPOLOGY:linear  
CLONE:HUMGS07570  
SEQUENCE DESCRIPTION:  
GATCTTCCCT GCGGCCTCTG CCCTGGCCTG CTTCCAGCA CACACTTCTT TGGCCTAAGG 60  
GCTTCTCTCT CAGGACCTCT AATTGACCA CAACCAACCT GGGCTTCAGC CACATCAGTG 120  
30 GGCAGTGGAG CTGGGGTGCA CATGGGGCCT GCTCACCTTG CCCACACATC TCCAGCCAGC 180  
CAGGGCCCTG CCCAGCTTCA ATTTACAGAC CTGACTCTCC TCACCTTCCC CCCTGCTGTC 240  
CAGAGCTGAA CATAGACTTG CACTTGGATG TCACCTGGAG TGTNACATGG GAGTGTTATG 300  
GCAGCATCAT ACCAAGGCCT ACTGTTGCAC ATGGGGCCAA AACCAGTAAA CAGCCACCTN 360

35 SEQ ID NO:6405  
SEQUENCE LENGTH:32  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
40 CLONE:HUMGS07571  
SEQUENCE DESCRIPTION:  
GATCTNACTA ATAAATGAAG GGAAAAAGGA AA 32

45 SEQ ID NO:6406  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
50 CLONE:HUMGS07572

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SEQUENCE DESCRIPTION:

GATCTGGTCA TTAAAAAGTG TGTGGCACCT CCCCACCACC TCTNTCTCTC GCTCGCTTGC 60  
 TCGCTCCTGC TTTNACCATG TNATGTGCCT GCTCCCCCTT TGCCTTCCGC CATGATTGTA 120  
 NGCTTCCTGA GGCTTCCCTA GAAGCAGATG TCAGCATTAT GCTTCCTNTA CAGTCTGCAG 180  
 AACTGTGAGC CAATNAAACT TCTTTCCTTA TAANTTAAA 219

SEQ ID NO:6407

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07573

SEQUENCE DESCRIPTION:

GATCCAGTTA CATGTATTAT NNTTTTCCTA CCTTATGGAC TATTTTGGAG GGATAAGCTA 60  
 TTAAGACTAA GACTATGNGT GANAGTNGGG GAAGGAGCAG GAAGGGAGGA ACCTGCACAC 120  
 CACATTGGAA CCNGCACACC ACATTAACAC AAAGGCAATC TTCTGGCTCG GACTGTTCTT 180  
 TACTACTGTN CTAAAGAAA ATGTTTCATTG TGCTGCAGCT ANCTAGCCTC CATCTNCTAC 240  
 ACCAAATACT ATTCCATGCC ATGGAAGTGC TATGCAATAA CTNTCCCAGG TAGGCACCTT 300  
 ATACCCGCTT AAANAGNCTT TAAANATNTG CANTTTTGGT NGGNGTN 347

SEQ ID NO:6408

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07574

SEQUENCE DESCRIPTION:

GATCACTCCT TATTTGCTGT TATTTTNGTN CTCTTAACCA TACATTTCCC AATGTTTAAA 60  
 GGGTGGTATT TNGAGAAAAGT NAATGGGTTT TGTAAGTGCC AGCNCTTTAT ATAAGCAGGT 120  
 AGACTAGCTT TTNCCCAGCA GACGCTTGTC TGTNTAGACT TCCTTAAAAAN AATTATCTTC 180  
 AAATAAAGCA AAATCTCCAT AAAANGNN 208

SEQ ID NO:6409

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07575

SEQUENCE DESCRIPTION:

GATCCATAGA CTTAGCAAGT CTTGCCTTAT CTATGGAGCT CGATGGTGAG AATTGTNACC 60  
 ATTGTCTGAT GTCCATAGTT CCTTCCCCCT AGATTGTTTC TTTCCACGGA TTGTGTTTCA 120  
 CTGAACCATT NNATTTTAA TTTACCAAAG TACTGTACTT GGCTATTTGC AGTGTTTTCA 180  
 AAACCAAATG TTTCTNTTTT GGTGTTTTTA ATCTCCGATA CTTGGTGCAA TAGAAGCTGC 240  
 AAAGATGTGC CACTTNATCT ATGAAATGGA GTNTTGATA CCAATAAATN CTAGTTTAAA 300  
 AACANTTNAN NANNNANN 318

SEQ ID NO:6410

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07576

SEQUENCE DESCRIPTION:

GATCTGTAA GGGGTGGATA ACATAATATG CAGCTTAGGA TGCTATTTTA AGATGTATGA 60  
TATTCAGTTC ATTCACCTGA TTACTTTGGT TGCAGCACAA CTGTATATAT NGTATAACCG 120  
AAATTGATTA TTTNCATTGT CCTTAATGCA GTGATTTATA ATTNAGCAT GTTTAATAAG 180  
TTNCTCTTC TNGTTAACTA GTCATTTGAC TGGNAANNNA TAANATNCTT TTN 233

SEQ ID NO:6411

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07577

SEQUENCE DESCRIPTION:

GATCCCACGA GGACCACTNT GTAATTGNCA GGGGGCTTCC AGNNAAGACA CTGAACCTG 60  
AAGCCGTGGT CTGGGGCAGG GTGGTGGGAG AGGTGGGCGG GGGNN 105

SEQ ID NO:6412

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07578

SEQUENCE DESCRIPTION:

GATCACCTTC CCACTTCATC CATCCCCACC CTTCCAGCTC CCCATCCATC CTGCTGAAAG 60  
CATTTCCACC ACTCAATAAA ACCTCGCATT CATCCTTCAA A 101

SEQ ID NO:6413

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07579

SEQUENCE DESCRIPTION:

GATCAGAAGG AATCCGNCGA GGCAGGGATG GGTGTGCCCA TGTNTGCCTT GACGGGACTT 60  
CATCTTATAG ACTGTTAAAC TGTCACACAC AAACAGGCTT TCCACCCTG CTCTGNNGC 120  
ACCACGCACA GNTTCCAGT TCTTAGTGTG GCTGTTTAAA GTAGAAAATC TGGGGGCTGG 180  
GTGAGGCCAC TCATGCCTGT AACCAGGGC TTTAGAAGGC TGAGGCTGGG GGGNTTGT 240  
GAAGGTCAGG AGGTTCAAGG CCCAACCTTG GGAACCATAG GCAACNACCC CCCATNNT 300  
NCCAAANTNG AAAAAACCAA AAAGGNNAC CN 332

SEQ ID NO:6414

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07580



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## SEQUENCE DESCRIPTION:

GATCTACCAG CATAAATATC TNCTNATTTG TCCCTATGCA TATCANTTGA GCTTCATATA 60  
 CCAGCAATAT ATCTNAAGAG CTATTATATA AAACCCCAA ACTNTTGATT ATTAGCCAGG 120  
 TAATGTGNN 129

SEQ ID NO:6415

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07581

## SEQUENCE DESCRIPTION:

GATCTAGAGG AATTAGTCAT GACATCAAGA AAGGAGTCTA AAGAAGAGAA AGAAAATCAA 60  
 GATGAAAGAG AAGTAAAAGA AGANGAACAA GAAGAAGAAG AAGAAGTCAG GTCAGCAGAA 120  
 ANTTCTCAA ANTCTCCAAA GAAAGGTCAC TGATTCCAAG GCANCCTGTG GNAAGANGAN 180  
 TTCAGATGTC AGTGGGAGCC TCCAGGTGGG NGGNGAGCAT GCCTAANCCC TGGTGGCCAT 240  
 TGTNCTGTAC TANGGAN 257

SEQ ID NO:6416

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07582

## SEQUENCE DESCRIPTION:

GATCCACAAG GCTTCTGTAT ACAGTTCACG GTCCTCGGCA TTGCTTCTNG TAATTTTNC 60  
 ATCCCAAAGG AGAGCTACTG TACTGACTGT ACTTGTGGAA TNCAGCGCTT CATTAAATTA 120  
 AGTTTATTAA AATGCAAA 138

SEQ ID NO:6417

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07583

## SEQUENCE DESCRIPTION:

GATCTAATGG GACACGGCCA GTGCCTAGGG GTGCCAAGTC CAAGGCCTCC CACTGGGNGT 60  
 AATCGCTGAG AAGATGCCAA TTTTCATCC ACCGGCTGCA CAGGCACAAA CTCCCCACC 120  
 CAGGACGGCT GTNATGAGGT GGCCCTCCCT NTNAACCCTG GTCCCTGGAG TCCCCAGCAC 180  
 CTGGGGCCCT GGTGGGGCTG ATGTCACAGG TGTTTACTGT GCTGCTGCAC TGGTCCTATG 240  
 NCAGCTTCAC CCCATGTGGG GACCACGGAA GGNACAAATNC CTTACCCCG NTTGCCGGN 300  
 CCGTGCGGTN NNCAAGANGG GNCAAGGANG N 331

SEQ ID NO:6418

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07584

## SEQUENCE DESCRIPTION:

GATCCAGCTT ATCCTTTAAT TTCAAAGTCC ATTCTTGGGG CTGGTGGGGA GGCAGGAGAA 60  
TACCCCTCCC TAAGCCCTTA GTGTGTGCCG AGCTTGCTTT GTNATGTTGG CAGGGGAGGG 120  
GAGACCTGGG TGGTGACTGA GTTCCCTTTA TCAAACCCTT CAATGGGCAC AAAATTNAGT 180  
GCTTGATTTT ANGGTTTNAT TTTTNNATGA ATGTCCAAAA TCTGTGTTTC CCCNNTGCC 240  
TCCCAAGANN TGTGTGGGCC AGTTGAAAGT GTCTTGTTT TGTGTGTCAT CTTTCCCTN 300  
AATTCTGGA GCANGNCCC TGAGNNCCNT GCCANAN 337

SEQ ID NO:6419

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07585

## SEQUENCE DESCRIPTION:

GATCATGGAT GTAGCATACA CCAAAATCCA CCGAGACCTT TGCAAAATNA GGCTACTTGT 60  
TTNATTTTGC CAGATTATCA TGGGAGAGTC TTAACTAGT NCTGAATATT TGTAAGTCTG 120  
AGTACTTCAT AGAATTATAA AGAAGGTACA GCTGACCCCT TCTCACCATG TNGTAAATAT 180  
TTCCTGAGAC TGGGTGCAGT ACTGAGGGAT AATAATCTCC TGNTTTATCA AATCCTGACT 240  
GTCTAGAGCA ANTTGTACAC TCTCTTGTG AATGGTCCTG TAACGTGTAT GNNCACATTT 300  
NTGGGTGCCT TAGANGTNGT NTTTTNCATG TGTGCTAATN TGCAGTTTCN 350

SEQ ID NO:6420

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07586

## SEQUENCE DESCRIPTION:

GATCCAGGGT CTNAACCGCC GTGGGACGAG GAGGGCATCC CGGCCACAGC AGGGGCCGAG 60  
GAAGAGGAGG AGACAGAGGG GAAAGGGGAG CCGGCCTGAC CCACACCCCC GGCCATCGCT 120  
CCCTGGGCCA GGTTAGAGC AGGGAGTTTG GCTGGTGCTG GGCTGAGCC AGGGGGCCGG 180  
GACACCTTG TTTCCGGTGG TCTTCCCGTT GTGGGAGCAG GTNGAGGGTG GAGACCTAAA 240  
CTTTGGGGTC CAGCTGCCTT CAGCCCNCT CCNCCAGACT AACAGACCCT TGGAGGCAGG 300  
GGCTGTGGAA ATAAATCTTT GCCTGNTGGG NTAAAAAAA ANTATNANNT GTGNNNNGTT 360  
GN 362

SEQ ID NO:6421

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07587

## SEQUENCE DESCRIPTION:

GATCTNCTCT CCCACCCACA CTTATCTCCC CCAGGGCCAC TCCAAAGTCT ATACACAGGG 60  
GTGGTCTCTT CAATAAGAA GTGTTGATTA GACCTGAATT TCTCCACCTA TAA 114

SEQ ID NO:6422

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SEQUENCE LENGTH:62  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
5 CLONE:HUMGS07588  
SEQUENCE DESCRIPTION:  
GATCTTTGCT ACTGGAGTCC TTAAACAACA CCTATAACGA TAAAAAATTC CTAATTNTTA 60  
AA 62

10 SEQ ID NO:6423  
SEQUENCE LENGTH:96  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
15 CLONE:HUMGS07589  
SEQUENCE DESCRIPTION:  
GATCCTTCAT ATTTAATTAA AAGTGTTCAT TCAGGTAAGG TGTATGTTGA AATTTTNCCA 60  
ATNATCTTAA TAAACCTGG CAATTTAAAA NCCAAA 96

20 SEQ ID NO:6424  
SEQUENCE LENGTH:88  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS07590  
SEQUENCE DESCRIPTION:  
GATCTATTTA TNTAAGTATG TAGTAAACAA TATCTNAAAG TGTCCGATTC ACTACTTGTA 60  
AATTAAAAAA GTNATGATTA ATGTGAAA 88

30 SEQ ID NO:6425  
SEQUENCE LENGTH:314  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS07591  
SEQUENCE DESCRIPTION:  
GATCAGAAGA AGCTACAGTT TTNTTTTAAA CTTGAAAAAA AATTAAGAAG TATTAAGGAA 60  
AAAGCTTAAT ACTCTGGAAA CCAGACATCT GGTCTTTCTC ATGCGTAGGG AGCAGTGTA 120  
ATGAAAGTGA AGTCAAACGG ACAGTTTTTT NCTGCATTAT GCACAAGGTG TTTTAAATTG 180  
40 TCAGCTTAAG GTTTAGATGA NGATAATCTT TAACTTTGTT TACAATTTTG NCTATTTNGC 240  
ATTATCCCCC TTTTNCCATA AAANNTAANG TGAATATGTG TGCATATNNN TNTNGAGTCA 300  
NAATTAAACT TATN 314

45 SEQ ID NO:6426  
SEQUENCE LENGTH:91  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
50 CLONE:HUMGS07592  
SEQUENCE DESCRIPTION:

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GATCCTGTGG TGTGTATAA AAATGAACAG CTAAAAATTT ACCCATGACA AGATTAAAGC 60  
 AAAAATAAAC ACAAAGTTGT TAGACTTTAA A 91

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SEQ ID NO:6427  
 SEQUENCE LENGTH:122  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07593

SEQUENCE DESCRIPTION:

GATCTTGTGC TATAACTTTT AAAGCCATAC AAATAAGAGT GCTAAACTNT GGACTTAAAA 60  
 GTAGGTGTNT AAATATTTT AATCAGTATT ACTTGGAAAA TAAATATAA CAAACCCATA 120  
 AA 122

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SEQ ID NO:6428  
 SEQUENCE LENGTH:293  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

20

CLONE:HUMGS07594

SEQUENCE DESCRIPTION:

GATCCTAACC CCTGCAGGC TCAGGGGTCA GCAGGGACCC ACTGCCCCAT CTCCCTCTCC 60  
 CCACCAAGAC AGCCCCAGAA GGAGCAGCCA GCTGGNATGG GAACCCAAGG CTGTCCACAT 120  
 CTGGCTTTTG TGGGACTCAG AAAGGGAAGC AGAACTGAGG GCTGGGATAT TCCTCATGGT 180  
 GGCAGCGCTC ATAGCGAAAG CCTACTGTAA TATGCACCCA TCTNATCCAC GTAGTAAAGT 240  
 GAACTTAAAA ATTCAATCAA ATGAACAATT AAATAAACAC CTGTGTGTTT AAA 293

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SEQ ID NO:6429  
 SEQUENCE LENGTH:209  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07595

SEQUENCE DESCRIPTION:

GATCTGAATT TGTAAGTTAT TAATGTGAAA GGGGGAGCAG GAAGCTCCCC GTTTGCACAA 60  
 AGGGGGATTT GTTTGCACAA AGTTCAGTGT AAATACTGTG AGANTNGANT TCTGAAAAGG 120  
 TCATATTTAG TGATTTCAA AGCACACATT TAANTGANGA CTGACTAAAT AANAGGTACC 180  
 ACACACTTCT NGGTTGGTTT CATTCCAAA 209

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SEQ ID NO:6430  
 SEQUENCE LENGTH:200  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07596

SEQUENCE DESCRIPTION:

GATCTCCCTC AGTNTGCCCC CAGCCCCCAA ACTCCTCCTG GCTAGACTGT AGGAAGGGAC 60  
 TTTTGTGTTT TTGTTTGTTC CAGGAAAAAA GAAAGGGAGA GAGAGGAAAA TAGAGGGTTG 120  
 TCCACTCCTC ACATTCCACG ACCCAGGCCT GCACCCACC CNCAACTCCC AGCCCCGGAA 180

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TAAAACCATT TTCCTGCAAA

200

SEQ ID NO:6431

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07597

SEQUENCE DESCRIPTION:

GATCTNATTC CAGGATTGCT CAGAAATTGG AAAAAAACTC ACCTGTGCTT CCCAAATTTA 60  
 TTTCCCAAGA CAAAGATGTC TATAGCACAG AAAAAAATGC ATGANTTAAA AAATCAAGAT 120  
 GTATTATTAA A 131

SEQ ID NO:6432

SEQUENCE LENGTH:42

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07598

SEQUENCE DESCRIPTION:

GATCCTGAGC TGTCCCATTA AACATGGCCC TGTCTCGGTA AA 42

SEQ ID NO:6433

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07599

SEQUENCE DESCRIPTION:

GATCCACTAG ACAGTTTNCA GTTTGCTTGG AGGTANCTGG GTAATCAAAA ATGTTTAGTC 60  
 ATTGATTCAA TGTGAACGAT TACGGTCTTT ATGACCAAGA GTCTGAAAAT CTTTTGTNA 120  
 TGCTGTTTAG TATTCGTTTG ATATTGNAC TTTTCACCTG TTGAGCCCAA ATNCAGGATT 180  
 GGTTCAGTGG CAGCAATGAA GTTGCCATTT AAATTTGTTC ATAGCCTACA TCACCAAGGT 240  
 CTCTGTGTCA AACCTGTGGC CACTCTATAT GCACTTNGGT TTACTCCTTT ATTNCAAATA 300  
 ANTATACTAA AAGNCTTTAA ANNANGNNNA NN 332

SEQ ID NO:6434

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07600

SEQUENCE DESCRIPTION:

GATCAATACG GGTCTATTTT NATGTCAACT GAACACTGTA GGGTACCTTC CAGTCTTTTT 60  
 CAAGATTGTN AAATTGAGAC AAGTAATTGA ATAATTTGTC CTATTTTAAT TTTAAAAAAA 120  
 GTGAATGGNC TGAAATGTTA AATGTGAATG TNCATTTCTN.AATTGCAACT TTNCTACTGA 180  
 GTGTTTGCAC TATACTTNCT GGAATCTNAT TTAACAAANN TANN 224

SEQ ID NO:6435

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07601

SEQUENCE DESCRIPTION:

GATCAAAAAG CACAAAGAGC TGGGGCAGAG GCAGGAAGCA GGGGCCCTCC TGGCAGCTCC 60  
TCTNAGTGGG GAGAGGTTGG GCAGTGAGTG AGGGACCCCT AATGCAGGGN CTAGAAGCCT 120  
CANTTTCCCC NTTTTACCCT TCCACACAAT AGCCTCTGTA GGNNAGGCTG CCCCATNCCA 180  
CCNGGNTN 188

SEQ ID NO:6436

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07602

SEQUENCE DESCRIPTION:

GATCTAGGAC TAANACTTAA AATGTGGTTG GAATCTCACT CAAGGCCTAC CCACCTAAAA 60  
CTGCGTTCTA GCAATTGCAT GCTGACTGCA CCTATGAGTC GTAAGNCTGT AGTTGCAAAG 120  
TGTGTCTAGT TTANATTCT TTCTAAATAC TGGTACGGGN AACAGGCATT CCAGNACTTG 180  
TGGCTTGCTG GNGGTGGTNT GAGTNATGNG GAATCTTGGG AAGGGGTTCC TGCCCTGGG 240  
ANTTGGGGGG TTTTNN 256

SEQ ID NO:6437

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07603

SEQUENCE DESCRIPTION:

GATCCAGGGC CTTTNAACA TCCCCAAAGT CATGGCCATA CTCACCATTA GCCAGTTTCT 60  
AACATCTGTT TCAGGGTATC CAGCTGTAGA TGTCTTATC CCCCATACTT GTGAGTTCTT 120  
GGGGTTGCTC ACAAATACTA GGGGTTTTTG TTGTATTTT AACAANTATA TCCTAATGTC 180  
ATATTNATNC TCTTTTGTA CTGCTGGTCT TTACANTAAA GGNGTCATCT GCCTTTCAAA 240

SEQ ID NO:6438

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07604

SEQUENCE DESCRIPTION:

GATCAGCACC CTTCTCCACA TCCACATGAC TGGTTTTTAA TGTAGCACTG TGGTATACAT 60  
GCAAACATCC GTTCAAAATC TGAGTCGGAG CTAAAAATAA AAAATGAAAA ANCAGAAATA 120  
AGAAA 125

SEQ ID NO:6439

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07605

SEQUENCE DESCRIPTION:

GATCCGCCTG CNTCGGCCTN CCAGAGTGCT GGGATAAAAG GTGTGAGCCA CTGTGCCTGG 60  
 CCACTCCCTT GAGACCCAGT TTCCACGTCT GTNAAATGGG GGAATACCA CAGTGAGAAT 120  
 TAGATGAGAT AGATGCATTT NAAACCACAA ATCGGGGTGC CCACCTGTGG TGGGTAGTTA 180  
 GGGTAGCTGT TACAAAGTGC CCCAGCAGAG ACCCCCTTGA CTAACCTTNA TTCTTCCATC 240  
 TTTTCCCACA GGTGGCAGCT GCCAACAAGA AGCATTAGAA CAAACCATGC TGGGTAAATA 300  
 AATTGCCTCA TTCGGTANTG N 321

SEQ ID NO:6440

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07606

SEQUENCE DESCRIPTION:

GATCTTTGTC CAGAAAATAA AGCTTTCTGT TGATTTTTTC TTTAAGCAAG AGGTAAGGAA 60  
 ATATGCACTT AAGANTATGT GTACAAGAAA ATAGTTTCTA AAATAAATTG AAATGTCTGC 120  
 AAA 123

SEQ ID NO:6441

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07607

SEQUENCE DESCRIPTION:

GATCCACTCT GGACACTCAA CAAGACCTGA ACAGGATTTN CCTACCTGGT CTTACACTA 60  
 CATCATCATC ATCTCATGCC CACCTGCCCC CACCCAGCAG AGCTTCTCAG TGGGCACAGT 120  
 CTCTTACTCC CATTTNTGCT GCCTTTGGNC CTGCCTGGCC CAGCCTGCAC CCCTGTGGGG 180  
 TGGAAATGTA CTGCAGGCTC TGGGTCAGGT TCTGCTCCTT TATGGGACCC GACATTTTNN 240  
 AGCTCTTTGC TATTGAAATA ATAAACCACC CTGTTCTGTG GAAA 284

SEQ ID NO:6442

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07608

SEQUENCE DESCRIPTION:

GATCTGGTAC GNGGTGGACG TCATGGCCCG ANATGCCCAC GGNAACACAG CGCTGACCTA 60  
 CGACCGGCAG GCCTCCAGCC ATGGAGTGCA TCAACGTGCT TCTNCAGTAC GGCTGCCCCG 120  
 ACGNGTGTGT ATAGTATCTG TTTTATTTGA CTGCAGTCTC CTTGGTGCAA AANCAAANTG 180  
 GGGGAANNATA GGATAACTCA GNATTTCAAA AGGAN 215

SEQ ID NO:6443

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07609

SEQUENCE DESCRIPTION:

GATCTNAGAC TTCTCAGTC CAGAACTGTA AGCAATAAAT GTCTGTTGTT TATAAATTAA 60  
A 61

SEQ ID NO:6444

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07610

SEQUENCE DESCRIPTION:

GATCCTTGCT CTACCTGGCT AGAGTTTCTN CTCATCAGAG CACTGGGACA TTAAACCAAC 60  
CTTTTACAAC ACAA 75

SEQ ID NO:6445

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07611

SEQUENCE DESCRIPTION:

GATCTCAGCT CAGAGAGAGA GCATGAGGTC TTTTAACT GTCAGGAAAC AGAGCTGTGC 60  
CCAATCCAC TCAACTTTTG GCACAACTGT TAATCTGGGC CTTACCTAC CTTAACTGA 120  
GTTTCTGCAA GCATAGCATT TTAGACACCC TGAATAACC TTTGGGAAT GATGCCACAG 180  
AATAAAGTTC ACTCTTAACT TTTCAA 207

SEQ ID NO:6446

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07612

SEQUENCE DESCRIPTION:

GATCTGATAG TGGTAGGTCT ATCAGGAATA TCAGGNAAAA TNCTTTTAAT GTTGTGGCA 60  
AAGTCAATTC CTATCATTTG TACTTGACAC CAGCTACCTA GCAGGCTCAT TGTGAACTTC 120  
AGGTTTCGCC CACGTTATTT ATATAAAGTA TCTCAGTGTA ATATAGGGAG TTGCTGGTTA 180  
TTTGAAAATA GTAACAAAGG TAACCCAAAC GAGAACTCC ATTTCCATAA TTNGCTTTCC 240  
TGAAAGTCAG GCATGTCTTT GAGGACAGGT TTTGGCAGTA TTNNTTNGT GCACAGGNGG 300  
GAAATTN 307

SEQ ID NO:6447

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear



# EP 0 679 716 A1

CLONE:HUMGS07613

SEQUENCE DESCRIPTION:

GATCTGCCTG TTTATTTTGG TGGGTGGTCT TTCCTCCCTC CCCTACCACC CATGCCCCCC 60  
 TTCTNAGTCT GCCCCTGGCC TCCAGCCCCT AGGGGACTAG CTGGGTTGGG GTTCCTCGGG 120  
 CCTTTTCTCT CCTNCCTCTT TTCTTTCTGT TGATTGTCGC TCCAGCTGGC TGTATTGCTT 180  
 TTNAATATTG CACCGAAGTT TTNAAATAA AATTTTAAA 219

SEQ ID NO:6448

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07614

SEQUENCE DESCRIPTION:

GATCTGGTGT AGTATATTTT ATCGCATTTT CTTATATTAA AAAATGTCTG CATGATTACA 60  
 TTTTATTTCC TTTGTAATTT ACATTTTCTG ATAGTGTATT GCTATATGGG TGCCAAGATT 120  
 GANTATGAAG AACCCGAGTN TTTGTAGTAT TATAGTTTAA AGCAAATCTG TGTGGTGATA 180  
 CAGCCATAAG ANTGGGGCTT ATATAANCTC TGTACATGTA AGATTTTGTA CAGAGAATTT 240  
 TTAACCTTAT AAATTGTATA TGANCATGTA NN 272

SEQ ID NO:6449

SEQUENCE LENGTH:300

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07615

SEQUENCE DESCRIPTION:

GATCCACCCG CCTCAGCCTC TGAAATTGTT GGGATTACGG GCGTGACACN CGCGCCTGGC 60  
 ATGTATATCA TTTTNNATTG TGTATTTTGT AATTTTGTG TGTNAATTTA TTTTAAATAT 120  
 AGTTTTCAAT TTAACCTGTT AGTTTCTGTA GTGGCAAATC CTTGTGTTTG CAATATTGGA 180  
 TTATTTCTCC ATAAGAGTTT CACATTTCTC CTGCTAGGAA ATCCATGGGG AATATTGGAA 240  
 TTGGGCTAGT TTTAATNNNA TNNCTAATGT TTAANGGTTT TGAAAAANAT TGGCGNCAAA 300

SEQ ID NO:6450

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07616

SEQUENCE DESCRIPTION:

GATCTCCACT TTNCCAAAGG GCTGCNAGAG GTGATTGANA AGAACCGGCC TGCTGATGTN 60  
 AGGGCGTCCA CTGCCCCCAC ACCGTCCACA GCAGCTGTCT GAGCCCTCAA TCCCCAAGCT 120  
 GGCAGCTGTC ATTCAGGACC CCAACCCCTC TNAGCCCCTC TTTTCCCACA TTCATAGCCT 180  
 GTAGTGCCCC CTCTAACCCC CAGTGCCACA GAGAAGACGG GATTGAAGC TGTACCCAAT 240  
 TTAATTCAT AATCAATCTA TCAATTACAG TCCGTCCACC ACCAAA 286

SEQ ID NO:6451

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07617

SEQUENCE DESCRIPTION:

GATCTGTGCA GAGAGAGATG GCAGCCACTC CCTTCAGTCC TCCCAGATTT CTGTAGCTAT 60  
TTATGTAGCA GGCTCAATAA AATGTCTTCT CTCTAAA 97

SEQ ID NO:6452

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07619

SEQUENCE DESCRIPTION:

GATCNNAGGC ATNNTTCTT CAGTCAGAGC ATTCAATCCT CAAGCCATTC ACACATTTAG 60  
GCCTCATGCT TTNTCCTGTC TTTAATCACA TCCATTCCT ACACTCATTG AGN 113

SEQ ID NO:6453

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07620

SEQUENCE DESCRIPTION:

GATCATAAGT CATTCCCCTC CCCTTCCAGG CCTCCTGCTA TATTTGGGGG ACCTGACTNG 60  
NTTNGCTGGA GTCCCATGAG GATGTGGGCC CNTTAATAAN GGATAGCAAA CAGGCAAA 118

SEQ ID NO:6454

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07621

SEQUENCE DESCRIPTION:

GATCCCAAAA TCCAAGGATG CTTCGAATCC CTTATATAAA ATGGCATGGT ATTTGCATAT 60  
AACCTACATG CATCTTCAAA TATGTTAAAC CATCTCTAGA TTA CTTATAA TACCAAATAC 120  
AATGTAATGC TATGTAAACA GTTGTTACAA TGGATTGTCA AAGGCAAGCT CTNCTTGCCC 180  
ANTNCGGGCC AANTGNGNGG TNCATGAGCA AATTAANTNN NTGCTGGTAT TTN 233

SEQ ID NO:6455

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07622

SEQUENCE DESCRIPTION:

GATCCGAATT TCCTGCTCTA AACCTCCAC TGCTTTCTGC TGTTTCCACT GAGGAAAGAG 60  
GATGTGTGTC ATTAAAGCTT TGTGGGACC TGTCACAGTC AAGGTGGGTA TAATTATGTT 120  
TAATTTATTG AAGTGTTTCT GGGCATCGTC TTTTCAAAT TCATATATNC TATCCAGAAG 180

# EP 0 679 716 A1

ANGTGNATTC ATTNNNCATT ATNAAAAAAN ATAAAAATATT ACCAGATAAA GCTCANCAC 240  
NCNCTCTNCC CCN 253

5 SEQ ID NO:6456  
SEQUENCE LENGTH:44  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07623  
10 SEQUENCE DESCRIPTION:  
GATCTTTCCT ATCAGTGTA TAAAAACTCA TATTATGGCA GAAA 44

15 SEQ ID NO:6457  
SEQUENCE LENGTH:320  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07624  
SEQUENCE DESCRIPTION:  
20 GATCAGGCAG GGTGCCATTN ATTGTCTTTC TCTCCTAGCC CCCTCAGGAA AGAAGGACTA 60  
TATTTGTACT GTACCCTAGG GGTTCCTGGAA GGGAAAACAT GGAATCAGGA TTCTATAGAC 120  
TGATAGGCC TATCCACAAG GGCCATGACT GGGAAAAGGT ATGGNAGCAG AAGGAGAATT 180  
GGGATTTNAG GGTGCAGCTA CGCTCACCCT AAACCTTTTG TGGCCTGGGG TATGTCTTGA 240  
25 GGCCAGACT GTTAAGCAGG CTCTGCTGGC CTGTTTACTC GTCACCACCT CTGCACCTGC 300  
TGTCTTGAGA CTCCATCCGN 320

30 SEQ ID NO:6458  
SEQUENCE LENGTH:179  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07625  
SEQUENCE DESCRIPTION:  
35 GATCCAAATN AGAACAGATT GGTTATTGCA GGTATCACAG CCTAAAGAAA TTATCTTTTT 60  
GCAAAAGAAA TATTAAATGA TTTAGCAGTC TCCACGTGTG TTAATGTTTC AAACGTGTAT 120  
CATAATGTGT ATAATTGTGT AACAAAATTG TCTACAATAA ATCTNTTGGT ATTTGTAAA 179

40 SEQ ID NO:6459  
SEQUENCE LENGTH:337  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07626  
SEQUENCE DESCRIPTION:  
45 GATCCATTCC CCCAAGGGG ACAACGGGGT GTNAGNGGAG TAAGGGGTGG AGGTAGGGGC 60  
CAGAGGGGCT TACACGATAT CCCATACCTT TAATGCCTTT GGCCTTCCAT TCTNATTTCN 120  
CTNATGAGAA TATTGCTGGC CCTGCTTTCC CTGGTAGGTA TTTGCCAGGC CCAATGCTTT 180  
AACCTTAAGC TGATACTTTG CTTTAGATGT CAGTCTCGTT ACCAGCAGCC TTTTGACCCA 240  
50 ACTACGGCGC TCTATATTTA AGTNGAGGGA TTTTNANCCA TTGTGCATGG NAAAAAGNTG 300

55

TTCATGGGTA CNATNGTAAG NAAANNTAAA ANTTTTN

337

SEQ ID NO:6460

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07627

SEQUENCE DESCRIPTION:

GATCGGTTGN GNCATGGAGT GGGGGCTTCC AGGTGGACCT NCCCGGCACA CATTCCATTT 60  
 NTTGAGCCCC AGTCCTGCCC CCCACCCNAC CCTCCCTACC N 101

SEQ ID NO:6461

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07628

SEQUENCE DESCRIPTION:

GATCCTTCTT GGTTAGTATT ACTTGTNCCG GAGCAATTCT NATTCCTCGT TTAGACATTG 60  
 NNATTTCTT CGTTGGAGCT GTGAGCAGCA GCACATTGGC CCTAATCCTG CCACCTTTGG 120  
 TNGAAATNCT TACATTN 138

SEQ ID NO:6462

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07629

SEQUENCE DESCRIPTION:

GATCTNATTA GNNTAGTAAT GTTTTCCCTT TAAACAGATT CATCATTATC CCTAAAGTAT 60  
 TGCTGTATTA ATACTGTCTT CTAGAAAGTA TACACCAGTN CCTACTTTCC TCCGATATCA 120  
 TTAGCTGTTT TCNGAAACTN AATTTCTCT TCAGAGATTN CTCATATGTN TN 172

SEQ ID NO:6463

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07630

SEQUENCE DESCRIPTION:

GATCCACAGA GTTCATAGGC ATGATTAAAT GGTAGTAGTT TTCCACCACG AAGTTTGGGA 60  
 ATAATTTGTC ACAAAGCAAT ANGGTAATTA GAAAAATAAC CTTTCAGAAG GAGACAGTTT 120  
 CTCCAAAGCT TGGGTACTTT CGCTTAATAT TAAANAGTGG ANGGAATTTT TTNCCTGCCA 180  
 GNCAAAAGGC AGNAGGTGTA TTTCTACACC ATGGNTAGGC AANTNNTTTT TTNCTAN 239

SEQ ID NO:6464

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07631

SEQUENCE DESCRIPTION:

5 GATCTGCATT TAGCAATGTG ATGTCAGTAA ATGGACATAA CAGGATTGTT GTAAAGGTTG 60  
GGCATGATGT ATGCAAAGTA CTGGCCAGGG TAGACTAATA ACTGATGGCA TTTATATGCT 120  
GTGCTGGAAT ATTGTTACCA AGCTGATGTG CCGTTCTCAC CCNGGGNGAA TACTGGTTTT 180  
GTCATTTTCAT AAATGATATT TTTATAANTA AAA 213

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SEQ ID NO:6465

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS07632

SEQUENCE DESCRIPTION:

GATCTGGCCA AGAATGAGGC CCTCCCAACA CTTTCACTCC CTCTCCAAGC CTTGATGGGA 60  
CCTCCACTTA TTTAGGCCTN ATGTGCTTTG AAGAAGCTTT GAGAGCCAAT NTGTCTTCCA 120  
CGGGTCTCTT TTTTGCTACA AGTAATCAGC CCCATGTNTT CTCTTAACT GAGAATTGCA 180  
20 CCGGGGGCAA TTCCTGTTTT CTAAGGTGGT CTCTGCTGCT ATTTAACAAC CCAGAGTAGG 240  
CCTCTGTNAG GCTTCAGTGG CCTCAGAAAC CAGAGGGTCC AGATAGGGGG CCTGCTTGGG 300  
CCCTCTGCTG NCAAACTGCT TAAAANTTN 329

25

SEQ ID NO:6466

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07633

30

SEQUENCE DESCRIPTION:

GATCCACGTG TGTGGCCATA TTGTAACACA TTTTCTGCA AATNACCTCT TTCATTTAAC 60  
AGCCCTTATT CAATGGCCTT TTNCTTTTTC AGTAGTACAT ACACATCTGT GTCATTNGTT 120  
GAATGACGNC ATGAATGTTT TGTAAGATAA ATATAATTAA ANGNTTTTAA GCATTTCTNA 180  
35 CTCATAGATA TTNATGTTAG CACCAAATTT GNTGTGCAAT GANCCTCCCT ANATAN 236

40

SEQ ID NO:6467

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07634

SEQUENCE DESCRIPTION:

GATCTATGCC TTAGTGTTGT TTTTNTTGTG TGCTTTGATG TAAAAGCAAG AGTATTTGGA 60  
GCAAGAAGCT GCAATGCGCC AAATACACAN TAGGCCTTTC NTTATCATT CACACGACAT 120  
45 TTCTGGTTTA GGTGTATGTA GTTGGGCCAT GTTACTTGTC CAGAGGAAGA GNCTAAAGAT 180  
ATACGGNTAA TTTTNTAGTC CNTAATGCTG TTTTGNTTAC NTNCTNTCAN GGTTATTTN 239

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SEQ ID NO:6468

SEQUENCE LENGTH:82

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07635

SEQUENCE DESCRIPTION:

GATCGAGCAA TTGCAATCCA GCCTGGGCAA CAGAGCGAGA CTCCATTTCA AAAAAAGAAT 60  
CAATAAAAAT GTTAAAAGCA AA 82

SEQ ID NO:6469

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07636

SEQUENCE DESCRIPTION:

GATCCGTAAG GCCATGACCA AGGAGGCCAT CCGAGAGCAC CAGATGGCCC GCACTGGCGG 60  
CACGAGACAG ACCTGTTTAC CTGCGGCAAG TGCAGGAAAA AGAACTGCAC CTACACACAG 120  
GTGCAGACCC GCAGCTCTGA TGAGCCCATG ACCACCTTTN TTGTCTGCAA CGAGTGTGGA 180  
AACCGCTGGA AGTTCTGCTG ACCCCTTGTG TAGATGTGCT GCAGCCTTNG GCCTTCNCGG 240  
GCCACGTTCT TCGTTGACAN AGGTTNTNTT GGGGNCCCCT AGGAAGGCGG TATGTNCCTN 300  
GCCNTTNAAN CTTGNCTGGN TTGGATTGNA NCTTTTTTGN CCTTTTTN 348

SEQ ID NO:6470

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07637

SEQUENCE DESCRIPTION:

GATCGTGAAA TCTAAGGCTG CTTGATGTTT TGATGCTTGT NAATGCCGTC GTGCTCTGTG 60  
ACTCCACGAA ACGCCAAGGA GCTTCTTCCG GACGNCTCCT CTTCTCTGT AACATACGTG 120  
TGAATAGTCA AGGTTTAATT TTNCTTTAAT CTAATAAAGT CGAAGTGGA CTNTTAAA 178

SEQ ID NO:6471

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07638

SEQUENCE DESCRIPTION:

GATCCAGCAC ACCTCCTCGG TTTTTTTTC AATAAAAGT TAGAAAGAAA 50

SEQ ID NO:6472

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07639

SEQUENCE DESCRIPTION:

GATCTCTGTG AAACAAAATN AAGCAAGAAC GGAGACGCTG AATAGTTTTA TTTCTNTATT 60

AGAAACTGTG ATTGGAACAA TTGAAGAAAT AAAATCATAA CAGAGAAA

108

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SEQ ID NO:6473

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07640

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SEQUENCE DESCRIPTION:

GATCTGAAGA AAGCAGCAAT ATCTGTNACT AGAGAACATT CCCATGTTTT TAAACTCTTC 60

ANTTCTTAGA TGCATTTAAN TTCTTAATGC AAATNACGTA GCAATTTGAA AACTTCTCCG 120

TATTACTNGT GTTTAAATG TCTTGCTTTA AATACAANNC AAATGGTAAA GGGGATTATC 180

15

TTTGGTTTAG ATGGTTAANT ATNATTNGN 210

SEQ ID NO:6474

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07641

20

SEQUENCE DESCRIPTION:

GATCAGCAGG ACTGTCTCCA GCACGGAGCT GACACTGTTC AGCTGCCTCA ACTGGTAGAC 60

25

GCTCCAAGA AGTCAGAGGC AGCNGTCGGG GCGGAGGTGT CCATNACCTC CCCAGGACAG 120

AGCAAAAAC TCTCCTCAA GAACAGAAAC GTTTTACCNN CTATTGTATG ACCTTTGCTG 180

AGGGTATGTC CTGCTCCTTT CCACCAGTGA TTTGTATTAA GNCAGCACTT ATATTGTACA 240

ATACTTCAGN CTGTTTTTTT TAAATACATA AAACCTTATG TTAAAAAAT CTATTANCAT 300

GGGCAAA 307

30

SEQ ID NO:6475

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07642

35

SEQUENCE DESCRIPTION:

GATCACAGGT TAGGGGTTTC TCTAGATGGG GGTTCGTAAA TTTGCAGTGT CTGCTCCTGG 60

GAGGCAGCAC CAGAAAGGGC ACTGAAATGT ACTAGCTGGA TGTNACCCAG TCTTAATAAN 120

40

CAGGTTTTCT AATCCAGAAA 140

SEQ ID NO:6476

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07643

45

SEQUENCE DESCRIPTION:

GATCAACTTT GTATATTCAC GTGTATTAAA ATATTGTGCA CTAAATGTTT TGCCCTTGTT 60

50

TGCTATTATA TGGTCAAGGC ATTTATCAGC ACTATTGTAA TGAATCATG TAAGTGGCAT 120

GGGTCAGGGA AAATTATTTT CTAATTNCT GCCTAATTAA ATTNCTGTTT TCCAGTATTA 180

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CATTAAA

187

5 SEQ ID NO:6477  
 SEQUENCE LENGTH:113  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07644  
 10 SEQUENCE DESCRIPTION:  
 GATCTTGAT ATTTNATTTT TAAAAAACTA GAATAAACAG AGAGGCATAA NCATATCTTA 60  
 GAGTCCAAGT GGTAGTGTTC AGCATTGGAT ATAATAAATG GATGTTTTAC AAA 113

15 SEQ ID NO:6478  
 SEQUENCE LENGTH:276  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07645  
 20 SEQUENCE DESCRIPTION:  
 GATCTCATT TGGGCTAAAA TAAGACAATA TTCAAAGGTC AGAGATATCT AGCCAGAATC 60  
 TNATGGAGGC TGGATTTTCTG ATTTTNTNAC AGAATTAGAC AGAGGAACAC AGAGGGGACA 120  
 GGCTCAGTTA GGGTGGAGGT GTGGGGTAGG GAAGCAGGNC TTGATATAAN TNATTGGAAT 180  
 25 CATTGTCTTT TAANCCAGTG GTTTATGTCA GGGTATAGCG TTTCANGGGA TTTGAGGGTC 240  
 AGATGGGGNA ATGTAGCCTC TTATTTTGCC AGTGTN 276

30 SEQ ID NO:6479  
 SEQUENCE LENGTH:160  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07646  
 SEQUENCE DESCRIPTION:  
 35 GATCTGTCAC TGNTCCCGT CACGCCCTGA TGGGACCGTC TAGTTGCTGG AAAACAAACT 60  
 CAGGGCTCCC ACTGATTCTA CATTATGGTG TGTTGTACAA TTATTTTATT ATATATNACA 120  
 AGGTAATANT AATAGANATA AAATCCACAG TAANTGCAAA 160

40 SEQ ID NO:6480  
 SEQUENCE LENGTH:158  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07647  
 SEQUENCE DESCRIPTION:  
 45 GATCATAAGT NNTAGGACCA AAGGTGTTTT TAATGAGATA ATCTTTTNA TTTNNTAACA 60  
 AGAAAGGAAA TATTCACCTT ACATTTTAAC ATCAACTTTT AAGTGATATT CAGANTTAAT 120  
 TGACCATGGT GATACGTTGT AAAANGTTN CATATTAN 158

50 SEQ ID NO:6481  
 SEQUENCE LENGTH:112

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SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07648  
 SEQUENCE DESCRIPTION:  
 GATCCAAAAA AAAAAAAAAAC GAANANAATT NATCCTCACA AATTGGTGTT CTAAATATCT 60  
 TAAGANCCTA ATTAAATAGC TGA CTACAAA AAAAAAAAAA AAAATNCAAA AN 112

10 SEQ ID NO:6482  
 SEQUENCE LENGTH:105  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07649  
 SEQUENCE DESCRIPTION:  
 GATCCTGTGT GGCCGGTGTT TGCATCTTCA GTGGCCACAA GCATAATAAA GCCCCTTTGC 60  
 CTTTCTCTGT ATTATATTCA ATACAATACA TCAATAGTCT TGAAA 105

20 SEQ ID NO:6483  
 SEQUENCE LENGTH:252  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07650  
 SEQUENCE DESCRIPTION:  
 GATCAGATTT AAAGNCTGGA TTCTATCTAC ATAAGTCCTT TNAATTCCAC CAGGGCCAGA 60  
 GCAGTCCAC CACTGTGCAC TTAGCCATGA TGGCAACAGA AACCAAGAGA CACAATTACG 120  
 CAGGTATTTA GAAGCAGNGG GNCAACCAGA AGGCCCTTAA CTNTCACCAG TGCATCACAT 180  
 CTGCACACTC TCTTCTCCAT TCCCTAGCAG GGGNGGCTAG CTCATTNAC NGGGTNNAGA 240  
 ANCTGAGGNC CN 252

30  
 SEQ ID NO:6484  
 SEQUENCE LENGTH:36  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07651  
 SEQUENCE DESCRIPTION:  
 GATCACGNGT AAAGAGAACT GTTTCCTGCC CTAAA 36

40  
 SEQ ID NO:6485  
 SEQUENCE LENGTH:125  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07652  
 SEQUENCE DESCRIPTION:  
 GATCAGCCTC ATCAATATTG CCGTCATCTG TTAACTACTC CCAGTATATT TCCTCAATGT 60  
 CTGTTTACTT AAAATTTTGT GGAGTGACAT AATTAATAAG NAATAAAGTC TGAATTATAC 120  
 AAAAA 125

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SEQ ID NO:6486

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS07653

SEQUENCE DESCRIPTION:

10 GATCCACACT GGGGNGAAGC CTTATNAGTG TACGANATGT GGAAGAGCT TCAGTCAGCA 60  
TGC GGGCCTC ANCTCCCACC AGAGACTCCA CACCGGNGAG AAGCCATATA AGTGTAAAGN 120  
GTGTGGGN 128

SEQ ID NO:6487

SEQUENCE LENGTH:329

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07655

SEQUENCE DESCRIPTION:

20 GATCCAGAGA GCTTCCTGAA GGACCTGTTG AACTCAGTCC CCTGACCACC ACACAGCAGC 60  
TGC GCGGCGC AAGAGAAGCT GGCTTGCCTT CCACCCTCTG TTCTCCCTCC TTGTGCATTA 120  
AGTTCCCTCC GNGGGATGCT GCATTGGTAC CCAGCCCTCC NCTATCTCAT TTTTCTTGGN 180  
GTGGCTTGGG GTTTTAGGC TTCCNGTTTT ATCTCGTGTG TGTGGTGCAC CAGCTATGAG 240  
GTTGTCTGTA ANCNAAGCCA TCAAAGGGNC TNTAAATANC TAGGNGCCAT GAGTNGTCCC 300  
25 GGNCANCTTT CANAACTTGA GTNTGANAN 329

SEQ ID NO:6488

SEQUENCE LENGTH:101

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07656

SEQUENCE DESCRIPTION:

35 GATCTGTA CT GTAATTTGT TTGTAATCCT GTATATNATG GTGTAATGCA CAATTTAGAA 60  
AACATTCATC CAGTTGCAAT AAAATAGTAT TGAAAGTGAA A 101

SEQ ID NO:6489

SEQUENCE LENGTH:215

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07657

SEQUENCE DESCRIPTION:

45 GATCATGTAT ATAATTGTAA CATCACATTG ATTTTACGGA AGATGTTATA TGGNCTTTAA 60  
TGACACAATG TTTAGNGATA AAATGTACAT TATTTTGGTT CAGTTTTTTA AAAAANNTAT 120  
GCTTTAACAA AATTCTTAGG AATNCTTTTA AGCAATGCAG GTATTGCGAT ANCTGTAGNT 180  
TTTACAATAA TGTTACTCTA CAGNTGGGAN AATNN 215

SEQ ID NO:6490

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SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07658

SEQUENCE DESCRIPTION:

GATCTCTTTG TATTCTCTTC AAGCCCAAAC CAATTCTGTN CCTTCAATCT AAATAGTGGT 60  
 AATATGAATG TTTAAGAAAT GAAATAAGAA ACATGTGCAG GCACTTTGGA AGGTGCTAAG 120  
 TGAQTGCCCT AAGGAATGAA AAGCAAGGGC CAGGTGGGAG TAGCCCAGCG AAGGCACTTG 180  
 GGCTGCCAGG AACAGGNGGC GTGGGAAACT CTGGCTTAGG NAAACATGAA CACNGGGGCA 240  
 ACAGCGGCAN ACTGTTGTTC GAGTTAAATC TAANTCTCAG GCTCTTTNAC GGTAANGGG 300  
 TTANGGATAC TCCATTNNGA TGAAGANAAG NGTGAGGCTG ANNGTAANGC ACATGGCAGN 360  
 TNNN 364

SEQ ID NO:6491

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07659

SEQUENCE DESCRIPTION:

GATCTTTCTT CTCCTTTAAG CTCTTTGTTA ACATTTCTCT AGACGCAATT TATTGAAAAT 60  
 AAAGATTNC TGTTTACTCA TGA 85

SEQ ID NO:6492

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07660

SEQUENCE DESCRIPTION:

GATCCTCATT TATGTTTGTA GTTGGAAGC AAAGCTAGGT AGCCATTCT TCTGTTCTAC 60  
 CAAGTTATAA TAGCATTCTT TTCCCTTTAT ATTTCCCTGA AATAAGCAC ATTCCACTTA 120  
 AA 122

SEQ ID NO:6493

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07661

SEQUENCE DESCRIPTION:

GATCCTACAT TAAGGTCATT TGTNAGAATG ATGTTTGTGT TTGTNTAGAG TTGGCTGACC 60  
 TCCAACNT GGGGTCAAGG AATCCTACTG CCTNAGCTTC CCAAATAGCT AGGACTATAG 120  
 GCATGCACCC GGCCATGTGT TTTATTTATA GCTCTTAAAG CCCAGATGAA GAAATCACAT 180  
 TTTNCCCAT AGTGAAGAAA CATTGGCCA TTGCTTAGTC CTTNNGGGG GTGNCTGTCC 240  
 TGTTTTTATT AGATTAGNGA GACCCTGTGT GGGCCACAGT TAATATANNC CATTATCACT 300  
 TTTAAGGTAA CCTGCACATC TTAGGTTTCA TAATTNCCTT ATTGTTCTNG NCTCAAANTT 360  
 GN 362

SEQ ID NO:6494

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07663

SEQUENCE DESCRIPTION:

GATCGGGGCA CTGCAGGGGC CGAGCCATTT TGGGGGGCCC CCCTCCTTGC TCTGCAGGCA 60  
CCTTAGTGGC TTTTTCCTC CTGTGTACAG GGAAGAGAGG GGTACATTC CCTGTNCTGA 120  
CGGAAGCCAA CTTGGCTTTC CCGGACTGCA AGCAGGGCTC TGCCCANAGG CCTCTCTCTC 180  
CGTCGTGGGA GAGAGACGTG TACATAGTGT AGGTCAGCGT GCTTAGCCTC CTNACCTGAG 240  
GCTCCTGTGC TACTTGCCT TTTGCANACT TTATTTTCAT AGATTGAGAA GTTTTNTACA 300  
GAGANTTAAA AATGNAATTA TTTNTAAA 328

SEQ ID NO:6495

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07664

SEQUENCE DESCRIPTION:

GATCCTGTTT CTACCAACAC TGCACCTTAT CCCAGGAACC TGCCCTAGAC CTCCAGAGAC 60  
CATATTTNNT CTCCTCCAT TTCTACCCAG ACCTCCAGGC CTCCTTCTGG AATNATAGAA 120  
CCGTAGAATT GGAAGGAATT TNAGAGGGGN TCTAGTTGGA GTTGTGTCCA ACAGAATTCA 180  
TTAACACCAG CCTGGGCTTG TTTTCCTCC TCCCTCTGGA CTTTTTAAT CTTTCCTCC 240  
ACCTCAAAAA ATACTTACAC ACAGATTCTT CTTGTACAGG CATCAAAACC AACTNCTNTG 300  
CCCCTAAGGC TGTGTNNGNG TGGTNTCCAG NNANCCNTAC CNCAGTCANT N 351

SEQ ID NO:6496

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07665

SEQUENCE DESCRIPTION:

GATCTGGTAG GGGAGAAATG GCGAATGTAA TACACATGAN ATGGTATATC CTTGCAATGT 60  
ACAGTATCAG AAGGTGGTTT GACAGCATCA TAAACAGGCT GACTGGCAGG AATGAAAACA 120  
AA 122

SEQ ID NO:6497

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07666

SEQUENCE DESCRIPTION:

GATCANTTGC AAACCTCCCC CAGCCCCTAC CATCCAATNT GGACGGAAAA CANGAACTGC 60  
CTGAAGAAGA GTCCAAGCTA CAGATACACA GCGTGTGCAT TGCGGCTGTC ACCTTCCTNC 120

TNCCACTTCT GTATCCTCAG AGATGCTGCG TGGATGTTTC CTTANCCTCA GCTGACTTCC 180  
CTGTGAATNT CTAATGCTAG TTCANGGGCC TNCNGGAAAT TGANTTN 227

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SEQ ID NO:6498  
SEQUENCE LENGTH:238  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS07667

SEQUENCE DESCRIPTION:

GATCTTGCCC TTCTCACTCC AGAGGCTAGT GGTCACAGAC AGCTGGGAAT GGCAGCCACA 60  
GAGGGTCCCC TCTGGGAGAA ACAGCTTCAC CCCAGCCTCA GGGCCCTGGG CCATCACTGC 120  
AGTGGCCCTG GGAGGTGAGG AAGAAGCTGG CTAGAGGAGG GGGCTCCCAC CTACCTTTTA 180  
TTTAAGCCAG TATTCTTTGT TCCTGCTTGT AATAAACTT CAGTTTATAA GAGTTAAA 238

15

SEQ ID NO:6499  
SEQUENCE LENGTH:142  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20

CLONE:HUMGS07668

SEQUENCE DESCRIPTION:

GATCTGTCAT AACTCATTTT AAAGTGTGAA ATATGCCATA TGAAGAGGN TTAAGAGGCT 60  
GNGAACTCA TATTCAACC AAATCCAGCA TTAGTTTTTC TTAGGTCTAA TANTTCCTNG 120  
TTAATAAAGA TTAAATGCA AA 142

25

SEQ ID NO:6500  
SEQUENCE LENGTH:160  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30

CLONE:HUMGS07669

SEQUENCE DESCRIPTION:

GATCTGTCAT TGTCTCCCAT CACCCCCAAA TGGGCCCCTC TCGTTGCAGG AAAACAAGCT 60  
CAGGGCTCCC ACAGTTTCTA CATTATGGTG AGTTGTATAA TTNTTTCATT ATATATTACA 120  
ATGTAATAAT AATAGAAATA ANGTACACAA TNNNTGTAAA 160

35

SEQ ID NO:6501  
SEQUENCE LENGTH:266  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40

CLONE:HUMGS07670

SEQUENCE DESCRIPTION:

GATCTGCCCC AGACTCCCAG AGGGTAATGC CACTCCCACA ATCTCAGGCC TGGTACCCAT 60  
CCTNTTCCA CTGTGAGCAG AGCCAGAAGG TAGGTCTNTT CAGAGTCTGT NNCCCTGGAC 120  
CTGGGGNGTG GATATGANAT GGGATATCTC CTTCATTCC CCGNTCCAGG GGAGAGTCAC 180  
TAGTTGTACC CTAATCCATT AGGTCCCAA TAGGGGCCCA ATTCACCTG TATNAGGNTC 240  
TGTGCATNCC AGCTGCCNNA AATNTN 266

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SEQ ID NO:6502

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07671

SEQUENCE DESCRIPTION:

GATCCAGACT TAGGGACGAG GCTGTCCTG GTGGGCACCC TCTGTTCTG TTTGTGTGTT 60  
TGAATAGTCT GAAATNCTGT GACTTTTTTT GTGTGAATAA AGNTATGAAA CTTCTGAAA 119

SEQ ID NO:6503

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07672

SEQUENCE DESCRIPTION:

GATCTTCGTG TGAGCCGCGN CGTCCGNCGN GACCGAGCTG CCTTCGCGTG CCCCCGNCCT 60  
GTGTTTTATA AAAAGAAAGA TTCTCGGAAA 90

SEQ ID NO:6504

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07673

SEQUENCE DESCRIPTION:

GATCTGTCAG TGTATCAAAA CAACATAAAT AAACCTGAAC AACTGATACG CAAAAAACA 60  
AA 62

SEQ ID NO:6505

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07674

SEQUENCE DESCRIPTION:

GATCAAGTTT GGTACAGTTT TGTCACCAAG CTTTGTAAT AAACCTGGTTT TCATAGCTTT 60  
TTGGAGATGA AA 72

SEQ ID NO:6506

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07675

SEQUENCE DESCRIPTION:

GATCTTTTTT CAGAATGTTG GAAAATCCTG TAAATGCAAA TAGTCAATAC TGTATTAAAT 60  
ACGTGCACTT GNGTNTGCT TCGCTTGAC AGTTGTAAAT AATCAGAACT TATGNAAAAG 120

EP 0 679 716 A1

GTACCCTACA GAGGAAATTC TGATACAGAT TATTGCTATA TTATAACCTN TTGCTGTTGA 180  
GCGGGCTGTA GGTAANCTAA TGTGTGGTT TGA CTATTAA A 221

5 SEQ ID NO:6507  
SEQUENCE LENGTH:42  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS07676  
SEQUENCE DESCRIPTION:  
GATCTTCATT TTTGTAATAA AACGGNAGAC TCATCCAGTA AA 42

15 SEQ ID NO:6508  
SEQUENCE LENGTH:62  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07677  
20 SEQUENCE DESCRIPTION:  
GATCTTAGAC TTCCCATCCT CTAGAACTGT GAGAAATAAA TTCCTGTTGT TTATGAGCCA 60  
AA 62

25 SEQ ID NO:6509  
SEQUENCE LENGTH:117  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07678  
30 SEQUENCE DESCRIPTION:  
GATCTGCCAT CTAGAACTCA TATTCTAAAG GGCAGTGNTT TCTCAGAACA GTGATGTTCT 60  
GGAATATGTA TTATTTATTT TAACACTTTT TTAATAAANT CTTTATTATA AACCAAA 117

35 SEQ ID NO:6510  
SEQUENCE LENGTH:113  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07679  
40 SEQUENCE DESCRIPTION:  
GATCTGTTTA AAAGATTAAA TCTCAAGTTA ATTAAAAATA AGCTTTTCAA AAATGTATTA 60  
TATTTATAAC AAATATACTG TAAATAGANT AAAGACATGC TATTCAGTGT AAA 113

45 SEQ ID NO:6511  
SEQUENCE LENGTH:159  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07680  
50 SEQUENCE DESCRIPTION:  
GATCTGTCAC TGTCTCCCAT CACCCTAAGA TGGGNCCTGTC TAGTTGCAGG GAAAGAAGCT 60

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EP 0 679 716 A1

CAGGGGCTCCC ACTGATTCTA CATTATGGTG ANTNGTAGNA TTATTTTATT ATATATTACA 120  
ATGTCAATAA TAGAAATAAN GTGTGCANTA AATGTCAAA 159

5 SEQ ID NO:6512  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS07681  
SEQUENCE DESCRIPTION:  
GATCAGCCGG AAGAGAAAAT NAAGACCCCA GAGACATTTA TTGGGGAGTA GGATGTGGCT 60  
GAGTGCTTTT TTTTGGCCA GACTAGCGGA TTCAGTCCTG GAAGAGAGTA TCATATAATG 120  
AGNCCCACAG GCACTGGCAC CCTTGGGTTG GNAATAGANG NNGNCCATGG ANTGGCGAAA 180  
15 ACCAGGGATT CCAGCTGGGG NATAGTANCT TGAAGGTGN 219

SEQ ID NO:6513  
SEQUENCE LENGTH:217  
SEQUENCE TYPE:nucleic acid  
20 TOPOLOGY:linear  
CLONE:HUMGS07682  
SEQUENCE DESCRIPTION:  
GATCTTGACC TACAGTTTGA AAAACAGAGT ACTGAAGAGT CTTGTTTCCT TTATTTAGAA 60  
25 CAGTGCAAGG ATGAGTATCT GGGTAGAGTT GTGCGTTGTA CATAACCTTT GATAGTCATA 120  
TAGTTGAACC AAAAGCAANN TCTGTAGTGN CATTGAAAAA ACATTTTGAC TTGATTATC 180  
CTGNCAGNNT NCNNTAATTT TTGGCTGGCT AATNCAN 217

30 SEQ ID NO:6514  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07683  
35 SEQUENCE DESCRIPTION:  
GATCTCTGCT CACGTTGCCT CCCTTCATCT TCCTGCATAA GTGGAAGCAG CCTGAAGCCC 60  
TCACTGTTTC TTGTACAGCC TGCAGAGCCG TGAGCCAAAT AAAGCTCTTT TCTTTTAAA 119

40 SEQ ID NO:6515  
SEQUENCE LENGTH:173  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07684  
45 SEQUENCE DESCRIPTION:  
GATCTGATGG TTTTATAAGC ATCTGGCATT TCCCCTGCTT GCACTCACTC TGTCTGGTG 60  
CGCTGTGAAG AAGGTGCCTG CTTCTCCTTT GCCTTCCACC ATGATTGTAA GTTTCCTGAG 120  
GCCTCCCTGG CAATGCAGAA CTGTGAGTCA ATTAACTTC TTTTCTTTAT AAA 173

50 SEQ ID NO:6516

55



# EP 0 679 716 A1

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07686

SEQUENCE DESCRIPTION:

GATCACCATG TNAGCCTTAG ACCAAGAAGC TGGCTAGTCC TTNCTGTGAA GCTAATACAA 60  
 TNGNCATTTC CAGACAAATT TAAAGGNAAC ACTAAGGCTG CTTCAAAGAT TATCTGATTC 120  
 CTTTAAAATA TATGTCTATA TACACAGGCA TGCTCTTTT TTAAGTGCTT ACATTTTAAT 180  
 AGAGATGANT CAGTTTNGA ATCTANGCTG TTTGCCCAAG NTGANGCTNC CAGGGTTN 238

SEQ ID NO:6517

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07687

SEQUENCE DESCRIPTION:

GATCTGTTTT TNACCACTTC ACTGAAAGAC ACCATTTATC TACCCAAGGG CAGAAAGTAG 60  
 AACTTACTAT TCATTAAATG TTTGACACAA TTGGAATTGT CTTTAATTTT TGTCAGAATG 120  
 CTATTGAAAA TGTGAATTGC ATGACTTGGT AGCATATTCT TTTCTGCAA AAATAGGCCA 180  
 TATTAACCAT GCTTATGACC ANTGNCCTGT GCTACTGGCT TTTGGNAAAA ATGGTTTGCN 240  
 TCAGNTGGG GAAGTAATNA AAGGANTNCA CCTGGNGNCC CNNGAATAN 289

SEQ ID NO:6518

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07688

SEQUENCE DESCRIPTION:

GATCCCCCAG GATTCTATTN TGTTTAATGG GCTTTTCTAC TAAAAGCATA AAATACTGAG 60  
 GCTGATTAG TCAGGGCAAA ACCATNNACT TTACATATTC GTTTTCAATA CTTGCTGTTC 120  
 ATGTTACACA AGCTTCTTAC GGTTTTCTTG TAACAATAAA TTTTTGNGT AAATANTGGG 180  
 TACATTNTAA CAAACTCNGT AGTNCAACCT AAACNGTAT NAACGGTGTG TAAAAAN 236

SEQ ID NO:6519

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07689

SEQUENCE DESCRIPTION:

GATCAGGTCT GCTTTNAGTT TCATTTTTGT TTCTTTCCCG TCCCACTCTT TAAAACTGG 60  
 TTCCGTGAGA AANGGCAGAA GCCGTTCCGT GTCTCTTGCA GGCTGGGCCG NCTTCATGNA 120  
 GTNCGAGGGC GTNCCGTGAC NACGTACATA CGTATGN 157

SEQ ID NO:6520

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07690

SEQUENCE DESCRIPTION:

GATCTTTCTG GATATAATGA AGCTTCCTGG AGAAACAGAC TGGCAATCAG AAAGATTTGG 60  
CTGCTTCCGA CACCTCCATC TTGGGCCTGC AGAGGCTGCA GCAATCTGTG AGGCAGCCGA 120  
ATCTGCGNGG CAGNCCACTC TTCTAGGACA TATGGGTTTC ANNAGGCACC NTTTTGCTAN 180  
GNAGGCATAN TTANN 195

SEQ ID NO:6521

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07691

SEQUENCE DESCRIPTION:

GATCGAAACC AAGTTATTAT TATCCTTACT GTATTCCATT GCTTGATCA AAATCTACTT 60  
TTTTNCTAGT AGGAAACTAT GCATTCCCTA TCAGTCCCTT TGATTATCAG GAATGTATAA 120  
GAATTGTGAT AAAATAGGCC AATATGCTAT TTGGTACCAT TTGTATGTAT TTTANGTGCA 180  
TAACCTAGGT AAAATAAGNN TAGTTTCTAT GTGTAAAGAA GCAAGTTTCA CAGTATGCAG 240  
ACTCCAGTGG ATGTATTTTA GGCTGTATAC ATNTTTAAGC TCTNTNTGGT ANATAGGGTA 300  
TACAAACTAN NTGCCTCNNA ATNCNAATAN NTTCGGN 337

SEQ ID NO:6522

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07692

SEQUENCE DESCRIPTION:

GATCATTTC TGGAACTTT GAAGTATCTT TGAATCTAAC TTTGACTTGG TGGTGGACCT 60  
TCCTTGGTTT TANTAACACC TAAGAGATAT CCTTTAGAAT TACATGTATT TTAGCATAAG 120  
GAAATGNA AAGTAAACA TACTGGTTTT TTTCAACAAG ACCATATGTA AATTAAATAG 180  
TGAAATGTGT ATGNGTTTCA GTAGAACTGT ACCATCAACA ATGTTTCCAT AAATATGCAG 240  
NGTTCTTCT NNTGTATTGT TATTTACAAT ATTGTTAAAT NGGATGCATT TGCAATNNCT 300  
CGGNTTCTAA AGNATTGNGG TNCNGANCGT N 331

SEQ ID NO:6523

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07693

SEQUENCE DESCRIPTION:

GATCTGGAAT GGTGTTTTGG TTTGGGGGGA ATTTTTTTTT TTCCNGGCA AATNACATGT 60  
GTTGTTGATG TGAGTATCTG ATGAAAAANC AATGNCAGAA TANCCGN 107

SEQ ID NO:6524

# EP 0 679 716 A1

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07694

SEQUENCE DESCRIPTION:

GATCTATATA TGTATAAATA TGTATTTTGT CAAATTTGTN ACTTAAATAT ATAGAGACCA 60  
GTTTNCCTCTG GAAGTTTGTT TAAATGACAG ANGCGTATAT GANTTCAAGA AAATTTAAGC 120  
TGCAAAANTG TATTTCTAT AAANTGAGNA GTCTCACTGN TAGCGGTTCT TTATTGCTCA 180  
TTTTTTAAAA ANTGGN 196

SEQ ID NO:6525

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07695

SEQUENCE DESCRIPTION:

GATCGGCTCT AGAAACACTG CTTTCCCTTC TTNCTTTTG TTTCTTTCT NTTATTATTT 60  
TTTTAAAGAG TAAACGAAAG TNCTGTATGA ATTCGGACCC AGGCAGCAAC CACAGGNCTN 120  
GGGGTGAGAC CCTCCTCCTC CCAAGNGAGC AAAAAGGACC CATGGCCCCC AAAAAAACCC 180  
CTCAACGAGA ATCCTCAGCN TTGTAAAATG CAAAANTGTC TAATGAATAT TTNTATNTGT 240  
NCCATTTTTG ATAANTN 257

SEQ ID NO:6526

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07696

SEQUENCE DESCRIPTION:

GATCCTATTT AACATGACAA GTAAAATGCT TGCCATAGGA TATTTATATC TAGAACTTTG 60  
ACAGACATAC CTAATCATTG TCACTCAGGC ATCCTGCATA TCATTCATTT ATTCATTGTC 120  
CTATCATTG TTGANCATTT AAAATGTCCT AGATACTTAG NATATGANTG TTGAATGTCA 180  
CAAACTGAA TGTCACTC CCTCCCCTTT AGANATTNC AGCATGGGAT GCGAGCTAAT 240  
GATATGTAAA TAANTACATA TTTNTAANTA ACACAACCNN AAAANAANAN AAACNAN 297

SEQ ID NO:6527

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07697

SEQUENCE DESCRIPTION:

GATCGTGGCC AACGTGGACC TGCCTACGNA GGGTGGGCTC TGACCCAAGT GGGGCCCTCCT 60  
TGTCCAGGTC TCACTGCTTT NCACCGTGGT CAGNGGGACT NTCAGCTGAG CTTNAGCTCC 120  
CATGGAGCCA GCAGGNN 137

SEQ ID NO:6528

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07698

SEQUENCE DESCRIPTION:

GATCAGCCTG AGAAGCCACT CAACTTGGCT CACATCGTGC CTCCCAGACC TGTAACCAGC 60  
 ATGAACGACA CCCNTGTTCT CCCACTCTGT TCCCTCCTCA GGAAGTCCTT TTATTACCAG 120  
 GAGCTCGGAC GGTGCTTTTG GTGGNTGCGT CTAGATGGAT AACATGACTT CTTCTACCCT 180  
 AAAATATTCC TATAATACTT TNAGCTGTTT TGGTTCCTCC AGGGTGNATG GTACCNATTA 240  
 ACCCAAAAATA CTGNTTATNT ACCCNTTNTT ACNATNTANN AGTCANTTTT GGN 293

SEQ ID NO:6529

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07699

SEQUENCE DESCRIPTION:

GATCCACGGG GCCAGGCCAC CCTGCGGGAG CGCCACACGC ATCCACTTCG GATTCAGTGG 60  
 GTGAAGACAG AACGCTNAGA GTCTGCAGGC GGCTCCTGTG CTTTAAATTT CTGGCTCTTC 120  
 GGATGTCTTC TAGACATTTA CTATCACTGC ACCTGAAGAA AAAATCACTT TTACCTTCCT 180  
 AATTTAAAAA GACAAAACAG AAATGTACGT TCCTTCGCTA GCTTTAGTCT TTCTGTTCCC 240  
 ATTTTNATAA ANTCTGAGGC ATTGATAATG NTCNNATCTA AAATTTGTAC AGTGTGATTT 300  
 CNNTNNTAAG NGTTAAANCT TTTANTAAAA GGGGCANGAN NTNAN 345

SEQ ID NO:6530

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07700

SEQUENCE DESCRIPTION:

GATCCAGAAA ATAGGTACGG TTTTAAAATA TTTNATATAG AAAAGCTACA AAGTAAATTG 60  
 AGCAATGCTT TTAAAGTTAT CTTTGTITTA TAGACTTTTT TGTGTATGT ATTACAGTCT 120  
 TTATAATCTT ATTTAATGNA TATNTGTACT TTCAAGTACT GATGGAGATA GNCTCAAAAC 180  
 AGTTATTTT TTACAATTAA TCTACAANGG GCATTANTAT TGTNGNCTTT TAAAACATCT 240  
 GCTGGNTATC TNATNTGCAA TTCNTN 266

SEQ ID NO:6531

SEQUENCE LENGTH:43

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07701

SEQUENCE DESCRIPTION:

GATCCACAC ACTAAATATA TGGTTGTTTT GCCACCTTTT AAA 43

SEQ ID NO:6532

# EP 0 679 716 A1

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07702

SEQUENCE DESCRIPTION:

GATCTGTTTT TCACCACTTC ACTGAAAGAC ACCATTTATC TACCCAAGGG CAGAAAGTAG 60  
AACTTACTAT TCATTAAATG TTTGACACAA TTGGAATTGT CTTTAATTC TGTCAGAATG 120  
CTATTGAAAA TGTGAATTGC ATGACTTGTA GCATATTCTT TTCTGCAAAA TAGCCATATT 180  
ANCATGCTTA TGACAATGAC TGTGCTACTG TCTNTGGAAA ANTGTTTGTC TCAGTTGGNA 240  
ATNCTAANNG NTTACCTGC GGANNAACG CCCNNNCCN CCCAN 285

SEQ ID NO:6533

SEQUENCE LENGTH:43

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07703

SEQUENCE DESCRIPTION:

GATCCTCTTG TGTATATGCA AATAAACCTA TTATTCACCT AAA 43

SEQ ID NO:6534

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07704

SEQUENCE DESCRIPTION:

GATCAAGACA CCTTTTATTA ATAAAGAAGN GACACAGGTG TAGATATGTA TATACAAAAA 60  
GATGTACGGT CTGGCCAAAC CACCTTCCCA GCCTTTATGC AAAAAAAGGG GAGANTCAAA 120  
GCTTTCATTT CAGAAGTGTT GCGTGGANAA GTATCTGTAA TTAAAGTTTC GANGTAATTT 180  
AACCTATTTT TAAA 194

SEQ ID NO:6535

SEQUENCE LENGTH:45

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07705

SEQUENCE DESCRIPTION:

GATCAAGCCC TGCTTAAAGT TAAATAAAAT AGAATGNATG ATAAA 45

SEQ ID NO:6536

SEQUENCE LENGTH:38

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07708

SEQUENCE DESCRIPTION:

GATCTTCTGG ATGACCTGAA ATNAGAACTA ATTGAAAA 38

# EP 0 679 716 A1

5 SEQ ID NO:6537  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07709  
 SEQUENCE DESCRIPTION:  
 GATCGCCCAA CTGCACTCCA GCCTGGNAGC AAGACTCTGT CTCGAAAAGA AA 52

10 SEQ ID NO:6538  
 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 15 CLONE:HUMGS07710  
 SEQUENCE DESCRIPTION:  
 GATCAGNACC ACTGCACTCC AGCCTGGGCA ATCANAGTAC GACTCCTGGC TCAAA 55

20 SEQ ID NO:6539  
 SEQUENCE LENGTH:252  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07711  
 25 SEQUENCE DESCRIPTION:  
 GATCAGTCTG AAGTCGATTA CTAACAGCTG AAGCTGATAA AACCATTAAA GTATACAGAG 60  
 AGGATGACAC AGCCACAGAA GAAACTCATC CAGTCAGCTG GAAACCAGAA ATTATCAAGA 120  
 GAAAGAGATT TTAATGAATG TGGAATTTT TCTCTCTCTT TTTTCTTCTT TTTAATTAAA 180  
 30 AAAAAAAGG CTTGGGGTTC ATGGGGTTTT CCNGTCATT NGTGCNCTGG CTGGGATTTT 240  
 AAGGGGGAAT TN 252

35 SEQ ID NO:6540  
 SEQUENCE LENGTH:48  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07712  
 SEQUENCE DESCRIPTION:  
 40 GATCGAGNCA CTACACTCCA GNCCGCCGAA GCAAGACTCT GTCTCAAA 48

45 SEQ ID NO:6541  
 SEQUENCE LENGTH:235  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07713  
 SEQUENCE DESCRIPTION:  
 GATCANACAT TTNCTACCTA TGAATNTTGC TGCATACAGA AAGTGCCCTT TCCTCAGGAA 60  
 50 GTTGCTGTGT NTCATTTCTT TAGATGGNCT CTTATCTAGA ATACATAGCA GCTCTGCAAA 120

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EP 0 679 716 A1

GAANCAGTTT TTAAAAATGG GAACTTCTAC ATTGAAAAGT CCCCNNTTTT GTGCCAACTA 180  
TGATTAGTGN GCGGAAGNAN TCTTATTCTA TGGCATATGT ATGGANGGGG GGGGN 235

5 SEQ ID NO:6542  
SEQUENCE LENGTH:36  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07714  
10 SEQUENCE DESCRIPTION:  
GATCCTTTTA AATTTAAAGC AAGTCCTAAA ATGAAA 36

15 SEQ ID NO:6543  
SEQUENCE LENGTH:155  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07715  
20 SEQUENCE DESCRIPTION:  
GATCCAGCGN GCGCACGCG AGTACCTGCA CAAGGCCGTC TTCAGGGGCC TNCTCACGGA 60  
GAAGNCGGCG CCCGTNATGA ACGTCATCCA CAGCATCTTC AGCCTCGTGC TCAAGTTCCG 120  
CAGCCAGCTN ATCTCCCAGG CCTGGGGGCC CCNNN 155

25 SEQ ID NO:6544  
SEQUENCE LENGTH:110  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07716  
30 SEQUENCE DESCRIPTION:  
GATCAAATAT CACTCTCTTA CTTACAGGAC TCAACATACT AGTCACAGCC CCTATAACTC 60  
CCNCTTACAA TANNTANCCA CAACCAAAT GGGGCTCANT CACCCAACCN 110

35 SEQ ID NO:6545  
SEQUENCE LENGTH:192  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07717  
40 SEQUENCE DESCRIPTION:  
GATCTGGTTG TNTAGAAGCA TGCAGCACCT CCTGCTTCAC TCTCTCTGTC TCTCCTGCTC 60  
CACCATGGCC AGAAACGTGC CTGCTTCCCC TTCGCCTTCT GCCGTGATTG TAAGTTTCTT 120  
GAGGGCTCCC CAGCCATGCT TCCTGTACAG CCTGCAAAAC TGTGAGTCAA TTAAACCTCT 180  
TTTNTTCATA AA 192

50 SEQ ID NO:6546  
SEQUENCE LENGTH:73  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS07718

SEQUENCE DESCRIPTION:

5 GATCATACTG GTTTGTTTCT TATTTTGATT GGAGAAAAAT NAAATTGCTG CATTTCGCAG 60  
TGACCCATTT AAA 73

SEQ ID NO:6547

SEQUENCE LENGTH:80

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07719

SEQUENCE DESCRIPTION:

15 GATCAAATGT GTGGCCTTTG ACTGAAATCA GCCAGCCCAT GGCCCCCAAT AAAGGCAGCT 60  
GCCTACTNCT CCNTCTGAAA 80

SEQ ID NO:6548

SEQUENCE LENGTH:115

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07720

SEQUENCE DESCRIPTION:

25 GATCCANATG CGTGTGGCAG CCNAAGGATT TGTGTAGGA GCAATGNCTG TTGGTATGGG 60  
CTATTCATG TATCGGGAAT TCTGGGNAAA ANCTAAGCCT TAGAAGAAGA GATGN 115

SEQ ID NO:6549

SEQUENCE LENGTH:98

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07721

SEQUENCE DESCRIPTION:

35 GATCATAGCA TATCTACTAT TTTATTATTT GATTTTAAAA ATTTAACATT ATATTATGGG 60  
TAACCTTACA TGTCAATAAA CAATTCACACA TTGTCAAA 98

SEQ ID NO:6550

SEQUENCE LENGTH:33

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07722

SEQUENCE DESCRIPTION:

45 GATCAACTTT GGAATAAAGT GATGCCCTTC AAA 33

SEQ ID NO:6551

SEQUENCE LENGTH:42

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07723

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EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCCACTGT AATATTTAAT AAAAAATGTT ACTATCTGTA AA

42

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SEQ ID NO:6552

SEQUENCE LENGTH:24

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS07724

SEQUENCE DESCRIPTION:

GATCAAATAT CACTCTCCTA CAAA

24

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SEQ ID NO:6553

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07725

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SEQUENCE DESCRIPTION:

GATCAGGACC CTNTCACGTG CACCCANTTA GNGTTGTGAG CCCTTAAAAG GACCAGGGAT 60

TGCTCACTCG GGGAGCTCGG CTCTTGAGAC AGGAATCTTG CCCATTCCCC GAACGAATAA 120

ACCCCTTCCT TAACTCAGAA A

141

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SEQ ID NO:6554

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS07726

SEQUENCE DESCRIPTION:

GATCAGGCAG CAGGAGTGAG GGGCACAGTC ACCCCAGGCC TTGCTGAGCC CAGGTCTGGG 60

TACTGAGTGT CCAGAGCTGC CTCCCAGGA GGTAAAGGTG GGGGCAAAGG GGAAGCTTCA 120

AGCACTTTGC CTACTTTTGT TCACTNCCCA GTGCACTGTG ACTCAGGCCT TCCCATCAGG 180

CCTATTTGTC TACCCAATAA AGCGTGTTTT TTCCAGAAAC AAGAAA

226

35

SEQ ID NO:6555

SEQUENCE LENGTH:46

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS07727

SEQUENCE DESCRIPTION:

GATCAGCCTG GCCATGGTNA AACCCCATAT CTAGTAAAAC TACAAA

46

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SEQ ID NO:6556

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS07729

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## SEQUENCE DESCRIPTION:

5 GATCCACTAT NAGGGTGGCA TCAGCCTGAA TTGAACATCC TATATCTNAA CATCTGCATA 60  
AATTCAGGT GACCACCACT GTGCACCACT CACCCATCCC AGTGTATTCA GGCCNNNTGA 120  
CCTGACCCAN TTTGGCCCAG AGGACTCTGC TGGTGACCTG AAAAGAGGGA CTACATATTT 180  
NAGGATATTG TTGGTCTCAC ATGACTCTTG ATAGAGTTG CCAGCCTTCA AATCACCAAC 240  
TGTGGGAACC AAGNNGGNN TTATTGCCTT GCTGTGTCA ATTACANAAA ACGNTGGAAA 300  
NGGCTN 306

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SEQ ID NO:6557

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS07731

## SEQUENCE DESCRIPTION:

20 GATCTGAATA CCCCTTCTCT GTAGCTGCTA GTGAGCCTTC CCATTTAGAT TAAAGATTGC 60  
TTTATCCAGC AGTCAATTAA CTCTCCAGTT ATCAGTACTC CCACAATTGG CCAGGGCAAC 120  
AATAATTGGA GTTCATACTG ATGCCCTGAG GCACTGAAAA AAAAAAAAAAT TCCAAGGNG 180  
CCTTNTGGGN TGNCTAAAGG TTNCATTGTG NTTGGNGGCT TTNGTGTTAG GTGTGCNGTT 240  
TANTTTCCTA NTTNN 255

25 SEQ ID NO:6558

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07734

## SEQUENCE DESCRIPTION:

30 GATCACGNCA CTGCACTCTA GCCTGGGCGA CAGAGAGAGA GACTGTCTAA AAAAGGAAA 59

35 SEQ ID NO:6559

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07735

## SEQUENCE DESCRIPTION:

40 GATCCTNAGG TCTCCTAGCC ATGTGGAGCT GTAAGTCCAA TNAACTTCT TTTCTTCCC 60  
AGTCTCAAA 69

45 SEQ ID NO:6560

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07736

## SEQUENCE DESCRIPTION:

50 GATCTGTCAA GTCCAGTAGA GCTTCAAGGT AAAATNAAAA TAACAATGTG AAA 53

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SEQ ID NO:6561  
SEQUENCE LENGTH:33  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07738  
SEQUENCE DESCRIPTION:  
GATCCAGAGG CCATGGAAGA GTCTCCAAGG AAA 33

SEQ ID NO:6562  
SEQUENCE LENGTH:158  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07739  
SEQUENCE DESCRIPTION:  
GATCAGCTCA AAAAGNTTGG GCTTAGNGTT TTCATTGCAA ATNATAATTG CTGTAGAGCC 60  
ACACACAAC TTTGAACTTT TAATTATAAG TGTATGGCT AAAGTTATTN NCTGAAAATT 120  
TCAGTAAAGT GTGTGAATGT TTCTTTATGT ATTANCNN 158

SEQ ID NO:6563  
SEQUENCE LENGTH:121  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07740  
SEQUENCE DESCRIPTION:  
GATCAGGGTT CTTTTTTTCC CCCATACAAG TATCCAGTCA TTGTAACACT GTTTATTGAA 60  
AGAATTATCC TTTCTCATT AAATTACCTT GCCAATTAGT AAAAAATCAA TTAACCATAA 120  
A 121

SEQ ID NO:6564  
SEQUENCE LENGTH:87  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07741  
SEQUENCE DESCRIPTION:  
GATCAGCATA CACAAATNAC AAAAGTCTGA ATTTTTTTTT ATCAAGAGGG ATAAACACC 60  
ATGAAAATAA ACTTGAATAA ACTGAAA 87

SEQ ID NO:6565  
SEQUENCE LENGTH:54  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07742  
SEQUENCE DESCRIPTION:  
GATCCNTTTT NCTGTGGCAT TTGGTGCCCT AAAAAATTTG CATTTATCTT GAAA 54

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5 SEQ ID NO:6566  
 SEQUENCE LENGTH:20  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07743  
 SEQUENCE DESCRIPTION:  
 GATCATTGA CAACTGCAA 20

10 SEQ ID NO:6567  
 SEQUENCE LENGTH:143  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 15 CLONE:HUMGS07744  
 SEQUENCE DESCRIPTION:  
 GATCGACTAT GAGACAGCAA AGGGGCCTAC CTNCTNATGG AGTTAGCCAA GAGCCAGGAC 60  
 AAGAGTCTCA AGATTTATGA CGGTGCCTAC CATGTTCTCC ACAAGNAGCT TCCTGACGTC 120  
 20 ACCANCTCCG TNTTCCNTGA ANN 143

25 SEQ ID NO:6568  
 SEQUENCE LENGTH:199  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07745  
 SEQUENCE DESCRIPTION:  
 GATCTGCTGC AATGCTCNAA GGCCAAGGAT TCATCTNTCT TNCACCGTA GGACCTGNCT 60  
 30 GGCATTGTAT TAGCAAATC TTTACTAGA CATCGTACTA CACGACACGT ACTACGTNGT 120  
 AGCTCACTGC CNCTGATGTC CTATCAATAG GAGCTGTATT TNCCATCATA GGAGGCTTCA 180  
 TTCCTGGTN TCCCNATN 199

35 SEQ ID NO:6569  
 SEQUENCE LENGTH:37  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07746  
 SEQUENCE DESCRIPTION:  
 40 GATCGTTTCC AGGACAATAA AAGTTTCGGA GTTGAAA 37

45 SEQ ID NO:6570  
 SEQUENCE LENGTH:57  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07748  
 SEQUENCE DESCRIPTION:  
 50 GATCAGATGT TTAATNAT TCCAAATACT TCATTAAT AATTATTTTA TTATAAA 57

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# EP 0 679 716 A1

5 SEQ ID NO:6571  
 SEQUENCE LENGTH:152  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07749  
 SEQUENCE DESCRIPTION:  
 GATCGAGGAA AGGGGCGGAG AATTTTTTTT TCTTCTTCCC ATTTCTTTAA AAAACCAACA 60  
 10 CAAGAAAACA CACACACACA CAACCAACGT TTGTTCCCGA GTAGAAACAT AAATAGGGCA 120  
 GAATCGAACA CTCTGTTCTT CTCTCTTCCA AA 152

15 SEQ ID NO:6572  
 SEQUENCE LENGTH:22  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07750  
 SEQUENCE DESCRIPTION:  
 20 GATCAGAGCT TGAAAAACA AA 22

25 SEQ ID NO:6573  
 SEQUENCE LENGTH:111  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07751  
 SEQUENCE DESCRIPTION:  
 GATCAACCTG TGGCTGTTTT CCCGTCTAGG TTCTCACAGG NATCTCCTGA CAGAGGTACT 60  
 30 TAACAATGGC TCTNCTGGAA ATTTCTATAA ATAAATGTC CAAAATGGAA A 111

35 SEQ ID NO:6574  
 SEQUENCE LENGTH:44  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07752  
 SEQUENCE DESCRIPTION:  
 GATCTCATCA CTGCTCCTTA TAATAAACCT AATAAGCAA GAAA 44

40 SEQ ID NO:6575  
 SEQUENCE LENGTH:42  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07753  
 45 SEQUENCE DESCRIPTION:  
 GATCCCGCCA CTGCACTCTA GCCTATGTGA CTCTGTCTCA AA 42

50 SEQ ID NO:6576  
 SEQUENCE LENGTH:48

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# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07754

SEQUENCE DESCRIPTION:

GATCATTGT AAGACCAAAA TATAAATAAA AAGTTTCAA AATCTAAA

48

SEQ ID NO:6577

SEQUENCE LENGTH:46

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07755

SEQUENCE DESCRIPTION:

GATCGATTAC AATAAATGTT TTTCTAAAAA GCCATTTTCC CACAAA

46

SEQ ID NO:6578

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07756

SEQUENCE DESCRIPTION:

GATCAAAAGC TTTGCATTGA TAAGTGCTC ATAATTTTG CTGTGATTGG AGAAAAAATG 60

TAGTCGTAGC CAATAAATTT TATCAGCTTT TAAGTTTCAG TATTATTAAA CCATTTTCAT 120

ATAAA

125

SEQ ID NO:6579

SEQUENCE LENGTH:36

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07757

SEQUENCE DESCRIPTION:

GATCAAATGT GAAATAAATA TGAATGGAGT GGTAAA

36

SEQ ID NO:6580

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07758

SEQUENCE DESCRIPTION:

GATCTCTGGC CCTTTGCGTT TCAGTATTTG TCCTTTTAT GCCTGAATGT TTAACCTGCC 60

ACATNTTTGT ACTGCAACAT GAATCTTGGA AATTTTAATG TTATGCATTT NAAANGTTT 120

TGGTTATCTG TAAACTAAAT GTGCCCTTAT TGGCTNGNG GTCAAGTNA GATGTTTGTA 180

TAATGTATTN GTCAGNAAA

199

SEQ ID NO:6581

SEQUENCE LENGTH:66

# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07759

5 SEQUENCE DESCRIPTION:  
 GATCTACTGT GATGTTGTCT TCAAAGGCAG GNGAAAATAA TGTTACAAT AAAATGTGCT 60  
 AACAAA 66

10 SEQ ID NO:6582  
 SEQUENCE LENGTH:135  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07760

15 SEQUENCE DESCRIPTION:  
 GATCTGTAAA GAATGACTTT CAAGGATAGT TCTTAGGGGA CTGTGAAAGT GTTGGGTCTT 60  
 ACTCNAGGAT GCCTGCATGG GACCCNACCC GGAGCTGGTG TGGCCATTCC CCAAGTGCCA 120  
 CTGGNCCATG GNNNN 135

20 SEQ ID NO:6583  
 SEQUENCE LENGTH:130  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

25 CLONE:HUMGS07761  
 SEQUENCE DESCRIPTION:  
 GATCAGCCTG GCCAACATGA TGAGACCCCA TTTGTACTGG AAATGCAAAA ATTGGCCAGG 60  
 CATGGTCGCG GGTGNCTGTG GTCCCAGCTG CTCGGGACGC TGAGGCAGGN NNNATCGTTT 120  
 GAACCTNGGN 130

30 SEQ ID NO:6584  
 SEQUENCE LENGTH:80  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

35 CLONE:HUMGS07762  
 SEQUENCE DESCRIPTION:  
 GATCAAAATGA AAGGCCTATA ACTAAAATCA GCCAGCCCAT GGCCCNCACT AAAGGAACCT 60  
 NCCTCTGCTC CCTNTGCAAA 80

40 SEQ ID NO:6585  
 SEQUENCE LENGTH:48  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

45 CLONE:HUMGS07763  
 SEQUENCE DESCRIPTION:  
 GATCAACAAT TTTTGTTTT ATTAAAATNA GTTTTTTGAA AGTTGAAA 48

50 SEQ ID NO:6586

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SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07764

SEQUENCE DESCRIPTION:

GATCCCCTGC TGGCTGGGGG CAGCTCCCAG GATATACTGC CTTACAACTG TTTCTAAAGC 60

CCATCCTNCT AACATGGCGA TTCCGGAGGT CAAGGCCTTG GGCTCTNCCC AGGGTCTAAC 120

GGNTAAGGGG GCCACATACC NGTTCCAAGG GGNNTGTCAA GTNGTGAAGT CGTTNTGN 178

SEQ ID NO:6587

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07765

SEQUENCE DESCRIPTION:

GATCAGATGG TTTATAAAAG TAATAACCAT AAAGCAAAAA ATAATTGAA AGCCCGTCTA 60

TTCCTATGCT CANTAAAGTT AAGGTTTTTC TTCATTAAA 99

SEQ ID NO:6588

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07766

SEQUENCE DESCRIPTION:

GATCCTTTGA GCCCAGGAGT TTGAGACCAG CTTGGGCAAC ATAGTGAGAC CCTGTCTCTA 60

CCAAA 65

SEQ ID NO:6589

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07768

SEQUENCE DESCRIPTION:

GATCACAGGG TCAGGAGTTC AAGACCACCC TGGACAATAT TGTGAATTCC TGCCTCTACT 60

AAAAATACAA AAATTAGTCG GGCATGGTGG CGGGTGCCTG TGGTCCCAGC TACTCGGGAG 120

GCTGAGGCCA GAAAATCGGT TGAACCTGGG AGGTGGAAGG TGCACTGAGC CAATATCACA 180

CCAGTGCACT CCAACCTGGT GACGN 205

SEQ ID NO:6590

SEQUENCE LENGTH:57

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07769

SEQUENCE DESCRIPTION:

GATCTCATAC TCAACAGAAG GAGACTCAGA GACTCCAGAA GGCACAGGAG CTGCCCN 57



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SEQ ID NO:6591

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07770

SEQUENCE DESCRIPTION:

GATCATGTTT ATTTACTGAT AAAACTCAAT ACCTAGAACT GCACCTAGCT CATGATGGTA 60  
CCTAATAAAT ACTTCAATGA AATGATGTGG TGATGCATGC CTATAGTTTT AGCTACTTGG 120  
GAGGGTGGCC TGAGCCCAGG GGTCTAGAC CAGCTTAGGC AACATAGCAA GACCCCATCT 180  
CAAA 184

SEQ ID NO:6592

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07771

SEQUENCE DESCRIPTION:

GATCTGAATG GTTTTAATAA GTGCCTGGNA TTTCCCCTAC TGGCTCTCAT NCTNACTCTT 60  
GCCGCCCTGT GAAGAGGTGC CTTCCACCGT GATTGTNAAG TTTCTGAGG CCTTCCCAGC 120  
CATGTGGAAC TGTGAGTCGA AAATNAAACC TCTTTTATAA TTAAA 165

SEQ ID NO:6593

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07773

SEQUENCE DESCRIPTION:

GATCCAAGCT TAATTTTCAA ACAGCTTCCC AAAAAGCTGT ATCCTGAATA TCATAAAGTC 60  
TATCATATGA TGTGTACTCA GTCATATTCT GTAGACTCAA ATCTTTTATC TGATTATACC 120  
AGCTTTCCCG NAAA 134

SEQ ID NO:6594

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07774

SEQUENCE DESCRIPTION:

GATCTGCCCC CGTTGGCCTC CAAAGTGCTA GGATTATAAG TGTGAGCCAC CACACCAGGC 60  
CCGTTTCATC CCTGNCTCAG CCTGCATGCC AAGCTCCCTN GGTGCCCCGNC CACAGGTGTC 120  
ACCCTTTNAG GAGAANGTGG CCTGGGGN 148

SEQ ID NO:6595

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07775

SEQUENCE DESCRIPTION:

5 GATCGCTTGT AGCTGGGAAC AGTGCTTACT TCAGGGAAAA CTGATTTTGA TAGAACCGAC 60  
 TAGTTGAGTA TTAAACTGTT TTGGAAATAA TTTATATATC TAAGTGCTGA AATATATTTT 120  
 TCTTCTCCCC ACTTATTCAA ATAAAAANGT TTTNATACTA TAAACTTTTC NNGGTTAGCG 180  
 CCACGCAGTC CTTGTCAAGN TTGTNCTGGG GGNCAANAAC TTGATGTATA AAGCATGN 238

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SEQ ID NO:6596

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS07776

SEQUENCE DESCRIPTION:

GATCTCTACT ACCANAAGGA AAATAGTTTA GGNGAAACCA GCTTTTANTG TTTTGTAAA 60  
 ATTAGCTTCA CCCTGTNATG TTANCAAGGT ATGTCTTTGC CN 102

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SEQ ID NO:6597

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS07777

SEQUENCE DESCRIPTION:

GATCGCGCCA CTGCACTCTA GCCTGGGTGA CCAGCCTGGG TGACAGAGTG AGNCTCCGTC 60  
 TCAAA 65

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SEQ ID NO:6598

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS07778

SEQUENCE DESCRIPTION:

GATCTAGAAG AAAGTATTGT ACGTTTGAAT GCAGATTTTN ATCCACAGAT AGTTGTAGTG 60  
 TTTAGACATG ACAGGACCTA TCGTTGAGGT TTCTAAGACT TACTATGGGC TGTAACCTG 120  
 TTTTNNAAAA CTATTTTAGA AACCTGAGAC TTGCCGTCTG GCATTTNAGT TTAATACAAA 180  
 40 CTAATGATTG CATTGNAAG NGNTNCTTGA CCTTATTCT AAACGTCTAG NGCTCTGAAA 240  
 TGTCTTGCTG GNNGGTATTA AACTATTTGC CTGTNGTACA TN 282

SEQ ID NO:6599

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07779

SEQUENCE DESCRIPTION:

50 GATCAAATGG CTTAGAGNTA GTCCTGGAAT ATTCATATTC-AAAGATTCCT TATTAATGAA 60

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TGTCCTTTAAC TTAAATCTAC CCAATAATTG CAACATGGTT CTTTGTACAT TTTCATTATA 120  
 TGGTGTTAAC AAGCTTCACT GCAAACAAAT AAATTACTTA AGTTATTTGN AAA 173

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SEQ ID NO:6600  
 SEQUENCE LENGTH:263  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07780

SEQUENCE DESCRIPTION:

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GATCAGTGTA GCAAATNAGG GATGAAGNGT TCAAACCTTT TGGCCCTTTC TTTCTTTNCT 60  
 AGGCTTCTCC CTCGCAGGGT GTTCCGTAGT TTCTTCTCGA GCCAATGCAT GTATTATAGC 120  
 AGCAGGTGTC TTTGTGCTTT CTCATCATAG TAACGTACTA CTTGTAAATA CATTTTNCTA 180  
 TTTNCTATTT TTTTGTATTT TTTTGTGACA TTTTGTTC A TTGGTGTGCT GNGNGNNCC 240  
 CATGCCCTCA CTCCTTTAAG AAA 263

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SEQ ID NO:6601  
 SEQUENCE LENGTH:51  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07781

SEQUENCE DESCRIPTION:

GATCCAAAAT TCTCAACAAA ATATTAGCAA ATTGAACCCA CCAAGGTAA A 51

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SEQ ID NO:6602  
 SEQUENCE LENGTH:283  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07782

SEQUENCE DESCRIPTION:

GATCAAAGGC CTCTNAGGGG TGTCCACCAA AAACCTCTCC TTCAAAAGAG AAGACTCCGT 60  
 GCTTCAGGGC TATGACATCA ACAGCCAAGG GGAAGAGTCC ATGGGAAATG CAGAGCCCT 120  
 TAGGAAGCCN ATCAAAAACC GGNGCNTANN GTTAANGAAA GTGAACTCCC AGGAAATACA 180  
 CATGCTCCCA ATCAAAAAC AACGGCTGGC CACCTTTTTT CCAAGAAAGT AAATAACGGC 240  
 TTTTAAANT NNGTATGNTT ATAATATGGG GAAAGGTGCA TTN 283

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SEQ ID NO:6603  
 SEQUENCE LENGTH:223  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07783

SEQUENCE DESCRIPTION:

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GATCGTTCAT CCGATTGCNA CGTTCCAAAG TGTCCAGGT TTTAAGACCT TACAAATGAC 60  
 TCAGCCCACG TGCCACTCAA TACAAATNTT CTGCTATAGG GTTGGTGGG CAGAGCTGTC 120  
 TTCCTTCTGC ATGTCAGCAC AGTCGGGTAT TGCTGCCTCC CGTATCAGTG ACTCATTAGA 180  
 GTTCAATNNN NATAGATAAT ACAGATATT TGGTAAATTG AAA 223

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SEQ ID NO:6604

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07785

SEQUENCE DESCRIPTION:

GATCACCTGA GCCTGAGAGT TCCAGACCAN CCTGGGCAAC ATAGCGAAAC TNCATCTCTT 60  
TAAAAATAAA ATAAATTA AATTAATACA AATAATTA 100

SEQ ID NO:6605

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07786

SEQUENCE DESCRIPTION:

GATCCCTTCC ACTCAGGATT CTCGCCGCCT TTTCTAAGAA AATAATAAAA AAAAAATNCT 60  
TGTTTCAAA 69

SEQ ID NO:6606

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07787

SEQUENCE DESCRIPTION:

GATCTGCCTG CCTCGGCCTC CCAAAGCGCT GGGATTACAG GCGTGAACCA CTGCGCCCAA 60  
CCTTTGGATT ATTTTTTGTG GAGATGGGGC TTCCCTATGT TGGCNAGGCT GGTCTCAAAC 120  
TCCTGGANTC CAGCCTGGGC GGCAGAGCAA AACCTTGTCT CAAA 164

SEQ ID NO:6607

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07788

SEQUENCE DESCRIPTION:

GATCACTCCT CTGCTTCAGC CTGGGCAATT GAGCCAGACT CTGTCTCAA AATAAACAAA 60  
AAAACCTGAC AAA 73

SEQ ID NO:6608

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07789

SEQUENCE DESCRIPTION:

GATCTTTTCTA CCTGGATATG TCTGTAAGGC TCCTGAAAGA GACAAATAAA GTCAATATAT 60

TTNCACAGTG CAAA

74

SEQ ID NO:6609

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07790

SEQUENCE DESCRIPTION:

GATCTTAGGT CAAATAACAG ACTTGAGAAT ACTTTATAAA CTGCCATGAT ACAGCAAA 58

SEQ ID NO:6610

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07792

SEQUENCE DESCRIPTION:

GATCGNGNGC GTTAAACGCT GGTGGGCAGC AATAAGGGGC AGATGTGACC AGATGCCTGC 60

NTCCCCAGGG TGCCGAGGGC AGCAGGAAAA AGTGGGGACC TCGGTGCATT TGCCCCACCC 120

NTCCCCTNNC TGGGCTAAN 139

SEQ ID NO:6611

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07793

SEQUENCE DESCRIPTION:

GATCATCGAC ACTTCGAACG CACTTGCGGC CCCGGGTTCC TCCCGGGGCT ACGCCTGTNT 60

NAGCGTCGCT TGAAA 75

SEQ ID NO:6612

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07794

SEQUENCE DESCRIPTION:

GATCTGGGGG AGGAAGTTCA AGGAAGGCAC CACACCAGAA ATNGGACCTA AATTAAGGCT 60

TAAAGAATGA GCATGGCCAC ACTGTCAGTN AGTGTCTTT AGGTGGTAGG ACTATGGTTG 120

ANATTTTCNT TCTTCCTATC TTCCTGCCTT TTTCAGGNNN TNAATATTAA N 171

SEQ ID NO:6613

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07795

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCACGATG TAAATAATTA AGCATTTTGG TTGGATTCT TTTGTAATAA ACTATTTTGG 60  
TACCATAAA 69

5 SEQ ID NO:6614  
SEQUENCE LENGTH:271  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07796

10 SEQUENCE DESCRIPTION:  
GATCTAGGAT AGCTAAGTNA CCTACATGGT GACTGTTCGG TCTAATTCAG AAACAGAAGT 60  
ACTAAAAGAA TACTAAAAAG TTTTACCCA TTATCTCTAT CCCTGTTTTN TTTTGTCAAT 120  
TCTCAGCNGN AGGGAGCAAG AAAATACACA GCAGNGGGGG GAATGTTGT TTGCATCCTG 180  
15 GCTTTCTCAA CCGCACTTA CGTCCTTGAA TATNCTAGAT ATTTACTCCT TCAAGAAGTC 240  
AGGAGTATAT CCAGGCCTAC CTATCANCCT N 271

20 SEQ ID NO:6615  
SEQUENCE LENGTH:237  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07797

25 SEQUENCE DESCRIPTION:  
GATCACACCA TGGAGACTTT CTACTAGAGG ACTTGAAAGA GAACTGAGGG GCCACAAAAT 60  
AAACTTCACC TTCCATTAAG TGTCAAGCA TGTCTGCAA TTAGGAGGGN GTTAGAAACA 120  
GTCTTTTCA TCCTTTGTGA TGAAGACTGA AATTGTGCCG TGTTGCCTTA TATGANTATG 180  
CAGTATGGGA CTTTGAAATA ATGATTCATA ATAAAATACT AAACGTGTGT CTTCAA 237

30 SEQ ID NO:6616  
SEQUENCE LENGTH:196  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07798

35 SEQUENCE DESCRIPTION:  
GATCTNAAAT AAAATTCAAA CTCTACTTCT GTTGTCTAGT ATGTAATTGA GCTAATGATT 60  
CATTGGAAT ATACCTTTT ATACTCCTT ATCATGGTAC TGTAAGTGA TCCATATTAT 120  
AAATATAATT ATCTNAAGGN TTTTNAATT TTNTNATGT CCAAGNGCCC ACGTGAATT 180  
40 NCTGGTGAAA GTNAGN 196

45 SEQ ID NO:6617  
SEQUENCE LENGTH:75  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07800

50 SEQUENCE DESCRIPTION:  
GATCATCGAC ACTTAGAACG TACTCCNGNC CCCGTGCTCC TCCAGAACCT ACGNCTGCAC 60  
TAAGCGTCGA TTAAT 75

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SEQ ID NO:6618  
SEQUENCE LENGTH:50  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07801  
SEQUENCE DESCRIPTION:  
GATCACGCCA CTGTACTCCT GGGCAACAAA GCGAGACTCC CTGTCTCAA 50

SEQ ID NO:6619  
SEQUENCE LENGTH:208  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07802  
SEQUENCE DESCRIPTION:  
GATCGAGGCT TGTNATGCCT TGTGAGAAAT AAGGGCCTTA ATTTGTACTG TCTGCGGCAT 60  
TTTTNATAAT ATTGTATATA GTGACTGACA AATATTGTAT TACTGTACAT AGAGAGACAG 120  
GTGGGCATTT TTGGGCTACC TGGTTCGTTT TTATAAGATT TTGCTGGGTT GGTTTTTTTT 180  
TTAATTAAAA AGTTTTGCAT CTTTTAAA 208

SEQ ID NO:6620  
SEQUENCE LENGTH:151  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07804  
SEQUENCE DESCRIPTION:  
GATCAGGAAG CCAAACCTAA GAAAGAGCTT GAAAATACTG CTCTAGAGCT TAGTCAGAAA 60  
GAAAAACAGT TTAATGCCAA AATGCTGGAA ATGGCACAGG CTAAGTACAG TGGAAATCAGT 120  
GATGCAGTGT CAAGACTGGA AACAAACCAA A 151

SEQ ID NO:6621  
SEQUENCE LENGTH:33  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07805  
SEQUENCE DESCRIPTION:  
GATCTNGGCA ACACAGTCAG ACTCCGTCTG AAA 33

SEQ ID NO:6622  
SEQUENCE LENGTH:321  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07807  
SEQUENCE DESCRIPTION:  
GATCCGGACG ACGTAATCAC TGACATTNAG ATGGTGGACG AGGGCTGGTG GCGGGGACGT 60

EP 0 679 716 A1

TGCCATGGCC ACTTTGGACT CTTCCCTGCA AATAATGTCA AGCTTCTGGA GTNACTAGAG 120  
CTCACTGTCT ACTGCAACTN TAATTTCCCA TGTCCAAAGN GGNTCTGCCT CCACCCCCTC 180  
CCTATTCCTG CTGCAAAATNT CTAACCAGAT GAGGTTCTGG ACAGACTTCC CTCTCCTGCT 240  
TCATTAAGGG CTTGGGGCAG AGNCAGCATG GGGAAGGAGG TCCCCTTCCC CAAGAGTCCT 300  
CTTCTATCCC TGGATGAANN N 321

SEQ ID NO:6623

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07808

SEQUENCE DESCRIPTION:

GATCCCAGCA CCCATTCTT AGCTATTTAT CCCTTTCCTG GTTTCGGAAA GGCAATTATA 60  
TCTATTATGT ATAAGTAAAT ATATTATATA TGGAAA 96

SEQ ID NO:6624

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07810

SEQUENCE DESCRIPTION:

GATCTAGGCT TCTNGCCTCA CTCCCATTAG GAATAACACC CAGCAAAATG GAACTATCCA 60  
AGCACTTCTT ATACATCTGT CTCCCCATTC TCTCTTAAGA AGTTTCTTCA GCTGGTGCGC 120  
CATCATCATC ACCATGACTG CCCCAGCTC TTGAGGAAAG GNATAATTAC CTCCATGGTG 180  
TTGCCTCCTA TTTGCCTAAA GCACCAGAAA TAATATTAAT TACACCAGAT TAACTACANA 240  
AA 242

SEQ ID NO:6625

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07811

SEQUENCE DESCRIPTION:

GATCCCGTCC TTGTCAGAGA AGTGTTTCCTT GGATGAGCGC CCAGAGGGAG GAGCCCATGG 60  
CCCTTCTTTC TGTNACTGAT TAAAAATCTC GATGAAA 97

SEQ ID NO:6626

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07812

SEQUENCE DESCRIPTION:

GATCCCTTCA AGACTTTGTC ACAGCCTCTA TCACACATCT GTTTTTCTCG AAGNAAAAAA 60  
TATAATTAAT AAAAATGTTT TACTCTTTTA CACTGAAA 98



5 SEQ ID NO:6627  
SEQUENCE LENGTH:36  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07813  
SEQUENCE DESCRIPTION:  
10 GATCCCGNTG TTCTTAATAA ATCCTGACTT CCCAAA 36

15 SEQ ID NO:6628  
SEQUENCE LENGTH:35  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07814  
SEQUENCE DESCRIPTION:  
GATCAAAAAT AAATACTGCA CATAAAANAA AAAAN 35

20 SEQ ID NO:6629  
SEQUENCE LENGTH:77  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07815  
25 SEQUENCE DESCRIPTION:  
GATCTTGTTT TTATTGTTAT TGCTTTTATT ATNATTGCTT TTATTATCAT TAAAACTCTA 60  
GTTCTTGTTT TGTCAAA 77

30 SEQ ID NO:6630  
SEQUENCE LENGTH:98  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07816  
35 SEQUENCE DESCRIPTION:  
GATCCAGTAC AGAAAGGAAA GGNTATTTAT TGATTAACAG AAGTTGTCTT TTAAAAAGTG 60  
TTTATTTTGG GCAATAAAGA GCACAACATA ATCTCAAA 98

40 SEQ ID NO:6631  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07817  
45 SEQUENCE DESCRIPTION:  
GATCAGGGAA CAAAATCCTC TCCTTGTTGA AATATCCCAT GCAGTTTGTT GATACAACTT 60  
AGTATCTTAT TGCCTAAAAA AAAATTNNCT TATCNTTGTT TCAAAAAAGC AANNTCATGG 120  
ANAATTTTGG TN 132

50 SEQ ID NO:6632

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SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07818

SEQUENCE DESCRIPTION:

GATCAACGGC TGACCTTCTG GCGTCTGGGG CATGGTGAAC CCACCTNCAT GAATAGCACT 60  
GTGTTCCATG TGCCTGANGT GGCTGACATG GACTGCTGGC CTGTAAGCCC TGAGTTTGGC 120  
CACCGTTGTG CCCTTGGGGG TCAGGGGNTT NAGGTTTACA ACTGGTATGA CTGAGGTATC 180  
CTGCGGTGGC TGGCGTGCTG GGCATGGGGC NTGCTCACAG ACAGNATGGA GCAGGGAAGG 240  
GCTGTCCTGT GCCCATGCTC AGCTTGNCTT TNNNGNNGAN GGAGGTNGTG GCCGTGGGTN 300  
CCTN 304

SEQ ID NO:6633

SEQUENCE LENGTH:35

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07819

SEQUENCE DESCRIPTION:

GATCTCAAAT AAAATTNCTG TAAAGAATTT CCAA 35

SEQ ID NO:6634

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07820

SEQUENCE DESCRIPTION:

GATCCAAATC GGGCCATCTT CATTGCCATG AGTGTTGGA CAGGCTCTGC GTGCCAGGCA 60  
ACAGTGGGCA GACAAAGGGC TCCCTGGCTA CTGGGAAGAT ACAGAACCAT CCTGTGAAAA 120  
TCATTTCAGC ACTGGAGACC TTCTTTGCTA TTAATTCTTT CATTAAACAT GACCTCTAAT 180  
TTAAA 185

SEQ ID NO:6635

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07821

SEQUENCE DESCRIPTION:

GATCCGTGGC CTGAAGGTTC CTAGAGNCGT CAAGAAATNA ATATCTTACA CTGTGATTCT 60  
GTGAGGAAAG ACTGGTAACC CAAACTCTC TTCTCTAATG TATTTTNA CGNAAATGAC 120  
AATATTCTT TAATAAGTA TTTATACCA A 151

SEQ ID NO:6636

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS07822

SEQUENCE DESCRIPTION:

5 GATCCAGGTC TAGGCCCTTN ATCTGCTGCT CTGTGGCCCA GGGCAGGTTT GCTTGACCTC 60  
TGCCTCAGTT CTCGACTCTA AAGGACATAC TGACCTACCT CACAGGGGTG TTGTNAGGAT 120  
TAATAAATNT TGGTACTCTG CTTTGGAAAT NTGAAAAAAA AGAAA 165

SEQ ID NO:6637

10 SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07823

SEQUENCE DESCRIPTION:

15 GATCAAATTC AGTGTGTAT GTATGTTTAT GGCAACATTT TGAAAATAAA AATTAAATGT 60  
TTNCTTCAA A 71

SEQ ID NO:6638

20 SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07824

SEQUENCE DESCRIPTION:

25 GATCTCAATA CTCCTTGAC ATCCCTTAAG ACTCAAGTCT TGATACTTTG TCTGCTCTCT 60  
GGCTCTTTCT TTGTCATTAC TATNATNNNA ATCTTCTTGA TGTTGACTCT TGCTAAAATT 120  
TTTNGTCTTC CTTATTGTTA ATGCTTATAG AAAATGATTC CTTGTTATCT TTNAGCCCAT 180  
GTCATCCGAA TCATTTGCTG TTTCTAGCCT AGGTGCTTTG ACTATGCCAG CTTGTATTTT 240  
TNCAGAATTT NCATTANCTA TATGTGTGGT ATTGTAGGCA TTACCATATT TNAATAATAA 300  
30 NTTTAGGCCA TTGCTTCAAA TCACAACAAA NNACAACNCA ACNNACNN 348

SEQ ID NO:6639

35 SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07826

SEQUENCE DESCRIPTION:

40 GATCTGAAGA GTGAAAATAA TGCTTTAAAT NAAAAATTGA AATCAGAAGG AAA 53

SEQ ID NO:6640

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS07827

SEQUENCE DESCRIPTION:

50 GATCTTTTNN AATTCAGTAC AACCCATAAT CATGTAAATN CTCATTTNCT TTAGGNCATA 60  
AAGAGAGCCC TAGGGTGCTC TGAATGTGTA CATGTNCTTG TCATAAAATG CATACTGTTG 120  
ATACAAA 127

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EP 0 679 716 A1

5 SEQ ID NO:6641  
SEQUENCE LENGTH:23  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07828  
SEQUENCE DESCRIPTION:  
GATCTGTTGT TACTTAACAG AAA 23

10 SEQ ID NO:6642  
SEQUENCE LENGTH:85  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
15 CLONE:HUMGS07829  
SEQUENCE DESCRIPTION:  
GATCTTNATG TTAATNTTCA GAGGACTCTA GACAACAACT TAGCAACTGA AGCTTATNAA 60  
AGAAGAATTA AGCGCCTTGA GCAAA 85

20 SEQ ID NO:6643  
SEQUENCE LENGTH:113  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS07831  
SEQUENCE DESCRIPTION:  
GATCTTTTGT GGATATTTGT CACTTGGTTT CAGAAAGTNC ACAAATGTAG CAACAGCTCA 60  
CATGACTGAG TAGGTAGAAA ATGTGAAATA AATCTCATAT ATATNGTTTT AAA 113

30 SEQ ID NO:6644  
SEQUENCE LENGTH:54  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS07834  
SEQUENCE DESCRIPTION:  
GATCGTCCCG CTGCACTCCA GCCTGGCCAA CANAGCGAGA CTGTCCCCC CAAA 54

40 SEQ ID NO:6645  
SEQUENCE LENGTH:59  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07835  
45 SEQUENCE DESCRIPTION:  
GATCTTGCTC CTCTGTAAGG AACAAGGGTG CCTAATAAAT ACATTNCTCC TTTATTAAA 59

50 SEQ ID NO:6646  
SEQUENCE LENGTH:184

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# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07836

SEQUENCE DESCRIPTION:

GATCCAGGGT CCCCCAGGGT GGGCTCAGCT CCAGGGAGAG GCCACCCACG TGGCAGCCCC 60  
ACCTCTTGAG AGCCCCAGT GCCGGAGCAG AAAGGACCCT GGACCCNGAG GCAGNNACTG 120  
CGGGGTGGTA GAAAAGGTAG AGTAGGCTGT GGCAATGGAA TAAANCACGA TTAAAAACGT 180  
TAAA 184

SEQ ID NO:6647

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07837

SEQUENCE DESCRIPTION:

GATCTTCCC CTGCAACCAG ACAGTCTACA ACTGCCCCCT CCAGCCCATT TNCTGCCGTG 60  
AAACCCAGC CAGCCANACC AGGCTCTGGA ACCCTTTTTC GACTAGGNCA ACTCTGGNC 120  
ACCAGGNGGG GTAGAACACC NAACACCAA CTGTACAGAN TNTCCN 166

SEQ ID NO:6648

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07838

SEQUENCE DESCRIPTION:

GATCTNTNAT GGTCAGCACC ACCCGCNTAC CCAGTTCCTC CAGTGGAGAC CAGTTGGGTA 60  
GTGGTGACTG GGTACGCTAC AAGCTCTGCA TTGTNTGCTG ATGGGACGCT CTTCAAGGTG 120  
CAAGTAACCA GCCAGAACAT GGGCTGCCAA ATCTNAGNCA ACCCCGGTGG AAACACTNAT 180  
TAAAGAACC CCAGAGGACA CCAACAGGTG TNTATCTGGN CNTGNCN 227

SEQ ID NO:6649

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07839

SEQUENCE DESCRIPTION:

GATCTTTGGG GTTGGAGTGA AGGTCTTATC TGCATTAATT TTGTTAATGC ACATTGTAGA 60  
TGTGGAGAAC ATCTTGACCT GCATAAGGAT TGCCTCTCAT TTTATTGTGT AGTGCTTTTT 120  
CGAAATATTT ACATTCTTTT GGTCCCCATG TTCATGTATT CTGGAGAAGT AAAATTTCTT 180  
GATTACTGGG CAGACCCTAA AACTACTAAG AGAAACATAA CATGTAGTTA GCTGTCTGCT 240  
CATGGTTTGT TCAAATCTAA GCTAACCTTA ATGGTGCTGT GTCCGCTGTN CACAGAAAAC 300  
GGCCTTAAAG TAGN 314

SEQ ID NO:6650

SEQUENCE LENGTH:104

# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07840

SEQUENCE DESCRIPTION:

GATCCCCTCC CCTGCCCTG GGTTCCTGCC TTCCNTCCTC AAGCAGGCAC NNAGGCTTTA 60  
GAGAAGTATA GGGGGCTTCT CCCCTGCNGG GCTTACCACA NTTN 104

SEQ ID NO:6651

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07841

SEQUENCE DESCRIPTION:

GATCAAGATG CCGAACCTG TGTTCAGAAC CTCCAAATAC TGCCATGAGA AACTAGAGGG 60  
CAGGTCTTCA TAAAAGCCCT TTGAACCCCT TTCCTGCCCT GTGTTAGGAG ATAGGGATAT 120  
TGGCCCCTCA CTGCAGCTGC CAGCACTTGG TCAGTCACTC TCAGCCATAG CACTTTGTTC 180  
ACTGTCCTGT GTCAGAGCAC TGAGCTCCAC CCTTTTCTGA GAGTTATTAC AGCCAGAAAG 240  
TGTGGGCTGA AGATGGTTGG TTTTCATGTTT TTGTATTATG TATCTTTTGT TATGGTAAAG 300  
ACTATAITTT GTACTTAACC AGATATATTT TTACCCAGA TGGGGATATT CTTTGTAN 358

SEQ ID NO:6652

SEQUENCE LENGTH:46

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07844

SEQUENCE DESCRIPTION:

GATCCAGTTT GGGATTATGA AATAAACCAC AAATNAAAAT TTAAAA 46

SEQ ID NO:6653

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07845

SEQUENCE DESCRIPTION:

GATCTGGGGG GATGGAAAGC AAAATAAAGG AGGTGCCTGG NTGCATTATT TGCAGTGGGC 60  
AAA 63

SEQ ID NO:6654

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07848

SEQUENCE DESCRIPTION:

GATCCACCCA CCTCGGTCTC CCAAAGTGCT GGGATTACAG TCTTGAGCCA CCGGGTGACC 60  
GTCTTACAGG GATATTTTNA ATCCCGTNAT GGACTCTGTC TCCAGGAGAG GGGTCTATCC 120

ACCCCTGCTC ATTGGTGGAT GTNAAACCAA TATNCCTTTC AACNGGTGNC TGNTAGGGAA 180  
AANCTACTCC TCATTATCAT CATTATTATT GCTCTCCACT GTATCCCCTC TACCTGGCAT 240  
GTGCTTGINA AGTNCTAGTT GTTCAATAAA TTTGTNAATA ATGCTGTAAA 290

SEQ ID NO:6655

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07849

SEQUENCE DESCRIPTION:

GATCTTCCTG GAAATNAGCA GTGACTAACG CTCACATAAC TGGTTTTTTT TTTNAACTGG 60  
GCTGATGAAT ACATTTACCT ANGAACTCA TTTTCGTTTA CTTAAGAGGG GANGTGCAGT 120  
TTTNTTTTGG NAGTTCAGAN TCCAN 145

SEQ ID NO:6656

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07850

SEQUENCE DESCRIPTION:

GATCCTCTGG TTTNTTCCAT TGGGGCGGAG TCGGGGGTGG AGGGAGCTGG CCACAACCCA 60  
CTGCTCTGAT GGGTGGTTTG TCCAAGNATG CTGAATGTAA TGCCTGGTCA ATGTGGAAGC 120  
CCATNAGGTT GCCCAGGGAA GCCTCCAAAA GCTGGGATGC TTGAGGGTAT CCAAGTTGAA 180  
AAAGACAAAA TCTGACCATC AGCCAGTGAC AGTCCTGGCA AATNAAGGTG GGGCGGGGCA 240  
GTNAGGGGTG GGNGANGGTG AATNNTTCAT TATTCCACCC NGCGGTTTNC TGGGGTGAGG 300  
GGGAAGANTC GNTGCTTGCT TTGGGCACTG ANGTTTTTC TGTNNGGGGA N 351

SEQ ID NO:6657

SEQUENCE LENGTH:346

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07852

SEQUENCE DESCRIPTION:

GATCATGTGA AGAAAACAGT GACCATTGAA AATNACCCTC ATCTGCCACC ACCTCCCATG 60  
TGTTCA GTTC ACCCATGCAG GCATGCTGAG GTGATGAAGA AAATCATTGA GACTGTTGCA 120  
GAAGGAGGGG GAGAACTTGG AGTTCATATG TATCTNCTTA TTTCTTGAA ATTTGTACAA 180  
GCTGTTCATT CAACAATAGA ATATGACTAC ACAAGACACT TCACAATGTA ATGAAGNGAG 240  
CATAAAANCT ATCCTAATTA TTGGTTCTGA TTTTNAAGA ATTAACCCAT AGATGTGNCC 300  
ATTGNCCATA TTCATCANTA TATACAGTTT CTCTANTAGG GGAANN 346

SEQ ID NO:6658

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07853

## SEQUENCE DESCRIPTION:

5 GATCCACACG CTGGCCCAGG AGTTCGACAT TNACCGCAAG GTGGGCGNAG AGCCTGTNCC 60  
 TGTAACGAGG GATNATTCCA GCAATGGCTT TCCCCGCACT CAGCATGGTT CCCCAGTAAC 120  
 CTCCTGCTGA CCAGTCCTC GGGGGAGCTG TGGAGGATGG TGGCATCGG TGGACAGCCC 180  
 CTGGGCTTTA ATGAATGTGG CATCGTGGCA CAGATTGCAG GTCCCCTGGC TGCCGCTGAN 240  
 ATCTCTGCCT ACTACATCAG CACCTTCAAC TTNNGNNNG GCCTGGTTGC CCGAGGACGG 300  
 10 TATCGGCAGC GTCATCGNGG GTCCTCCAGN GGNGGGNAGG AATGN 345

SEQ ID NO:6659

SEQUENCE LENGTH:47

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS07854

SEQUENCE DESCRIPTION:

GATCTTTGTT AAAAAAATAA AAAGTACTAA CATTACAGAC ATGTAAA 47

20 SEQ ID NO:6660

SEQUENCE LENGTH:35

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS07855

SEQUENCE DESCRIPTION:

GATCCTGCCA CTGCAGAGTG AAACCCTGTC TCAAA 35

30 SEQ ID NO:6661

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07856

SEQUENCE DESCRIPTION:

35 GATCCCCCGG AAGTCTTCAC AGGCACTGCA TCGGGTTGTC TGGCGCCCTT TTCCTCCAGC 60  
 CTAAACTGAC ATCATCCTAT GGAAGTGGCC GGCACTCTC TGGCCGAAGT GGCCGAGTG 120  
 TTGCCCCCGA GCTGCCCGCA CCCNCTCACA GGGTCCCTCA GNTTATAGGT GCCCAGGCTG 180  
 AGGTGAAGNG GCCTGGGGGN CCTGCNTTCC GGGCGCTCCT GGACCNTGGG GCAAACCTGT 240  
 40 GACCNTTTTN TACTGGANTA GAAATNNGTT TTATNATTN 279

SEQ ID NO:6662

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS07857

SEQUENCE DESCRIPTION:

50 GATCATAATA TAATTGGTTA CAAAGTGGAA GTGCCAGCTG GCTTAAGTAC CCAAAGAANA 60  
 GAATGCAGCA GCCTAACTTA GTGTTACCAT ATGTTACTGA ATTTGAAACT GACCTTTTTT 120  
 CCCACCCTAC TTCACACACC TAAACTCTT TTTTGTGAG ACCAAAGNGC AAA 173

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# EP 0 679 716 A1

SEQ ID NO:6663

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07858

SEQUENCE DESCRIPTION:

GATCCAGTTG TCATCCACCA CAGACATCTC ACATCAGATA CAGACAGTTC CAAGATTGAC 60  
AACAGAGAAC AACCTGCTGG AAAGACCTGG GCAGAAATGG AGAGCCCTGC GGGAAACCATG 120  
CTACATTTTC ATCTAAAGAG AGAATGCACA TCTGATGAGA CTGAAAGTNC TTTNTTGTTC 180  
TAGATTGTAG AATGGTATTG ANTTGGTCTG TGGAAAATTG CATTGCTTTT ATTTCTTTGT 240  
GTAATCAAGT TTAAGTAATA GGGGATATAT AATCNTAAGG CNTTTTAGGG TGGCN 295

SEQ ID NO:6664

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07859

SEQUENCE DESCRIPTION:

GATCATGGTC AGANTGGAGT ACCTGGGGGC TGTCCATGCC CCCCTTTGGA CCTAATCCTA 60  
CCCGTCCCCG CCAGCCCCTC TCCACACCNT TNCTCCCCAA GTACCCGCC ACCGTTTCCA 120  
TGGTCGAAGG TCAGGGCGAG AAGAACGTGA CCTTCTGGGG GAGACCGCTG CCACGGTGTG 180  
AGGAGCTACA AGGGCAGAAG CTGGTGGTGG AGGNGNACG ACCATNTNTA CACGTGCCTG 240  
CTTGCAAAGA CCCTGAGGAA GAGGAACTCT AACANTTNTT TCCTN 285

SEQ ID NO:6665

SEQUENCE LENGTH:47

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07860

SEQUENCE DESCRIPTION:

GATCCTGTTA GTCAGTGTGG TTCATCAAAT AAAACTGTTT GTGCAA 47

SEQ ID NO:6666

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07861

SEQUENCE DESCRIPTION:

GATCTCTAGA GCTGTCTTGT CGCCGCCAG GATTGACCTG TGTGTAAGTC CCAATAAACT 60  
CACCTACTCA TCAA 75

SEQ ID NO:6667

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS07862

SEQUENCE DESCRIPTION:

5 GATCCTGCCT GGNCAACCCT TTCCTGTCCC AGGCCCTACA TTCAGCAGAA ACGCACTTTG 60  
 GACTTTNTCC TTTANATAAA AGAAAGACAT CCCAGGAGAA GGACAAACCA GAGGAGTGAA 120  
 CCAACAAAGA GTACCTAGGA ATGGAAGTTG AGCCCTGGAA TGGGGCTCCA TGGAGAGGTG 180  
 CATAGGACTC GGCAGAAATG GCCTCTCCCC AAAGCCTCTT TTTNAGAGGA GAGGGAAGCC 240  
 10 TATTTTNTTA ACTGGTTTGG GATAGGGAAT GGGGTTNCTT TTTNTN 286

SEQ ID NO:6668

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS07863

SEQUENCE DESCRIPTION:

20 GATCCCGCC TGGCCAGGNG CAGGCACGGG TGGTCCNGT TCCACCCCAA GAGAACTCGC 60  
 GCTCAGTAAA CGGGAACATG CCCCTGCAG CCAA 95

SEQ ID NO:6669

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS07864

SEQUENCE DESCRIPTION:

30 GATCTCCTAA TGATGTATTG TGCCGTGGNA GTACTGTGTG TGAATAGCAG TAGTGGGGGC 60  
 AAAAGCAATC TTCTCATTTG GAAATGTTGT AAATAATTTT ATTATATAGT GTTTGGATG 120  
 TATTTGTTGT AGAAATGGNC CAGTGAATAA AGAGAATCTA AGGNTTTGTA CAATGTGAAA 180  
 TAACGTGTTA AATAANTGTC ATTGTCATAG AAA 213

SEQ ID NO:6670

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS07865

SEQUENCE DESCRIPTION:

40 GATCTAAAGA CCCGGGAGCG AGAAGCCAAG GCCAGGTTCT GGGNGNAGGG CCCAGAGAAG 60  
 CAGAACAGCC CAGAGCCCCA GGTGCCTGGC CTGGGCTAGA CCTCTGGAAT TGAGATTAAA 120  
 CAATTTGGAG TTGAAA 137

SEQ ID NO:6671

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS07866

50 SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

GATCCGCTAC AGCAACGTGA AGAAGCTGGA AATAAAGCCA AAGTACCCGC ACTGCGAGGA 60  
 GAAGATGGTT ATCATCACCA CCAAGAGCGT GTCCAGGTAC CGAGGTCAGG AGCACTGCCT 120  
 GCACCCCAAG CTGCAGAGCA CCAAGCGCTT CATCAAGTGG TACAACGCCT GGAACGAGAA 180  
 GCGCAGGNTC TACGAAGAAT AGGGTGAAAA ACCTCAGAAG GGAAAACTCC AAACCAGTTG 240  
 GGAGGCNTTG TGCAAAAGGN CTTTTCAGN TTNAAA 276

SEQ ID NO:6672

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07868

SEQUENCE DESCRIPTION:

GATCCTGGAC CAGTCAGAAG CCGAGAAAGC TCGCAAGGAA CTTTGGAGC TGGAGGCTCT 60  
 GAGCATGGCC GTGGAGAGCA CCGGGACTGC CAAGGCGGAG GCCGAGTCCC GTGCGGAGGC 120  
 AGCCCGGATT NAGGGAGAAG GGTCCGTGCT GCAGGCCAAG CTAAGGCAC AGGCCTTGGC 180  
 CATTGAAACG GAGGCTGAGC TCCAGAGGGT CCAGAAGGTC CGAGAGCTGG AACTGGTCTA 240  
 TGCCCGGGCC CAGCTGGAGC TGGAGGTGAG CAAGGCTCAG CAGCTGGCTG AGGTGGAGGT 300  
 GAAGNAGTTC AAGCAGGTTG CCAGAGGCCA TAGGCCCAGC ACCNTNAN 348

SEQ ID NO:6673

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07869

SEQUENCE DESCRIPTION:

GATCTGAGGC CAGCTCCCGT TCCCTGAGCT GCCTCCTGCT TCTCCCTCAA AGTCTCCTAC 60  
 CCTTCTCTT CTCTTTNAAG CCCTCTCTTC CTCGCTTTC TTCCTACCTA GCTCCTTGTT 120  
 GGTGAGCTTN TTGTGCCTTA ATNCTGTGAC CCAGGCCCTT ACACCANTTT NCACCTTCCT 180  
 GTNCGGAGNA CAAGGNCACT AGCTGCCCA GGAAGTTGTG TGATTTTAAA TCACTTCTGT 240  
 CTTTGCTGGA AAGTGTATTT GTGCATAAAT AAAAGTCTGN GGATTTGTTA AAAANAAGA 300  
 AAAANACNNA AAAANAACAN TNAAN 325

SEQ ID NO:6674

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07870

SEQUENCE DESCRIPTION:

GATCAATGGA ATAGAATTC ATTGGAAATG TAAACACTT TCCCAACAAT GGTCATGACT 60  
 TTCTNCTGTT TTTGAGAAGA GTTTCATATG CTGGACCACA TTNAGCTTT TATTGTTTTT 120  
 TTTNCCCAT TGTCCAAAAA GTTAAGCAAC AAGTGGCCAC ACTTTACGT GNCTACAACC 180  
 TGGAGTCTG CAAAGAAGGT AATATTTNCT TGGNCTTGC CTAANGTTAT CTCCCATTG 240  
 TATGGTTACA TTTTATTTG GCCTATGGGG CCTTCTAATA CGTTTGGTA AAGAGGCGAG 300  
 TNTAANGNAA TTNCTTGTC AATTTACCT CAAAGGTAAT TTCNTGCN 348

# EP 0 679 716 A1

SEQ ID NO:6675

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07871

SEQUENCE DESCRIPTION:

GATCAACTCT CTAATGGTGC TAATGGCAAT CTAGCTAATG TGCAAATTTA GGAAGTCTTC 60  
AGTACTAAGT ACATAATTTT CAAATAATAT TTTTNAATTG TCTACTTTGG ATGTTAGCTA 120  
TGTCTTGTGN GTATAGGATT CCAATTTTAA GCACTATTTT GATGCAAAAN AATGCATAAN 180  
NAATTANTT TATAAA 196

SEQ ID NO:6676

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07872

SEQUENCE DESCRIPTION:

GATCATAAAA ATGTGCGCCA ACAACGGCAG GCGCCATCTA AAGCAGCTTC TAAACAGAGA 60  
GAGATGCTCA TNGAAGATGT NGGCAGTGAG GNAGAACAAG AAGAGGAGGA TGAGGCACCA 120  
TTCCAGGAGA AAGATTCCGG CAGCGATGAA GATTTCTTAA TGGACGATGA TGACGNTNGT 180  
NACTATGGCA GTTCGAAAAN GAAAAACANA TNNN 214

SEQ ID NO:6677

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07875

SEQUENCE DESCRIPTION:

GATCCCCCAA GCCTGACGNG CCGNTNACCA TCCCCTCTGC CCTGCAGAGN CAGCCGCCAA 60  
GGNTGACCTC AGCTTCGGAG CCACCTCTGG ATGAACTGCC CCCAGCACCC GCCCCATTAA 120  
AGACCCGGAA GCCTGAAA 138

SEQ ID NO:6678

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07876

SEQUENCE DESCRIPTION:

GATCCATCGC AGAGTCCTAA AGAAGAACCC ACTGAAAAAN TTGAGANTCA CAAGCTCCGG 60  
GTGGATAAGG CAGCTGCTGC AGCANGGCAC TACAAGCCAA ATCAGATGAG AAGGCGGCCG 120  
TTGCAGGCAA GANGCCTGTG GTAGGTAAGA NAGGAAAGAN GGCTGCTGTT GGTGTTAAGA 180  
NGCAGAAGAN GCCTCTGGTG GGAAANN 208

SEQ ID NO:6679

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07878

SEQUENCE DESCRIPTION:

GATCTCCTGG AGGCTACAGG GAGCAGAGGC GATGCCCCGA GCGGCGAGCG TGTTCCTCAGG 60  
AGCAGGTGGG CAGGGGCCTT GCAGACTCTT CATTTCTTCC TTCCCTTATC ACCGTTAGCC 120  
ATTTTATG GATAGAGATA CAGAGGAGCT CCCATTACAA AGCGCCATTA AACTGTCATC 180  
TGTGCAAA 188

SEQ ID NO:6680

SEQUENCE LENGTH:35

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07879

SEQUENCE DESCRIPTION:

GATCTTGGTG GTAGTAGCAA ATATTCAAAC GCAAA 35

SEQ ID NO:6681

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07880

SEQUENCE DESCRIPTION:

GATCTTCCGT GGTCAGAGTG CCACTGCGGG AGCTCTGTAT GGTCAGGATG TAGGGGTAA 60  
CTTGGTCAGA GCCACTCTAT GAGTTGGACT TCAGTCTTGC CTAGGCGATT TTTTCTACCA 120  
TTTGTNTTTT GAAAGCCCAA GGTGCTGATG TCAAAGTGTA ACAGATATCA GTGTCTCCCC 180  
GTGTCTATC CCTGCCAAGT CTCAGAAGAG GTTGGGCTTC CATGCCTGTA GCTTTCCTGG 240  
TCCCTACCC CCATGGCCCC AGGCCACAG CGTGGGAACT CACTTCCCT TGTGNTN 297

SEQ ID NO:6682

SEQUENCE LENGTH:22

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07881

SEQUENCE DESCRIPTION:

GATCCAAGAT ATCACTTAGA AA 22

SEQ ID NO:6683

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07882

SEQUENCE DESCRIPTION:

GATCCAGCTG TGGTTCCAGA GCAGTGAGCT GGTGAGCTGG GCAGATGGGG GCCAGCACAG 60  
CAGNATCCAC CCAGNCTGAG GCTCAAGCTG CCCTTACCAC CCCATCCCC ACGCAGGACC 120

AACTACCTCC GTCAGCAAGA ACCCAAGCCC ACATCCAAAC CTGCNTGTCC CAAACCACTT 180  
ACTTCCCTGT TCACCTNTGN CCNACCNCAG CCCAGAGGAG TTTGNGCCAC CAACTTCAGT 240  
GNCITTTTGT ACCCNAAGNN AGCACAAGAT TGGACCAATA NTTTTTGNAG TN 292

SEQ ID NO:6684

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07883

SEQUENCE DESCRIPTION:

GATCTGCCTT AGCCTCACTG CTTGCCCCTA AGTGGTGGGA TTGCAGGTGT GAGCCACTGT 60  
GCTGGCCTCA AATAGTTTTN ATCAAAGCTA CTTCAATTAG TGGTTAGCAA GGCTTAAAGA 120  
CTAATTCAGT GCTTTATTTT NAACTNGNT CGCAACATGT TGCTTTTTTN CCTGTGTCCT 180  
ATGGGACCTA GTCATCTGTA TGTNAGATTC ACAGAGGAAT TAAAGAGATA AACATGCATG 240  
TNCTAAA 247

SEQ ID NO:6685

SEQUENCE LENGTH:37

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07884

SEQUENCE DESCRIPTION:

GATCCACAAC TACACACATC ATAACCACAC CATCAAA 37

SEQ ID NO:6686

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07885

SEQUENCE DESCRIPTION:

GATCTCTGAG GAGTTCCTG GGGACAACCTG AGCAGCCTCT GGAGAGGGGC CATTAATAAA 60  
GCTCAACATC ATTGNACNAA A 81

SEQ ID NO:6687

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07886

SEQUENCE DESCRIPTION:

GATCAGCCTT TCCAGGTGCT TTAGTCGTTT GCCTAGACAC GTTCCTGTCTG CCTCTGACAG 60  
CTGCAGTTGC TCTGCGCTGC TAGACATGGT GGACATTNA GCAGCCTGAC CTGTGGGGAG 120  
GGGGTCTCTC CCGAAGAGTT TCTGTTTTTA CTCAAATAA TGTATTCTC AGATGCTTGA 180  
TGCACTGTTG GAAATGTGCT CNATTTAATC ATGCAGATAA ACCATTATAA TGTCAAA 237

SEQ ID NO:6688

EP 0 679 716 A1

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07887

SEQUENCE DESCRIPTION:

GATCTCTTGA GCCCAGGAAG CCGAAGCCAC AGTGAGCTGT GATTGCACCA CTGCACTCCA 60  
GTCTGGGTGA CAAGAGTGAG ACCCCATCTC AAA 93

SEQ ID NO:6689

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07889

SEQUENCE DESCRIPTION:

GATCGCAGCA TTGCACTCCA NCCTGGGCAA CAAGAGTGAA ACTCTGNCTC AGAAAAGAGA 60  
AA 62

SEQ ID NO:6690

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07890

SEQUENCE DESCRIPTION:

GATCCTCCTG CTTCAGCCTC CCAAAGTGCT AGGATTATAG CCACCGCACC TCGTCTTGAA 60  
ATAGCCTTTT AAATGTTTAC CTCAGCTTGC CTCACAGTGG GTCTGTTTCT GGTTCCTCAG 120  
ATGCATAAAG GAAGACATAT CCCTCCCCTG GGNAGCAAGG CTACAATGGG AGGGAGGGAG 180  
AACATGGGAG CATGTGAATA AAATGGCATT AANTACTGAA A 221

SEQ ID NO:6691

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07891

SEQUENCE DESCRIPTION:

GATCATCAAG AAAAAAGAAA CTAAATGGA CACTTTTAAT GCTGCAAATN AGCTTGTCGT 60  
GAAGTTACCT GATTGTNTAA TTAGAATGAC TACCACCTCT GTCTGATTCA CCTTCGCTGG 120  
ATTCTAAATG TGGTATATTG CAAACTGCAG CTTTCACATT TATGGCATT GTCTTGTTGA 180  
AACATCGTGG TGCACATTTG TTTAANCAAA 210

SEQ ID NO:6692

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07892

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTGTCAT CTTCATAGCA CAACAAAACG AAATGATGGA AATNCTCTTN AGCTCACAAC 60  
 ATTTGTTTTN CTTTAAAGT AAATGCAAGT ACCAAAGCTC ACTACTGCGG TTTGCCTGTN 120  
 CCTGGNCANT GAGGCGGAGC NCTGTTGTTT TGTTGGGGCA CCCCTTNN 169

SEQ ID NO:6693  
 SEQUENCE LENGTH:226  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07893  
 SEQUENCE DESCRIPTION:

GATCTCTGCT TACCGTTCAA GAGGCGTGTG CAGGCCGACA GTCGGTGACC CCATCACTCG 60  
 CAGGACCAAG GGGGCGGGGA CTGCTGGCTC ACGCCCGCT GTGTCCTCCC TCCNTCCCTT 120  
 CCTTGGGCAG AATGAATTCG ATGCGTATTC TGTGGCCGCC ATCTGCGCAG GGTGGTGGTA 180  
 TTCTGTCATT TACACACGTC GTTCTAATTA AAAAGCGCAT TATAAA 226

SEQ ID NO:6694  
 SEQUENCE LENGTH:31  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07894  
 SEQUENCE DESCRIPTION:

GATCTCTTAA ATAAACTTGC TTCTGGTTAA A 31

SEQ ID NO:6695  
 SEQUENCE LENGTH:182  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07895  
 SEQUENCE DESCRIPTION:

GATCTAAATT TGTTTATTTA AGCTGCAAGN AAGTTACATT AATTTGGAAT GTGTCATCAC 60  
 TTGGNCCCAG TATATCAGAT TTTNATTGAG TAAAATGTTA AAAATAATAA GTGTA ACTCA 120  
 GATTCTGGAT GTNCGNGTTT ACAATACATT GCCTGTAATA AAAGCTGATT CTGANGTGCA 180  
 AA 182

SEQ ID NO:6696  
 SEQUENCE LENGTH:203  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07896  
 SEQUENCE DESCRIPTION:

GATCCCAACC CTGTGTCCTG CCCTGACCCC TGTTCTCCCA CTCGTGGCAC TGTCAGCCCA 60  
 GNCCTCCCTA CCGGCGAGAG TCCAGAGTGG GTACAGGAGC AAGGGGCACT GCTGGGGCCT 120  
 GATGGCTGAA GGAGACGCCG GCATCCTCGG GGGCCTGGGG AAGTTGTGTG TTGTGCAGTC 180  
 AGTAAAATCC TCCCACTGCN AAA 203



SEQ ID NO:6697

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07897

SEQUENCE DESCRIPTION:

GATCAAAATGA AATAATGTAA CGTGAGNATA CAGTATAAAT GATAAAGGAA A 51

SEQ ID NO:6698

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07898

SEQUENCE DESCRIPTION:

GATCTCCGGG CAGCCACCAC CTCCTCGGTC TGCCCCNTCA TAAAAAAGTC CTCCTTCCAT 60  
AGAAA 65

SEQ ID NO:6699

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07900

SEQUENCE DESCRIPTION:

GATCTAGTGC CTAGTGTTGC TTTTCTGATG TAATAAAAGG TGGTCTGGCA GAACCTAAA 59

SEQ ID NO:6700

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07901

SEQUENCE DESCRIPTION:

GATCCAGAGC CACAGAAAGA AATGTAGGTG TGAAGTATTA GGCTGCTGTC AGGGNGAGGA 60  
TGGCAGATGG AGGCATCAAG CACAAGGAAA ATGCACAACC TATGCCCTNT TATACANNNN 120  
GTTTCATGTN 129

SEQ ID NO:6701

SEQUENCE LENGTH:39

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07902

SEQUENCE DESCRIPTION:

GATCTTAAGT TTACAATTAA AAACCTCAGTA CTCAATAAA 39

SEQ ID NO:6702

SEQUENCE LENGTH:56

# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07903

SEQUENCE DESCRIPTION:

GATCCCCCG GGCATGGCCT GGGCTGGTTT TGAATGAAAC GACCTGAACT GTCAAA 56

SEQ ID NO:6703

SEQUENCE LENGTH:31

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07904

SEQUENCE DESCRIPTION:

GATCCTTTTA AAATAAAAAT NTTGATGCAA A 31

SEQ ID NO:6704

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07905

SEQUENCE DESCRIPTION:

GATCAGGAGC CTTCATTAAC ACAGAAATTT TAGGGAAAAC CACAAAAACC TTCGTAAAGT 60

GAATTGCATT AAACATCAAT TATAATAAAA TTTCATATTT TGANTAAA 108

SEQ ID NO:6705

SEQUENCE LENGTH:29

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07909

SEQUENCE DESCRIPTION:

GATCAAAAGG GACAAGCATC AAGCACAAA 29

SEQ ID NO:6706

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07911

SEQUENCE DESCRIPTION:

GATCATGGGC AAAATCTAGC CACAGTCCTG AGAGTCCAGG CTTCTGGGAT GCCCAGCTGG 60

GTATAAAAGT CCCTACTAAC CCTGNITCAA ATTCAGAGGT TTCTTTGGTT NAGAATGCCT 120

CAATGAGATT TTGATACATC CAAGAGCGCA AA 152

SEQ ID NO:6707

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS07912

SEQUENCE DESCRIPTION:

GATCTAAAAA ATACAAAATG TAGACAATTA CTATTCAGGT GCTTACTTTT AAGCCAATAT 60  
GTAGCAGNGN AAAACTAATT TCTCTGTGGC AGTATTTTAA TTTTGGNAT GTCCCNNGNN 120  
TTAACTGAN 129

SEQ ID NO:6708

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07913

SEQUENCE DESCRIPTION:

GATCCGCACT GGGGGTTCTG CAGGGTGGGG NCAACCACAG CCTGTCACAA GCTCACCGTC 60  
AGCCTCTNTG GNGCCATTG GCAGCATGAA GTCCCTATCA CCCACATAAT AATGNGNN 118

SEQ ID NO:6709

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07915

SEQUENCE DESCRIPTION:

GATCTTTCCC AGTATCTNNA GTGGGTGACC ACACTTGTC GTGGGAGNCT NTGAAACTAC 60  
CCTATCGNCT CCTTAAGGGC GGGATGAACT GCTTTGTGAC TTGGAAAGGT ACGCTGCTGG 120  
CCAGCATTGG AGANGAAGCT NCTGAGCAN 149

SEQ ID NO:6710

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07916

SEQUENCE DESCRIPTION:

GATCAGGTGG TCAAGGTGCT GCACGATGCC CAGCAGCAGT GCCGAGACGG CCACCCGGTT 60  
GTGGTCAACA TCCTCATTGG GAGGACGGAC TTCCGCGATG GCTCCATTGC TGTATAGGGC 120  
CTTGTTGGGTC AGNACGCTTN GCTGCCTTCC TACCCCTGGA CTGTNTCCAA NTGGTTTTNG 180  
AGTCTCATNA TTGCTTACCC CTGGNGCTNA TCCCATGAGG NCCCANTGNA CTTCAN 236

SEQ ID NO:6711

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07917

SEQUENCE DESCRIPTION:

GATCCGCAAA GAGGAAGACC GCCTCTTCAT TCTCAGGACC NTCACCTATT GATGGGAATN 60  
TGTGCGGGCT CAGGGTTCCT NNACACACTA GNTGTGGGAA GCCATAGGAG CCTCCAGATG 120  
GGGGCTGGCC TCTCTTGCCC AGCNAGNGGG CAGGGCCTGT GGGNTGGTGA ATN 173

# EP 0 679 716 A1

SEQ ID NO:6712  
 SEQUENCE LENGTH:48  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07918  
 SEQUENCE DESCRIPTION:  
 GATCACGNCA TGGCACTTCA GCCTGAGCGN CAGAATGAGA CTATTAAA 48

SEQ ID NO:6713  
 SEQUENCE LENGTH:50  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07919  
 SEQUENCE DESCRIPTION:  
 GATCGTGTCA CTGAACTCCA GNCTGGGTAA CAGTGCGACT CTGTCTCAA 50

SEQ ID NO:6714  
 SEQUENCE LENGTH:156  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07920  
 SEQUENCE DESCRIPTION:  
 GATCTTTGTT TAAATGCCAA AATGTACTTA AATGAGTTAC TTAGAATGCC ATAAAATTGC 60  
 AGTTTATGT ATGTATATAA TCATGCTCAT GTATATTTAG TTACGTATAA TGCTTTCTGA 120  
 GTGAGTTTTA CTCTTAAATC ATTTGGTTAA ATCAAA 156

SEQ ID NO:6715  
 SEQUENCE LENGTH:208  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07921  
 SEQUENCE DESCRIPTION:  
 GATCGATACC CCCACCCCTC CACTNGCCAG CCTGGGGGTG CCCTGCCTGC CCTCCTGGTA 60  
 CTGTTGTCTT CCCCTCGGCC CNNTCACATG TGTATTCAGC AGCCCTATGG CCTTGGCTNT 120  
 GGGCCTGATG NGNAGGGGTA GAGGGAAGNT GAGCATAGCA CATTTTCCTA GAGCGNGAAT 180  
 TGGGGGNAAG CTGTTATTTT NATATTAN 208

SEQ ID NO:6716  
 SEQUENCE LENGTH:57  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07922  
 SEQUENCE DESCRIPTION:  
 GATCAGACA CTACACTCCA GCCTGGGGGA CCGGGCAAGA CTCTGTCTGT CTTTAAA 57

SEQ ID NO:6717  
SEQUENCE LENGTH:333  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07923  
SEQUENCE DESCRIPTION:  
GATCTTGAAA AAAAAAGCAA AAGCTTAAAT ATTTGATACA AGTTTACTTA GCTACAACAT 60  
ACTTTACATT GTTGCCTTTA GTTATCTCAC AGGCACTGAC ATTTTATATT TAGAAAATAC 120  
TTTTAATCTT NCTAATCTTT TTTTGTAAT ATTAGTGTC ATTCTGTATG ACTCGCTAAC 180  
CTACTTTGCA AGGCTTTGGG CAACATTTA GCTCATTAAAC TTCAAGATGA TGTGTCATCT 240  
GTATAGGTCA AAGAATGGGN CTTCTGAACT GAGGAATTTT GCTGTTGACA GCCAAAGTNT 300  
AGTGTACAAG GTTTGATGNA ACTNGNTTAT GTN 333

SEQ ID NO:6718  
SEQUENCE LENGTH:57  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07925  
SEQUENCE DESCRIPTION:  
GATCTTGGAC TTCCAGCCT CCAGAATTGT GAGAAATAAA TTTCTGTTGT TGATAAA 57

SEQ ID NO:6719  
SEQUENCE LENGTH:63  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07927  
SEQUENCE DESCRIPTION:  
GATCTTTGCT TAATAAGANG AAAAAAGAGG CAAGGAGAAA ACGAAGAGAA AGAAATTTTG 60  
AAA 63

SEQ ID NO:6720  
SEQUENCE LENGTH:22  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07928  
SEQUENCE DESCRIPTION:  
GATCCNGTGT TCTTCTGTGA AA 22

SEQ ID NO:6721  
SEQUENCE LENGTH:186  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07932  
SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCCGGCTT GGACAGGCAC CTGAGATGGT GCCAAAGTGC AGCTGACTCT TCCCACGACA 60  
GCCCTGCCCT TCCCATGAGG CAGGCTCTTC AGTGAGTGTT TGAACGTAAT TATGTAGTTT 120  
TCTGTTTAAT TGAAAAAGNG AGCTATGCCT TTTTCTTT TTGGANGTAA AGCAGCTAAA 180  
ANCAAA 186

10 SEQ ID NO:6722  
SEQUENCE LENGTH:45  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07933  
SEQUENCE DESCRIPTION:  
15 GATCCAGGTG TTTGTTTCTA ACTTCTGTAA TACATACAAT GCAAA 45

20 SEQ ID NO:6723  
SEQUENCE LENGTH:173  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07934  
SEQUENCE DESCRIPTION:  
25 GATCATGGTG ATTTNACTGC TGCTTGTGGN TATCGTGGTT GTTGCAGTCT GGCCGACCAA 60  
CTGATGGCAG TAAAGAGACC ACCAGCAGTG ACACCTGCCA ATNACAGATG CAAGCCCAAC 120  
ACCCTNTTGG TACGCAAAAC CTNATCTCAA TAAATCCCC CAAAGCTCTG AAA 173

30 SEQ ID NO:6724  
SEQUENCE LENGTH:61  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07935  
SEQUENCE DESCRIPTION:  
35 GATCCCAAGC CCTGCATTGT AAGCCACAG TAGGCACTCA ATAAATGCTT GTTAAAGGAA 60  
A 61

40 SEQ ID NO:6725  
SEQUENCE LENGTH:269  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07936  
SEQUENCE DESCRIPTION:  
45 GATCCTGCAG AAGAATAACC TGAATCTGCT CAGAGACCTA AGCTGTGCAC ATTGCCATA 60  
GCCTCAGGAA CAGTCCAGAC TGGGGCGGTG TGGTCATATT ACACAGNNAG GAGGGTGATT 120  
CAGAGTTCAT GAATATCATT GCCAATNAGA TTGGGTCAGA GGAGACCCTC CTGTTCTTAA 180  
CTGTGCGCGA TGAGNAAGNT GGTGGNCTNT TTTACTGGC AGGGCCACNA NCGCTCATGT 240  
GGAGACCCNG GGGCCAGGG TGGCTGATN 269

50 SEQ ID NO:6726

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# EP 0 679 716 A1

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07937

SEQUENCE DESCRIPTION:

GATCCCTCAT CCCTGAAATT GAGTTTATGT AGTCATTTTA CTTATTTNAT TCATTAGCTA 60  
 ACTTTGTCTA TGTATATTN TAGATATTGA TTAGTGTAAT CGATTATAAA GGATATTTAT 120  
 CAAATCCAGG GATTGCATTT NGAAATTATA ATTATTTCTT TTGCTGAAGT ATTCATTGTA 180  
 AAACATACAA AATAAACATA TTTNAANACA TTTGCATTTN ACCACCAAA 229

SEQ ID NO:6727

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07938

SEQUENCE DESCRIPTION:

GATCCATGAA CTCTGACCCC TCCCAGTAA AGGCTTCTGT AGAGAGCAAA 50

SEQ ID NO:6728

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07939

SEQUENCE DESCRIPTION:

GATCCCCGCA CCAGCCTCTC CTCTCTTTCC CTGCAACCTG TTACCTCACA CAGCTGCTCA 60  
 GGAACAGCAG AAATAGTAAA ACTCTTCCAT ATATGTGGCA CCTCAGCCGC CCCTCCNTTA 120  
 AA 122

SEQ ID NO:6729

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07941

SEQUENCE DESCRIPTION:

GATCAGGAAG TTCTTAGATT CTTGGATGAC AGATGCATGT TGATGCCCTA TGGAGATGTC 60  
 CTTNTGTTTT GAGGTCACTG AGGTAGGAAG ACCTGTCTAC TCTTGGTTTC ACCACTAGAA 120  
 CAGTCTTGGG CTGGATGGGT TATAGAGCTG AGCGGCTGTA ATGGTTCTNT TTTTACATTA 180  
 ACAAAAACAA TTA AAAACAC CAAAAACAAC AAA 213

SEQ ID NO:6730

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07942

SEQUENCE DESCRIPTION:

GATCCCAGGN ATTCAAGGTT AGAGTGAGCT ATGATTGCAC CACTGTACTC CAGCCTGGGC 60  
 ANCAGAGANN GACCTGTCTC ACAA 85

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SEQ ID NO:6731  
 SEQUENCE LENGTH:313  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07944

SEQUENCE DESCRIPTION:

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GATCCAGCTG GAATTTGAGG AACTGGAAC AATGAGGTCA GCTTCCAAAA CAAAACAAAA 60  
 CAAAACTTTA AACATCTGTG TAAGTACAGG GTGGAATATA ATGAATTCCA GGTACCCATC 120  
 ACTTAGGTTT CACAATTAGC CATGGCCAAT CTTGTGTGAT AGGTATGTCC CTACCTATTT 180  
 CTCCCCTGCC CTNATTGTGA AGTAAATATT TTCCTAAAAG GTCTTTTAA AATTAAGTTA 240  
 TAACCATGCC ATCATTGTAC AAANNTAATG CTATTANNTT CCTTANTNTN ATCAAATNTT 300  
 CNNGNCTNAN NTN 313

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SEQ ID NO:6732  
 SEQUENCE LENGTH:73  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07945

SEQUENCE DESCRIPTION:

GATCACTTGA ACCTAAGAGT TTGAGGCTGC GCACTGCACT CTGGCCTGAC AGAGCGAGTC 60  
 ACTGTCTCTT AAA 73

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SEQ ID NO:6733  
 SEQUENCE LENGTH:257  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07946

SEQUENCE DESCRIPTION:

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GATCTGAATT CTAATGCTGG CTTGTGCCTC TAACTATGTG GTTTGGTCAT TATAGATAAT 60  
 GCCCAGTTTA ANTTTCCCA TCTTTGAAAA GGAGATAATA TGTNATCTCT TGGGAGTAGT 120  
 TCTGAATATG AAGTGTGTTG ATACAAGAAG CACTGACAAT GTTTCTGTNN NNNAAATTTA 180  
 AAAGTGGCCT GGTTCCTT TTTAATCAAG NGNGCTTAAC AGGTAAAAAN TTGGAATTAG 240  
 NCCTAAAAAN AAAAACN 257

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SEQ ID NO:6734  
 SEQUENCE LENGTH:148  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

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CLONE:HUMGS07948

SEQUENCE DESCRIPTION:

GATCCTTTAG CCTCCTGGNA GTGCCCCAGT TGTACCCCCT ACACACCCCT CTTGGCATTG 60  
 AGTGCCAGTC CTCTGCCAGG CTNTGTGTTA CAAGTTGGGG NGGCGGCAA AGTACCGAAT 120

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TAAAGATGTC AGTTCTAAAG GAGGNAAA

148

SEQ ID NO:6735

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07949

SEQUENCE DESCRIPTION:

GATCATATCC AATTCATATG GAAGTCCCGG GTNTGTCTTC CTTATCATCG GGGTGGCAGC 60  
 TGGTTCTCAA TGTGCCAGCA GGGCCTCAGT ACCTGAGCCT NAATCAAGCC TTATCCACCA 120  
 AATACACAGG GAAGGGTGAT GCAGGGAAGG GTGACATCAG GAGTCAGGGC ATGGNNTNGN 180  
 NAGATGANTA CTTTGTCTGGA TGAAGCAGGC TGCAGGGCAT TCCAGCCAAG GGCACAGCAG 240  
 GGGACAGTGC CGGGAGGTNT NGGGTAAGGG AGGGCAGTNA CNTNAGAAA 289

SEQ ID NO:6736

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07951

SEQUENCE DESCRIPTION:

GATCAGGCTT TTAAATACTC ATTTACAAGT TTTCTATCCT CCTTCAGTGT TAAAGTAGAA 60  
 AGTAAAAAGA GTATCTNATA CATGCATGAA ATTAAAGCAT ATACCAAATG CAAA 114

SEQ ID NO:6737

SEQUENCE LENGTH:229

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07952

SEQUENCE DESCRIPTION:

GATACCCAG CATCCTTCCC CACCCAGCT GTGTATTTAT ATAGATGGAA ATATACTTTA 60  
 TATTTTGTAT CATCGTGCCT ATAGCCGCTG CCACCGTGTA TAAATCCTGG TGTATGCTCC 120  
 TTATCCTGGA CATGAATGTA TTGTACACTG ACGCGTNCCC ACTCCTGTAC AGCTGCTTTG 180  
 TTTCTTTGCA ATGCATTGTA TGGCTTTATA AATGATAAAG TTAAAGAAA 229

SEQ ID NO:6738

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07953

SEQUENCE DESCRIPTION:

GATCTCTTGT NCTTTAATTT TAGGGTCTTG TTCCAGGACT CAAATCAGTA ACTTGGTGAT 60  
 TACAAGGTGC TGAATGTGTT GGTAACCATA TCGCAATACA CCTCAAGGAA AAGGTTTCAG 120  
 TTTTNAATTT TAAAAATTTT NCATTTTTTC CTTGAATTTN ATATCCGTTT GTCCACTCGT 180  
 ACATGCCTAG CCTACAGAAG GGGATATATA TNATGANATG GTCATTTTCC TGAAGNGNAT 240  
 ATTTTGCTTG AAATGCAAAG GNCTGAAAGN GNTTGTAGG TTGTTGGTTT TTTCN 295

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SEQ ID NO:6739

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07954

SEQUENCE DESCRIPTION:

GATCATAACA CTACTCCAGT CTGGGTGATG AAGTGAGACC TGTCTACAAA AAAAAGAAGC 60  
CCAAACTAAA CCTAAAGCAA GCAAA 85

SEQ ID NO:6740

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07955

SEQUENCE DESCRIPTION:

GATCAGGCTG GTCTCAAACCT CCTCGGTTCA AGCAATTCGC CCACCTTGGC CTCCCAAAGT 60  
GCTGGGATTA CAGGGGAGCC ACTGCACTGG CCTTCATTGT CTTTTGCTG CACAACCTAA 120  
AAAACCAAGT ACCCTGTATT GGAAA 145

SEQ ID NO:6741

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07956

SEQUENCE DESCRIPTION:

GATCCTAACA TGTATTGATT GTAAAAGTGA AATATGTAAT AGCCACACTT CACTGTTTTA 60  
AAATAAAAGT GCAATTTCAA A 81

SEQ ID NO:6742

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07957

SEQUENCE DESCRIPTION:

GATCTTGTCT CCAATTAAAC CGAGGCTTTC ACCGATAAAA AAAAAACAAA 50

SEQ ID NO:6743

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07958

SEQUENCE DESCRIPTION:

GATCTGATGA AGTATATNTT TAATTGCCAT TTTGTCCTTT GATTATATTG GGAAGTTGAC 60  
TAAACTTGAA AAATGTTTTT AAAACTGTGA ATAAATGGAA GCTACTTTNA CTAAA 115

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SEQ ID NO:6744  
SEQUENCE LENGTH:175  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07959  
SEQUENCE DESCRIPTION:  
GATCGGGCTA CTACAAAGTT CTGGGAAAGG GAAAGCTCCC AAAGCAGCCT GTCATCGTGA 60  
AGGCCAAATT CTCAGCAGA NGAGCTGNGG AGAGATTAAG AGTGTGGGG GGGCCTGTGT 120  
CTTGGTGGGT TTAAGGCNCA TTGGNNGGNA NTTCATTNAA TTNTTACTTC TTTTN 175

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SEQ ID NO:6745  
SEQUENCE LENGTH:61  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07960  
SEQUENCE DESCRIPTION:  
GATCAAAAGT AACACGTNNA GACTCTGAGC TTAATCCATT AAATGGATTT NAGCATCTAA 60  
A 61

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SEQ ID NO:6746  
SEQUENCE LENGTH:118  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07961  
SEQUENCE DESCRIPTION:  
GATCATNAAC TACTGTGTT ATNTGGAAGT CTAGGTTCTG GTCCTGCTAC CCCTTTAACT 60  
TGAGTNATTT ACAAGTCTGT TTAAGGTTT CTAGACATAC ACTGGTTTGN TTTTAAA 118

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SEQ ID NO:6747  
SEQUENCE LENGTH:140  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07963  
SEQUENCE DESCRIPTION:  
GATCGCCCAA CGTTTTTGGN TTATAGAATT ATTATTCCT GCTTCTTTC TTTGGGTCTT 60  
TTGAATTTCT TTGGTTTCGT NTTAAGAAG TAACCCANCA TTTCTACAA CACTAAATAA 120  
AATGGTACTT ACCTTTCAA 140

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SEQ ID NO:6748  
SEQUENCE LENGTH:68  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07964  
SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

GATCCCCGTT CCACCCCAAG AGAACTNGCG CTCAGTAAAC GGGAACATGC CCACTGCAGA 60  
CACGTAAA 68

5 SEQ ID NO:6749  
SEQUENCE LENGTH:79  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS07965  
SEQUENCE DESCRIPTION:  
GATCCCCCT GCCTATCAGC TTCTCCTGTG GNGCCTGTTC CTCACTGGAA ATTGGCCTCT 60  
GTGTGTGTGT GTGTGTGTN 79

15 SEQ ID NO:6750  
SEQUENCE LENGTH:28  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS07966  
SEQUENCE DESCRIPTION:  
GATCGAAAGG GAGGCAGGT TGCCTAAA 28

25 SEQ ID NO:6751  
SEQUENCE LENGTH:294  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07967  
SEQUENCE DESCRIPTION:  
30 GATCTCAAGC CAGCCCCNTC CAGCTCATGA CACTGTTTGG CCTTTCTTGG GGAGAAGGCG 60  
GGGTATTCCC ACTCACCAGC CCTGGCTGTC CCATGGGGAA ACCCTGGAGC CATCCCTTNG 120  
GAGCCAACAA GACCGCCCA GGGCTATAGC AGTAAGAACT TTAAAGCTCA GGAGGGTGAC 180  
GNCCAGATNC GNCTGCTGGG AAGAGCTCCC CTNCACAGCT GCAGCTGAAT GCATTAGGGC 240  
35 TACCGNAGGN CCCGGACTTA NCAAACTTG NCNACAANNG TTCCTAGGGN TTTN 294

SEQ ID NO:6752  
SEQUENCE LENGTH:160  
SEQUENCE TYPE:nucleic acid  
40 TOPOLOGY:linear  
CLONE:HUMGS07969  
SEQUENCE DESCRIPTION:  
GATCCCAAG TGTGAACAGT CTGAAAAGGG CTTTTGCTT GCTGCAGGGA CCTGAGAATT 60  
45 GAGAAACAGC TGTGAACTT TGAACCCTGG CTGGAAGGTC CTGGTATTGA CTGTGGCANG 120  
AAACGGGGG AGCTAATCTG TAATCTGCTT AGACGCCAAA 160

50 SEQ ID NO:6753  
SEQUENCE LENGTH:98  
SEQUENCE TYPE:nucleic acid

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# EP 0 679 716 A1

TOPOLOGY:linear  
 CLONE:HUMGS07971  
 SEQUENCE DESCRIPTION:  
 5 GATCAGATTC ACGGACCCAG AGCTTTTCCA TGTGTTTATA TTGTAAATAT TTTTNATTTC 60  
 ATCAAATTAT TTATTCATTA AAAGAAATTT TTGTGAAA 98

SEQ ID NO:6754  
 10 SEQUENCE LENGTH:35  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07973  
 SEQUENCE DESCRIPTION:  
 15 GATCCTGTCT CTTAGGAAAA AAGAAAACCT CTAAA 35

SEQ ID NO:6755  
 SEQUENCE LENGTH:64  
 20 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07974  
 SEQUENCE DESCRIPTION:  
 25 GATCAAAGAC CCTGCCTCTA TTNACCCCG CACTGACTGA ATAAAGCTCC TCTGGCCGTT 60  
 NAAA 64

SEQ ID NO:6756  
 SEQUENCE LENGTH:38  
 30 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07975  
 SEQUENCE DESCRIPTION:  
 35 GATCATCTGA GCTGAAGAAA TAAAAAACA CACACAAA 38

SEQ ID NO:6757  
 SEQUENCE LENGTH:56  
 SEQUENCE TYPE:nucleic acid  
 40 TOPOLOGY:linear  
 CLONE:HUMGS07976  
 SEQUENCE DESCRIPTION:  
 GATCATTCAT ACACTATATT TATTTTNNCA TTAAANTATT TAAAAACCTT TGGAAA 56

SEQ ID NO:6758  
 45 SEQUENCE LENGTH:105  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS07977  
 50 SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

GATCTTTCAT CAAGATTTTA CCTGCATTTA TGTCTAAGGG TCCCTGATAA GGCTTGAGGC 60  
ATGTAACCTA TGTCTAATTA AAAATGATTT GTTGAATGAA NCAAA 105

5 SEQ ID NO:6759  
SEQUENCE LENGTH:65  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS07981  
SEQUENCE DESCRIPTION:  
GATCTACAGA AGCTTTNATT CTCTTACCTT AACAGTAGTA ATAAAGTTAA CATTNTCACA 60  
TCAAA 65

15 SEQ ID NO:6760  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

20 CLONE:HUMGS07986  
SEQUENCE DESCRIPTION:  
GATCTGTGTG TTGTGGGAAG AGAATTTTCA ATATGTAAC TCGGAGCTGT AGTGCCATTA 60  
GAACTGTGA ATTTCCACAT AAATCTGAAC ACTTGTCTTT ATTAAA 106

25 SEQ ID NO:6761  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07987

30 SEQUENCE DESCRIPTION:  
GATCTCATGG CTTTGATTGN TTTGGGCTGT TCAAAATGTT TATTGNAAA ACGTATACAT 60  
TAATAAACTT AACAAAGCGN TATAAAATAC AGCGNAATCA CCCAAA 106

35 SEQ ID NO:6762  
SEQUENCE LENGTH:335  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS07988

40 SEQUENCE DESCRIPTION:  
GATCGAAAGG GCCACCATGA ACTTGATACG TCCGTGTGTC CCAGATGCTN NCATTAGTCT 60  
ATATGGTTCT CCAAGAACT GAATGAATCC ATTGGAGAAG CGGTGGATAA CTAGCCAGAC 120  
AAAATTTGAG ANTACATAAA CAACGCATTG CCACGGAAAC ATACAGAGGN TGCCTTTTCT 180  
45 GTGATTGGGT GGGATTTTTT CCCTNTTAT GTGGGATATA GTAGTTACTT GTGCCAAGAN 240  
TAATTTTGGC ATNATTTCTN TTANTATCAA CTCTGANGCT AACTTGTACT AATCTGAGAT 300  
TGTGTNTGNT CCNANTAANC GTGANGTGAA CCTGN 335

50 SEQ ID NO:6763  
SEQUENCE LENGTH:169

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07989

SEQUENCE DESCRIPTION:

GATCTTGGAG ACAGGCCATC CATCCTGGAG CCTCATGGAA CAGGATGATG GCACTGAGAA 60  
AGCCAATGAC CGAATCTCTT TTCTCTGTAA AAATGTAGAC TGAAGGCCA TGTGTATTTT 120  
CCTATGTGCT GTAGCTCTCC TTTGGAAATA AATCACAGGC ATCTGGAAG 169

SEQ ID NO:6764

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07990

SEQUENCE DESCRIPTION:

GATCTGGGCT GCAGGAGCTG GGGCCACCCA CAGCCCCCT ACCGACCTGG TGTGGAAGGC 60  
ACAGAACACC TGGGGCTGCG GGAACAGCCT GCGTACGGCT CTCATCAAAC TCACTGGGGA 120  
AGAAGTGGCC ATGCGGAANT GGTGCGCTCA GTGACTTNTG GTTNAGGACG NCGNGGNTTG 180  
AGGATTGAGA NTACNTATT CATTNACCAC NN 212

SEQ ID NO:6765

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07991

SEQUENCE DESCRIPTION:

GATCATACCA CTGCACTCCA GCCTGGGCGA CAGAGAACCT CTCTAAAAA AAAGGAAAAAT 60  
NAAAAATAAA TGGGGGCGA AGCTGAGCCA AGCAGAGGCG GGCAGCTCCT CCTCCAGGGC 120  
CCACCTGGCC TGCTGGGGAA A 141

SEQ ID NO:6766

SEQUENCE LENGTH:360

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07992

SEQUENCE DESCRIPTION:

GATCTGTTAT NAAACGAAAC ACCCCCCGTG TTAATAACTT GGTATGAAAT CTGTTTTTAT 60  
GAGCCGGGCC CCCTGTGCCT CTAGTATACT TGTATTGACT CTCATAGTTA CCCTTTTAGT 120  
TTTACTGTGT TCTGTGAAAA TTTGTAATTG GTTGNGAATC ACTGTGGGCG TCCATTCTTA 180  
TTCAACTAAA TCTCCACAGG TTTTGTGAGC TGGTGTGGAT TAGTTTAACT CTTGTATTCA 240  
ACCATTAGTG CTACCACCTT CTCACATTAC AATACANTTN CTGGAAGCAA GTACTGCATT 300  
TCCTATGCAA CAAAAAAGG GCAAAANTAC ANANATTGCT AAATGATAAA CAAANACTTN 360

SEQ ID NO:6767

SEQUENCE LENGTH:88

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS07994

SEQUENCE DESCRIPTION:

5 GATCAAAAGG GCTATGGGAA GGGCAGACCC CGCCAATGAT TTCTCTTCAC CTGTCTTAAG 60  
ATTAAATAAA AAAGAGTGTC CTGGCAAA 88

SEQ ID NO:6768

SEQUENCE LENGTH:65

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07995

SEQUENCE DESCRIPTION:

15 GATCTTGCCA AGAACCATCA CGTGTTAATT TAGTTGCTTA AACAAAAGGT GTTCTGTTTC 60  
TTAAA 65

SEQ ID NO:6769

SEQUENCE LENGTH:246

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07997

SEQUENCE DESCRIPTION:

25 GATCAGTGGT GAAATATAGT GATTTTNACC TGTGCTTCCA TTCTGAAGTT CTGGAAAGAA 60  
GTACTGGATG GACTGAAGTC CAGGACAACG TTCCAAAGAA AGGCAGAGTC CAGGTAGGCT 120  
TGGAGGACCA AGCCCTGGAT GAGCACTGGA GGGCAGAGGC CTCAGTGTCC AGCACTGTGC 180  
CCTGCACATG GAAAGCCCCT ACGTTTGTGG AATNAATGAN TANTAAAAAT ATTTTATNA 240  
GTGAAA 246

SEQ ID NO:6770

SEQUENCE LENGTH:23

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS07998

SEQUENCE DESCRIPTION:

GATCCTGTCC CTGCCCTGCC AAA 23

SEQ ID NO:6771

SEQUENCE LENGTH:46

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS07999

SEQUENCE DESCRIPTION:

45 GATCTGTATA TCCTCCAGTC CAAGATTAAA GAGGCGGACT GTGAAA 46

SEQ ID NO:6772

50 SEQUENCE LENGTH:108

55



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08000

SEQUENCE DESCRIPTION:

GATCCAAACT CATTCTTNT GTAACTCAT GATGACGTAT AACNTTTC ACCTCACTNG 60  
GAGGTGGNT CTNCATTCTG AAGGCTTCTA TGTATACATA TTAAATAN 108

SEQ ID NO:6773

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08001

SEQUENCE DESCRIPTION:

GATCAACGAC GACCTTTTTC CTTTNATAC TAAAGTAAGA AATAAGAATG TNAGCCCAAA 60  
CTGCACTATT TTGCAGACCC CTACCATTTT ACAAAGTGGT CAGAGTGGAA AATTCCACCA 120  
GGGCTGAGC TGTGAGAAAC ATCCTGTCAG GCAGGNCCCA GGNCTNAACC CCTGGCTGCA 180  
CTAANTTNT TCATNATCAN CAGCCTAACA NACCGTCN 218

SEQ ID NO:6774

SEQUENCE LENGTH:38

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08002

SEQUENCE DESCRIPTION:

GATCAACAGT GCAGAGAATC TAGCAAGTAT AAAAGAAA 38

SEQ ID NO:6775

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08003

SEQUENCE DESCRIPTION:

GATCTGCAAC ATGAANCCCG AGGCATGGGT TGGTGTGATG CCAAGGCAAA GTGGTGAGGA 60  
GAAAACAGGA AACGGNCTTT CTCTGAATTG GTAAATGGGA AAGAAGTGAG CAACTTAAGA 120  
TTGTACANT TAATCACAAG TGTACAGGAT TAGACTGGGT TTATATTAA CTCTTGCTTC 180  
ATAGGTGTAC CATTTAAAGN GTGTTATNTA NTGCTAAGAA NTAAGTCTT TNATAAGCT 240  
TATTNNNAA TN 252

SEQ ID NO:6776

SEQUENCE LENGTH:34

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08004

SEQUENCE DESCRIPTION:

GATCAAAGGG AATAAGAGA ACTCTTGGCT GAAA 34

# EP 0 679 716 A1

SEQ ID NO:6777

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08005

SEQUENCE DESCRIPTION:

GATCATATNC TTTTCTNTT TTGTTCTTA CAATATCAAT CTAATTTAAT ATTCTCTTGT 60  
GAGAACACAA ACATNNGTAA ATTGCTCAGT AGTGGCAGCA GTAAGGN 107

SEQ ID NO:6778

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08006

SEQUENCE DESCRIPTION:

GATCAAGGTT TGTNTGCCCA TTACCTTTCC TCTGCCTGAA AGACGTGTCT CAAGAAAAAT 60  
AAATTCTATT TNAGATGCAG GTACTNATAN TAATTCTAAG ANTTGATATC AN 112

SEQ ID NO:6779

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08007

SEQUENCE DESCRIPTION:

GATCAGAGNA AACGNCTTTA ACNCCACCAT TAGCACCCAA AGCTAAGATT CTAATTTAAA 60  
CTATTCTCTG TTCTTTCATG GGGAAAGCAGA TTTGGGTACC ACCCAAGTAT TGACTCACCC 120  
ATCAACAACC GCTATGTAAA 140

SEQ ID NO:6780

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08008

SEQUENCE DESCRIPTION:

GATCAATCTC ATATTCATTC CCTGGGATGT TTAGTTACCA GTTTTCCCAA AGTGTCTGG 60  
TAGCATCTAC CATATTTNAT CAAATCTGTG ATTCCTTTGA TTATNATATG AACCATTATT 120  
TTATGTATCA TTAAGAAAAA ATACTGCCAA TTAACTCTG TCATGNNAAC AAA 173

SEQ ID NO:6781

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08009

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCCAAGTT GAGATTTTAA TTCTGTGACA TTTTACAAG GGTAATGT TACCACTACT 60  
TTAATTATTG TTATACACAG CTTTATGATA TCAAAGACTC ATTGCTTAAT TCTAAGACTT 120  
TTGAATTTTC ATTTTAAAA AAGATGTACA AAACAGTNTT GNAATAAATT TNAATTCGNA 180  
TATAAA 186

10 SEQ ID NO:6782  
SEQUENCE LENGTH:102  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08010  
SEQUENCE DESCRIPTION:  
15 GATCCATTTT TNATATGTCT TGAAGTACTG TGTCTAGTGG GCAAATGTCA TTGTTACCTC 60  
TGTGTGTAA GAAAATAAAA ATATTNCTA AAGGTCTGTA AA 102

20 SEQ ID NO:6783  
SEQUENCE LENGTH:198  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08011  
SEQUENCE DESCRIPTION:  
25 GATCAAGTAG ATTTTAAAA AATCAGAGTC AATTAATTTT AATTGAAAAT TTCTCTTATG 60  
TTCCAAGTGT ACAAGAGTAA GATTATGCTC AATATTCCCA GAATAGTTT CAATGTATTA 120  
ATGAAGTGAT TAATTGGCTC CATATTTAGA CTAATAAAAC ATTAAGAATC TTCCATAATT 180  
GTTTCCACAA AACTAAA 198

30 SEQ ID NO:6784  
SEQUENCE LENGTH:278  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08012  
35 SEQUENCE DESCRIPTION:  
GATCAGAGTA AAACNTGGAG CTAGATTGAT TACAGAGTGC AAGGACTAGG CACCCCGGGA 60  
TTGGAGAGCA TCCTTGAAAG CAAGGGTCT TCATTTATTT ATAAAAATTT NATTGCCTAC 120  
TAGAAGCCCA GCTAAGAGTA TGAAGCAATT AAGACAACAN TCTTGCTCA AGAATCTCCT 180  
AGACAATCCT GATTCAAGCA CCAGAAACAA AGGGNNAAGA AACCTCCCAG TCTNGTGNG 240  
40 NAAGTNGTAC ACATCNTGTC AACAGNTAGG TTNTTTN 278

45 SEQ ID NO:6785  
SEQUENCE LENGTH:339  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08013  
SEQUENCE DESCRIPTION:  
50 GATCCCATGT NAGCTACACA GTGCAGAGGC TCTTGATGGT GGAATAAGCA ATTCCTCCC 60  
TCGTGCGCAT CTCAGAACCC ATCGGTAGGC AAAGGAAAAT ACGCTCAGGT GGTGTGGNN 120

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# EP 0 679 716 A1

5 NAGNCTGTNT CAGGCCTACG GAGTCAGCCA GTGGCTAGCG CAAGACCAGT CACTCCCTCT 180  
GCNTTCAGGC TTCTTTCAAT TTCATTATCA TCAAGCAGGA ATTATGTCGT AAGTCACTGA 240  
CCCTAACTGC AGACCATGAA GTAAATTATG TAACTAGGTT TTTNNCTTCT CCAGTGGTGA 300  
CCACCNNCNC NCATNCCCCG GTNANAACCT GGGTTTTTN 339

SEQ ID NO:6786

SEQUENCE LENGTH:80

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08014

SEQUENCE DESCRIPTION:

15 GATCGCCTAT TACTGACAGT CTCATTGTAG CTCTAAAAAG CCTAATGTAT CCACTGTGGA 60  
ATAAACTCCA TAGACTCAAA 80

SEQ ID NO:6787

SEQUENCE LENGTH:279

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08015

SEQUENCE DESCRIPTION:

25 GATCTTGAAG AGACCGCTGG CAGCACCAGT ATTCCCAAGA GGAAGAAGTC TACACCCAAG 60  
GAGGAAACAG TTAATGACCC TGAGGAGGCA GGCCACAGAA GTGGCTCAA GAAAAAGAGG 120  
AAATTNTCCA AAGAGGAGCC GGTCAGCAGT GGGCCTNNAG AGGCGGCTNG CAAGAGCAGC 180  
TCCAAGAAGG NAGGAAAAAG TTCCNTTAAG CATTNCCNGG GAGNTTTGAA TTCAAAATTG 240  
GGCATNTTN TTTGGGGGTT GGGNNATTCC CTTGGCCCN 279

30 SEQ ID NO:6788

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS08016

SEQUENCE DESCRIPTION:

40 GATCCACTCA CCTCGGCCTC CCAAAGTGCT GGGATTACAG TGCCCGTCCG TGATGATGGG 60  
AACATGNCCG ACGTGCCAG NCACCCCAAG GACCCTCAGG GCCCCAGNCT GGAGTGGCTG 120  
AAGAACTGT GAGCACCTCC ACTGACAGAG GCGGCCCTC CCACGGCTCC CAATAAAAT 180  
GTGAAAACCA AA 192

SEQ ID NO:6789

SEQUENCE LENGTH:303

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08017

SEQUENCE DESCRIPTION:

50 GATCCGTATC GNTTTAAGAA GCGGACGGAG CTGTTTATTG CCGNCGAGGG CATTACACG 60  
GGCCAGTTTG TGTATTGCGG CAAGAAGGCC CAGCTCAACA TTGGCAATGT GCTCCCTGTG 120

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# EP 0 679 716 A1

GGCACCATGC CTGAGGGTAC AATCGTGTGC TGCCTNGAGG AGAAGCCTGG AGACCGTGGC 180  
AAGCTGGCCC GGGCATCANG GGACTATGCC ACCGTTATCT CCCACAACCC TTNGACCAAG 240  
AAGNCCCGTT TTGAANGTTG CCCTNCGGTT TCCAAAGAAN GTTTATCTCC TTAANGCCAA 300  
TCN 303

SEQ ID NO:6790  
SEQUENCE LENGTH:267  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08018  
SEQUENCE DESCRIPTION:  
GATCTAAAAA TCAATGAGAA CATAATTTTA ATTGGCAGTT CTTCAGAAAA ATGTGAATGG 60  
CTTATAAACA TAAATGTAAT ACTCAGCTGC TGTCATCATC AGAAGAATGA AGTTGTTTTT 120  
AAGCTCTTCA NCTGTCAAGN GTAAGAAGCA ATGTTACTAA TACCGGCAAG NTATGAAAAG 180  
ACGCTCATAC ATTGTTGGAA ATNAANGTTG GTATNGCTTT TCAGCGGCCN ATNAACATAA 240  
TCCCNNTNTT TCTTCCTAC NNACTCN 267

SEQ ID NO:6791  
SEQUENCE LENGTH:189  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08019  
SEQUENCE DESCRIPTION:  
GATCATCTGG CAAGACAGCC CAAGAATAAA GCCGTCACCA TGGAGACTAA GAAGNGNCAG 60  
AAAGNCACTG GGTCTTCATT GTNTCGTCCA GCTGTTTCATG AGGCCTTATC TGAAGCCCAC 120  
GTGACCTCCG GNCTACTCAC TTACATGCGN GAATAAAAGC TCTATTTTGT TTTAGGNCCN 180  
AAATAANTN 189

SEQ ID NO:6792  
SEQUENCE LENGTH:129  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08020  
SEQUENCE DESCRIPTION:  
GATCTGCTGG CAGAGGNCAA TCAAAAACGA CAACAAGCTT CTCCCAGGG TGAGGGGAAA 60  
CACTTAAGGA ATAAATATGG NGCTGGGGTT TAACACTAAA AACTAGAAAT AAACATCTCA 120  
AACAGTAAA 129

SEQ ID NO:6793  
SEQUENCE LENGTH:267  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08021  
SEQUENCE DESCRIPTION:  
GATCAGGACC CACCTCCAGT TCTNCTGAAA GTNTGACAGT GTCCAGCCGG TTCTGCAGCA 60

EP 0 679 716 A1

CTAGGGGAGG GGGCAGATGG TGGTTGCATG GGCTTCCTGG GTCTCCACTC TCCGTCTGGC 120  
CTAAAGGTGA TGTATTGGT GTTTGGNCCT GCAGTCCCCA CTNTTAAGGC TTAAGGCGGA 180  
TGTGGAACAN CACTTTCTTT CAGGAGTAGG TNGTNTACT TGTACCTCAT TTAGGGCTTA 240  
GAAAGTTTTN CCNCANACTN NAAAAAN 267

SEQ ID NO:6794

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08022

SEQUENCE DESCRIPTION:

GATCTACAAA ACAGATAGNG NAAAGTACAA CAGAATAGCT CGGGAATGGN CTCAGAAGTA 60  
TGCGATGTAA TTAAAGAAAT TATTGGATAA CCTCTACAAA TAAAGATAGG GGNACTCTGA 120  
AA 122

SEQ ID NO:6795

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08023

SEQUENCE DESCRIPTION:

GATCCCACTT GTAGATGCTT GCACTCACAC AATAAAAACG TCTGNTATTT GCCAAA 56

SEQ ID NO:6796

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08024

SEQUENCE DESCRIPTION:

GATCCGTGGT TCCCTGCAGA CTGGCAGGAG CAGATTCCAA AGGCACAGGA AGAAGCTTGC 60  
AGGTAAGATG TGTCATTAC CTTCTGCGCA TTATACCACA AAAAAGCTGG GNATAAAAAT 120  
GCTAACCAAAA 130

SEQ ID NO:6797

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08025

SEQUENCE DESCRIPTION:

GATCTGCCCC ATGATTGGTT CCTTAGGANC AAGNAATTTA CAAGTAGNAA TTATTCCTTT 60  
CAGAGTAACA TGCTGTATTA CTTCAATCCC TATTTTGTG TGTTCCATTT TCTTTGGATT 120  
CCCTATTCAC ATTGAATCCT NTTTGCCCTT CTGAAACAAT ATTCAGTCAC AAGNGNTTTT 180  
GGTCATGTTG GTCTTTGTAA CAAATNAAAN TTACCTTATA TCCTTCTGGA CAAA 234

SEQ ID NO:6798

# EP 0 679 716 A1

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08026

SEQUENCE DESCRIPTION:

GATCACAAGG TCAGGAGTTC GAGACCAGCC TGGCCAATAT GGTGAACCTC ATCTCTATTG 60  
 AAAATACAAA AATCAGCCAG GCACGGTGGC AGGCGCCTGT AGTCCACCTA CTCGGGAGGC 120  
 TGAGGCAGGA GAACTGCTTG AACCCAGCGG CAGAGGTTGC AGTGAGCCAA GATTGAGCCA 180  
 CTGCACTCCA GCCTGGTGNT AGNGCGNGCT CTGTCTCTAA ATAATNANNT AAANTNCNTT 240  
 AANNNN 246

SEQ ID NO:6799

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08027

SEQUENCE DESCRIPTION:

GATCAGTGTT AAAC TAGATT GTATTCATTA CTAGATAAAA TGTATAAAGC TCTCTGTACT 60  
 AAGGNGAAAT GACTTTTATA ACATTTTGAG NAAATAATAA AGCATTTATC TAAA 114

SEQ ID NO:6800

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08028

SEQUENCE DESCRIPTION:

GATCTTTTGT GCCAAGATGC AGGGAAATNA AGAAAGCTCT TTCCAGCTGT TTTNATGGAT 60  
 TCATGGAGTG GGCTCATGTT GGGACCAGCT GACTCTGGGN GGAAGACTGC CTCTCCATCG 120  
 CTGTGAGAGA GCCTGAAAGG ACCAACAATG AGNTGTTCTT GGGACCCGCC ATGGGGATGA 180  
 TTGCTTCTCT AGGCTNCTGG CTGTTGCTGC ATTCTAAGGN TTAACCTCCT GGTCTNATGG 240  
 TAGTGANCTT GAGCTTTTNN ATTCNATAGN AGNN 274

SEQ ID NO:6801

SEQUENCE LENGTH:42

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08029

SEQUENCE DESCRIPTION:

GATCTGTGNA GNAATGAAAT AAAATGGAGA AGAAGACAGA AA 42

SEQ ID NO:6802

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08030

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCAGTTT CAAGAATGGG CAGGTAAACG CAGNANGAGG AAAGGAATGT GGAATGAGAA 60  
 CTTGGTGGTT CACCGCTGTA CTATTGTGT AAATGTTTAC GTATGTNATA AGCTACATGT 120  
 ATGTAAATNT TGCAATACCC CTAACAGTCG AGTAGTAGTC TCCCTTACAG GAATTTTGA 180  
 CGGGGTTTCT CATCATCAAT ACCAAATAAN TATATGTAGG NNTGGAAA 228

SEQ ID NO:6803

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08031

## SEQUENCE DESCRIPTION:

GATCATATTC TTGAAATTTT TATAAATATG TATGGAAATT CTTAGGCTTT TTTTACCAGC 60  
 TTTGTTTACA GACCCAAATG TAAATATTAA AAATAAATAT TTGCAATTTT CTACAGAATT 120  
 GAATACCTGT TAAAGGAAAA TTACAGAATA ANCTTGTGAC TGGTCTTGTT TTACATTAAA 180

SEQ ID NO:6804

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08032

## SEQUENCE DESCRIPTION:

GATCATTCCG AGGTCATTG AGGACGCACA CTGGAGAGAA GCCTTATNAG TGTAACAAT 60  
 NTGGAAAAAC CTTCATTGG TNCTCAACGT TTAGAGAACA TGTNAGAATT CACACGCAAG 120  
 AGCAGCTCCA TAAATGTGAA CACTGTGGGA AGGCCTTTAC CTCTTCCAGA GCATTCCAAG 180  
 GTCATTTGAG GATGCACACT GGAGAGAAGC CTTATGAGTG TACACAATGT GGANAAACCT 240  
 TCACTNGGGG CCTCAANCCT TACNTAATAA TGTGGTN 277

SEQ ID NO:6805

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08033

## SEQUENCE DESCRIPTION:

GATCTACCTC AGTATTCAAG TTCAGTGGGG ACACCAGTGG CTTCAAACCTT CCTGGTTTCA 60  
 TGATATCTTG AGACGCCTTA CAAATGATGG AGGATTCCAA AGAGTTTTTG TTTATTTGGG 120  
 TTAATATTTG TTGGTATTTA TGGCATTGGA GATTGAACT AAGNAATGTT TTAATTTATT 180  
 ACCTTTACAA CATTATTTA CATTACATAC ATACATTTAC AACATTTATT AATTTATNTT 240  
 AAAATAGCAT GNATAAGCCA ATTATNGGTT AGN 273

SEQ ID NO:6806

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08034



EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCCACTCT TCTCGNCCTC CCAAAGTGTT GGGATTATAG GCGTGAGCAC ANCGCCCCGG 60  
 CCTGNTNTGG ATATTCTTA TAAATGGAAT CATACAGTGC TTNTTTCAGT TAGCATAATG 120  
 TTTCCCAGGT TCATCCAGGT CATAACACAT AATCAGGCTT CATTNTTTT TATTACCANC 180  
 TAATATTCTA TGAATATAAA NNNACCN 207

SEQ ID NO:6807

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08036

SEQUENCE DESCRIPTION:

GATCCTGAAG AGATTGAAAA AGAAGAGCAG GCTGCTACTC AGCCTGAGGT TGCAGACTGG 60  
 TCTGAAGGTG TACAGGTGCC CTCTGTGCCT ATTCAGCAAT TCCCTACTGA AGACTGGAGC 120  
 GCTCAGCCTG CCACGGAAGA CTGGTCTGCA GCTCCCACTG CTCAGGCCAC TGAATGGGTA 180  
 GGAGCAACCA CTGACTGGTC TTAAGCTGTT CTGTCATAGG CTCTTAAGCA GCATGGNAAA 240  
 ATGGTTGCTG GCAAATAAAC ATCAGTTTCT AAA 273

SEQ ID NO:6808

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08037

SEQUENCE DESCRIPTION:

GATCTCCAAC ATCTTTGTGT TGAAGGGCCT ACAGAGTAAA CTGTGGGACT CAATAAACAT 60  
 TCGTTACTTG AAA 73

SEQ ID NO:6809

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08038

SEQUENCE DESCRIPTION:

GATCACAGCA GACAGGGTCG CTGCCCTGAT GGCGCTTACA TTCCAGTGGG TCTAATGACC 60  
 ATATCTTAGG ACACAGATGT GCCCAGGGAG GTGGTGTAC TGCACAGGAA GTATGAGGAC 120  
 TTTAGTGTC TGAGTTCAA TCCTGATTCA GGAACCTACA AAGCTATGTG ACCTTACACC 180  
 AGTCACTTAA CTTGTAGCC ATCCATTATC GCATCTGCAA AATGGGGATT AAGAATAGAA 240  
 TCTTGGGGTT AGTGTGGNGA TTAGATTAAA TGTATGTAAG GCACN 285

SEQ ID NO:6810

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08039

SEQUENCE DESCRIPTION:

GATCAGTTTC TGGCACATAA ATGCCTCAAT AAAGATTTAA TTACTTTGTA TAGTGCTTTA 60  
AA 62

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SEQ ID NO:6811  
SEQUENCE LENGTH:237  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08040

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SEQUENCE DESCRIPTION:

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GATCATTGGC TATGACAGAG AACCCGTCTC TCAAGCAGCA GCTCTTCTCC TATGCCATTG 60  
TTGGCTTTGC CTGCTGAGG CCATGGGGCT TTTNTGTTG ATGGTCGCCT TCCTAATCCT 120  
NITCGCCATG TGAGGNTCCA TGGGGGGTCA CCGGANCTGT TGATACTGCA ACTACACACC 180  
ATTNTTGGTG CTGGGGTGTG TTAAGATTTA ACCATTNANC ACAACGTTTC TCTNAAA 237

SEQ ID NO:6812  
SEQUENCE LENGTH:215  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08041  
SEQUENCE DESCRIPTION:

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GATCAGCAAA TTTAAGAGAA GACCTAGCTA TGTTGGCTGG TTGCTTTCTA TTATCATGGT 60  
ATTTGACCAT TTAGTTTTA ATTCCATGTC AGATAAGTGT AAATAGAAGA GTTTAAAAGC 120  
ATGANACATT TCAGANGGTA TCAGTTATAT GATATTCTTT AANCANNTAT GACACATGTA 180  
AATCCTCNTG ANTGACAATN CATCTNTNTG TGAAA 215

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SEQ ID NO:6813  
SEQUENCE LENGTH:181  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08042  
SEQUENCE DESCRIPTION:

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GATCTAAAAG CCATATCCTG TCTTTGGTGG TGGCCTGGTA GGAATGGCTT GTNCTAGTTC 60  
TTCAAAGGTA AGATTGACCA AAGCAAGTTC TCATTGGTGG TCTGTGTTTA CATCTTCCGT 120  
GTCAAGNTAT TTAAAGCAT GNAAATAAAG CCATTCTTGC CCTTTTTCGT GTGTTTGCAA 180  
A 181

SEQ ID NO:6814  
SEQUENCE LENGTH:162  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08043  
SEQUENCE DESCRIPTION:

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GATCTCAGGC TTCTGCAGTT CTCATGACTC CTACTTTTCA TCCTAGTCTA GCATTCTGCA 60  
ACATTTATAT AGACTGTTGA AAGGAGAATT TGAAAAATGC ATAATAACTA CTTCCATCCC 120  
TGCTTATTTT TAATTTGGGA AAATAAATAC ATTCGAAGGA AA 162

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# EP 0 679 716 A1

SEQ ID NO:6815

SEQUENCE LENGTH:431

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08044

SEQUENCE DESCRIPTION:

GATCTCAGCG GGGAGCCACG TCTCTTGCAC TGTGGTCTCT GCATGGACCC CAGGGCTGTG 60  
GGGACTTGGG GGACAGTAAT CAAGTAATCC CCTTTTCCAG AATGCATTAA CCCACTCCCC 120  
TGACCTCACG CTGGGGCAGG TCCCCAAGTG TGCAAGCTCA GTATTCATGA TGGTGGGGGA 180  
TGGAGTGTCT TCCGAGGTTT TTGGGGGAAA AAAAAATTN TAGCATATTT AAGGGAGGCA 240  
ATGAACCCTN TCCCCANCT NTTNCCNGCC CAAATNTGTC TCCTAGNATC TTATGTGCTG 300  
GGAATAATAG GCCTTNACTG CCNTCNGNT TTATAGGCCN ANGGGTCCCG GTTCCCCGGG 360  
AACTGGAACC CTTCTTGAGG GGGAATCCCG GGGCTCAAAT TACCCCNAA AGGAAAGTGG 420  
CCAAGGCGGT N 431

SEQ ID NO:6816

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08045

SEQUENCE DESCRIPTION:

GATCTGTTTC TAAAGCGTTA CGCATCTTTN CTGAAGTATG CTGGAGAGCC TGTCCCTTTC 60  
ATTGAACCCC CTGAAAGCTT TGAATTTNAT GCACAGCAGC TAAGAAAATT GAGGGAAAAC 120  
TCTTCTGAA ATAACCAGGC GATACTTTGT TTTGTATATA TTTGTGATTC TGTGTCTACA 180  
TGTTATTTTG AAGTATATCT GAGGGAANNG GGAATGGAAA TTTTCTTTAA A 231

SEQ ID NO:6817

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08046

SEQUENCE DESCRIPTION:

GATCCTTCCA GCTGCTCTTC CATAACTTCA TCTCTCCCCT CAACACCTGC AACCCTAAG 60  
CCATTTTCCC CCTACCCGTC TGTAATTTTG TAATTTTGAG AATGCCAGGT AAATGGAATC 120  
AGAGCGGATA ATCTTTGGAG CATGAAA 147

SEQ ID NO:6818

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08047

SEQUENCE DESCRIPTION:

GATCATTAT ATTTAAGTTT AAAAGGAGGN TGAGACTGAG TTTTGTAGA GTTATAATNA 60  
CATTCAAAT ATACTTTTTT GCATTGNNA AATGTTAANT N 101

SEQ ID NO:6819

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08048

SEQUENCE DESCRIPTION:

GATCAAGCCA AACAGTAAAA ACTACCAAGA GAACACGAGG AAGGCAGAAA CGNTGTTTAG 60  
CAACAGTATT CTGCATGGTT CACTGCTTAA GAAAAATGCCT TCTGGAATAT TTGTAAACTG 120  
AAATTCTGTA TGTGTAAGNG NTGTTTAAAT ATGTTTGGGT CCTAAACAGC TTTTAAAAAT 180  
TATACTTGGG CNTAANTTCA GCATCTTTTC AAATCANCTC TNTGCNCCGC CGCTGN 236

SEQ ID NO:6820

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08049

SEQUENCE DESCRIPTION:

GATCATTTTG TTTGTGCTC TCTCTAGTGT CTTCTTCTCT CGTCAGTCTT AGCCTGTGCC 60  
CTCCCTTAC CCAGGCTTAG GNTTAATTAC CTGAAAGATT CCAGGAAACT GTAGCTTCCT 120  
AGCTAGTGTC ATTTAACCTT AAATGCAATC AGGAAAGTAG CAAACAGANG TCAATAAATA 180  
TTTTTAAATG TNAAT 195

SEQ ID NO:6821

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08050

SEQUENCE DESCRIPTION:

GATCATAAAT ATTTTGTAAT GAAATACTTC CNCTTTTCCA GGGCTTTGTA TGCACTTGTA 60  
TAATTACATT GATGGCAATG TAGNGTTTGA ATTTCACTCT GTAAATACTT TTNTGGNAAA 120  
TAGNAATTTT NATTGCTTTA AAGTTTGGGA TATGGGTGGN 160

SEQ ID NO:6822

SEQUENCE LENGTH:157

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08051

SEQUENCE DESCRIPTION:

GATCTATAGG AAGATTGAAC CTGAATATTG CCATTATGCT TGACATGGTT TGCAAAAAAT 60  
GGTACTCCAC ATACTTCAGT GAGGGTAAGT ATTTTCCTGT TGTCAGAAGT AGCATTGTAA 120  
AAGCATTTTG TAATAATAAA GNATAGCTTT AATGAAA 157

SEQ ID NO:6823

SEQUENCE LENGTH:150

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08052

SEQUENCE DESCRIPTION:

GATCCAGNTT GTTGCATCAA TAGTTCGTGTT TTTAGTACTG AGTGGGATGT CAGTATAGAT 60  
GTACCATAGT AAACACCTGT GGAAGGACGT CAGGAATGTT TCCTGTTATT AGGTATCTAA 120  
ATAAAGTTGC TGTAAACATT TGTGTACAAA 150

SEQ ID NO:6824

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08053

SEQUENCE DESCRIPTION:

GATCTGTCCA CTTTGCTCTC ACGGACGTGG CATTGTCAG GAAGGAGAAC CCAGCAGGAA 60  
CGGAGGTCTC TGCCTCACC TACAGTGAAG GGGCTGGTAT GTGAAATACT TTCACTGAGC 120  
TTAGTGAAAA ATTCATTTTA CACCCTAGTT AGCTCCCAGA AAGGTTNAAC TTTCAAGANG 180  
GTCAAAATAT GNAGCCTGTT ATATGTGTAA TAAAAAAGN NNTAGNATAT CCCAAATGGN 240  
ACATTTCAGG NATTAANTAA TTGNAATN 268

SEQ ID NO:6825

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08054

SEQUENCE DESCRIPTION:

GATCTGAGAA GTGAGTGTA GAGTTTAAA TCAACCTCTG TTCTGTGCTA GTTAAGGTAA 60  
TAAAGTTGCT GCAGTCCAGG GGGTAGGTAC CTGTGGACGG CTCTGCGAAT AGGNCAGTTG 120  
CATTTCTTGG GAATCAAGTG CATCCCTAGG CTGGCAGTGC AGCAGAAATA CTGAATAAAA 180  
TGTGACAAAT CTCAAAA 197

SEQ ID NO:6826

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08055

SEQUENCE DESCRIPTION:

GATCAAGTAA AAATGAAGGA CAACGTGAAG TTAAAGTTC GATGCAGCAG ATACCTTTAC 60  
ACCCTGGTCA TCACTGACAA AGAGAAGGCA GAGAAACTGA AGCAGTCCCT GCCCCCGGT 120  
TTGGCAGTGA AGGAACTGAA ATNAACCAGA CACACTGATT GGAAGTGTAT TATATTAAAN 180  
TNCTAAAAAT CCTAAA 196

SEQ ID NO:6827

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08056

SEQUENCE DESCRIPTION:

5 GATCATCAGT ACTGTTGTCT CATGTAATGC TAAAACTGAA ATGGTCCGTG TTTGCATTGT 60  
TAAAAATNAT GTGTGAAATA GAATGAGTGC TATGGTGTG AAAACTGCAG TGTCCGTTAT 120  
GAGTGCCAAA AATCTGTCTT GAAGGCAGCT ACACTTTGAA GTGGTCTTTG AATACTTTTA 180  
ATAAATTTAT TTTGATAAAT AATATTGAAC AAA 213

10

SEQ ID NO:6828

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS08057

SEQUENCE DESCRIPTION:

GATCGTCCTG CAGGTATTTT GCAAGCCCCT ACTGTCCGCC GACATCAGCG TGAATCTCAC 60  
ATGGTGCAGT TGGTCCCTG GGGGAGTNTT NGCNTCTCCT GTTGTCTTTT CCCAAAACCA 120  
20 NTA AAAACCA TGN 133

SEQ ID NO:6829

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS08058

SEQUENCE DESCRIPTION:

GATCTGCTAC ATTTTAAAG TGGGCATGAA AATCTTCTGT TATGTATGTA CTGTCATTAA 60  
TTCTGTATT TTNCCCCT AGTACTATCA ACTACAGTAA AGACCTTCCT CTGGCCCAAG 120  
30 GAATCAAGTT TCAGTAAAGG TGTTTTAGAT GANCATCCCT TAATTTGAGG TGTTCCAGCA 180  
GCTGTTTTTG GNGANGACAA AGNAAATTAA NGTTTTCCT GAATAANTGC ATTATTNTGA 240  
CTGTGACAGT GNCTAATCCC CCTATGGTN 269

35

SEQ ID NO:6830

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08059

40

SEQUENCE DESCRIPTION:

GATCTATCCA ATAAAGGAGA GAAACAACCG CACACGCCTG GCTCTCATCA TATGCAATAC 60  
AGAGTTTGAC CATCTGCCTC CGAGGAATGG AGCTGACTTT NACATCACAG GGATGAAGGA 120  
GCTACTTGAG GGTCTGGNCT ATAGTGTAGA TGTAGAAGAG NATCTGACAG CCAGGGATAT 180  
45 GGNGTCAGCG CTGAGGNCAT TTGNTACCAG ACCNGNGCAC AAGTCCTCTG NCAGCACATT 240  
CTTTGGTACT CATGTNTCNT GGCATCCTGG NGGGGTNTCT TGCGGAACTT GTTCTGN 297

SEQ ID NO:6831

SEQUENCE LENGTH:174

50

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS08060

SEQUENCE DESCRIPTION:

GATCATGGTG GTTTGGCAGC AGGGAATTTG TCTTGTGGA GCCTGCTCTG TGCTCCCCAC 60  
TCCATTTCTC TGTCCCTCTG CCTGGGCTAT GGGAAAGTGGG GATGCAGATG GCCAAGCTCC 120  
CACCTGGGT ATTCAAAAC GGCAGACACA ACATGTNGCT CCACGCGGCT CAAA 174

SEQ ID NO:6832

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08061

SEQUENCE DESCRIPTION:

GATCAATTTT GGAGACCTTG GCCGCCCAGG ACGTGGCGGC AGGGGAGGAC GAGGTGGACG 60  
TGGGCGTGGT GGGCGCCCAA ACCGTGGCAG CAGGACCGAC AAGTCAAGTG CTTCTGCTCC 120  
TNATGTGGAT GACCCAGAGG CATTCCCAGC TCTGGCTTAA CTGGATGCCA TAAGACAACC 180  
CTGGTTCCTT TGTGAACCCT TCTGTTCAA GCTTTTGCAT GCTTAAGGAT TCCAAACGNC 240  
TACTGTAATT AAA 253

SEQ ID NO:6833

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08062

SEQUENCE DESCRIPTION:

GATCATGAAC CAAAGGAATT TATGTTTTGT AACTTGGGTA CTTTATTTTG CATTTGTTA 60  
TACTATTAAT TANTTTNTC CTGAAA 86

SEQ ID NO:6834

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08063

SEQUENCE DESCRIPTION:

GATCCAAGTT TCACTTTTTG TGATATAATG AGCCAGTTTT CTCAGTAATG TCTACTAAAA 60  
AAAAAGCCAT TAACCNGGNT CTAATATTTG CATGATTCTA ATAAANGTAT GTCAACTTCT 120  
TAAA 124

SEQ ID NO:6835

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08064

SEQUENCE DESCRIPTION:

GATCCCCTCA GAAGGCAGGA GTGCTGCCCT CTCCCATGGT GCCCGTGCCT CTGTGCTGTG 60

TATGTGAACC ACCCACGNGA GGGNATAAAC CTGGCACNNG GACCAAA

107

SEQ ID NO:6836

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08065

SEQUENCE DESCRIPTION:

GATCCTCCTG TCTTGGTTTC CCAAAGTGCT GGGATTGCAG GTGTGAGCTA CTGCACCCGG 60  
CCCAATAAAA AAATCTCGTT CTGTGAAAGA AATGTTTAAAT AAAAGTTGTA TTGTCAAATT 120  
TTAAA 125

SEQ ID NO:6837

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08066

SEQUENCE DESCRIPTION:

GATCACTAAG ATTAGCTATA TCTATACAGT CATTAGTTTG ACAAGAAATA GNATCCTGTC 60  
AGATGCCAAA GAGTGGGATT TTNATGTTTA ATGATTAAAC ACCATTATTT ATTGACAATT 120  
TACCCTGTGG AACTGTATTA TTTCTAACTA TGAAATAAAG GGGTGATGTA AACACAAA 178

SEQ ID NO:6838

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08067

SEQUENCE DESCRIPTION:

GATCCCCGGC CAAGCCCAGT CACGNGAATT TAAGGCTCTT CTCTCCGGCT CCAGCCTGTG 60  
CCTGTAATTG TCCAGGANTG GCCTAGGCCG ACACCTTCTG CTGCCCCGGA GTCCCTCCC 120  
TGGGTGGGAT GCTCACTACA GCTCTGATGT ATATAGCACA CAGCCCAANT CCGACCCTCC 180  
GGTCTGTGCG CAATAAAGNG GGGTGTGTTT CANTCCGGA AA 222

SEQ ID NO:6839

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08068

SEQUENCE DESCRIPTION:

GATCCCAACA GGCCCTGGCA GCGTCTGGAC ATGTGTAAAC AGCAGCAGTC ACGTTCCTCG 60  
GCTGNCACAA CCAACACNNN AGCAGGTTTT CCATTTTCTG TACTTTNATA TTTCTGTTCA 120  
ACCTGTTGGT TTCTACAATG ATTTTAAACA TTGGNAAGNC AGCCTTGNGT ATATTTTAA 180  
AAATTATATT NAAAATGN 198

SEQ ID NO:6840



# EP 0 679 716 A1

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08069

SEQUENCE DESCRIPTION:

GATCATGAAA CTTAGTAGAG GGGATTGTGT GTATTTNATA CAAATTTAAT ACAATGTCTT 60  
ACATTGATAA AATTCTTAAA GAGCAAAACT GCATTTAATT TCTGCATCCA CATTCCAATC 120  
ATATTAGANC TAAGNTATTT ATCTATGAAG ATATAANTGG TGCAGAGAGA CTTTCATCTG 180  
TGGATTGCGT TGTTTCTTAG GGTTCCTAGC ACTGNTGCCT GCACAAGCAT GTGNATATGT 240  
GANATNNNAT GGATTCTTCT ATAGCTAAAT GNGTTCCTC TNGN 284

SEQ ID NO:6841

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08070

SEQUENCE DESCRIPTION:

GATCCACCTG CTTCGGCCTC CCAAAGTGCT GGGATTACAG CTGTAAGTCA CTGATNCCGG 60  
NTGCATGTCA AGCACATTGG NAAGTTCTTA CAACAATTCT GNTGGAGGNT TTTN 114

SEQ ID NO:6842

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08071

SEQUENCE DESCRIPTION:

GATCTGTCTC TCAAAGGAAG AAACAAAAAC CCAAAATTTT GACTGCAAAA GATTGACTAA 60  
TTCTAGGTGC AAATAACTGG AAATTTAGGA TTGTTATTGT ACTACACAGG TCACAANGTT 120  
CCAAACCTAT TTCCCTTGTA ATTTTATAGT CATGATTTT CAGAATGCAG TTTCTATCTT 180  
TTTAGGTGCA ATATTACGAA CTGCTTAGGT CAGANCANTT TNGTNTCTCC AGTTTTTCT 240  
CCCTANGTTA CAN 253

SEQ ID NO:6843

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08073

SEQUENCE DESCRIPTION:

GATCTTATAA CCTCATTGTT TCCTAATCAT TTTATTTTCT CTCCTGCTAG TACTGTGCCG 60  
CTTCCCCCTC CCCCCACACA AAATAAAAAC AGTATCTGCC AAA 103

SEQ ID NO:6844

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS08074

SEQUENCE DESCRIPTION:

GATCCGTGCC CCACCTCTCC CCAGTTAAGT GCCTTCACAC AGCACTGGTT TAATGTTTAT 60  
AAACAAAATA GAGAACTTT CTTATAAAT AAAAGTAGTT TGCACAGAAA 110

SEQ ID NO:6845

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08075

SEQUENCE DESCRIPTION:

GATCAGGGCT GAGGGTAAGG AAAAGAAGAG ACTAGGAAAG CTGGGCCCAA AACTGGAGAC 60  
TGTTTGTCTT TCCTGGAGAT GCAGAACTNG GCCCGTGGAG CAGCAGTGTC AGCATCAGGG 120  
CGGAAGCTTT AAAAGCAGCA GCGGCNTGTG CCCAGGGCA CCCAGAATGA TTTCCCTATG 180  
GGCACCAGGC CAGNGAAAAA ATTGGGCAGC NTCTTTAAAG GGNGGAAAAT TGTTTGTGAGC 240  
CCCAAA 246

SEQ ID NO:6846

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08076

SEQUENCE DESCRIPTION:

GATCTACCTG CATATAACAG TCTCTAAGTT TTTTTTCAA TCTTGCANTT TGATAATTTT 60  
GATTTTGGCC ANATTAGNNT AATTTGGGAC TATCCTGAAA CAGNN 105

SEQ ID NO:6847

SEQUENCE LENGTH:26

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08077

SEQUENCE DESCRIPTION:

GATCAAAAGA GCTGTCTGAC TGCAAA 26

SEQ ID NO:6848

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08078

SEQUENCE DESCRIPTION:

GATCCCTTGA GCCCAGGAGT TCCAGACCAG CCTGGGAAAT ATAGGGAAAC CCTGTCTTTA 60  
CAAAAAAAAA TTTTAAAAAT TAAA 84

SEQ ID NO:6849

SEQUENCE LENGTH:217

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08079

SEQUENCE DESCRIPTION:

GATCAGATTC CTGACTAACC CCTCTCTTAG AGCTACAGCG AGCTGCATTA CCAGCTTAAA 60  
ACACTTCTTA GGGATTAAAT ATAGNTGTNA TTTTCAAAA TCGTTTTTAA TTTAACTGT 120  
GTTTtagtGT AAAATTGTTA ACCTTGTAAG ATGGATANTG TGTATANGAN TGTAGGCCTT 180  
AACTATTTCA CATGAGTCAA ANCANGGCNG CTTTAAN 217

SEQ ID NO:6850

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08080

SEQUENCE DESCRIPTION:

GATCTCACCC AGTGTGCAAT TTGTGAAAAT GAACCAAATG TCATTACTTT TGTCTTAAAG 60  
CAAAGTCTAT TTCAAGNATA TGNACAGCAN AAA 93

SEQ ID NO:6851

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08081

SEQUENCE DESCRIPTION:

GATCAATGAA CCATCTCTTC TGGGCAGTTT TGTGAAAAT AAAGGTTTCT CTTTGATTTC 60  
AAGAATGACC AAA 73

SEQ ID NO:6852

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08082

SEQUENCE DESCRIPTION:

GATCACCGGT TTCCGACTGA GTCTGGGGAT TTNGGCCTTG TTGAACCCCTC CTACGGTGCC 60  
CNGGGAATTT GAAANACGCT TTCTGCATNG ATATNTGGGC CCTN 104

SEQ ID NO:6853

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08083

SEQUENCE DESCRIPTION:

GATCAACATC ATTAAAGATT ATGTAAAAAG TTAAGGCT TATGAGCCTA AGTTTGTTC 60  
TATATTACCA TATTTACTGA ATNTTCTGGN AAAGNAACTT TANTAAAGTT TAATCTNAGG 120  
AAA 123

# EP 0 679 716 A1

SEQ ID NO:6854

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS08084

SEQUENCE DESCRIPTION:

10 GATCACTTGA GCCTAGGAGG CAGNGGTTCA AGTGAGCTGA GATGGCACTC CTGCGCTCCA 60  
GCCTNGGTGA CAGCGTGAGA NNCTGTCTCA N 91

SEQ ID NO:6855

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08085

SEQUENCE DESCRIPTION:

20 GATCTGTCTAG NACCATTTGA AAAGCTGCTC AAGAGCAGTT GCTTATATAT AGTAGGATTT 60  
TACTTTTTCC TGCTTATGTA NTACTATATG CTTAAAAAAC CTGGAGGAAT ACTTACCAAA 120  
GAGGAGTAAC CATCTCTGAG GGTGGGATTC TGGGGGANTT TTTGTTTTTT TCTGTTTTCT 180  
ATANTGTGCA NCTNTTNTAG TATGTNTNTT NCTAATTGN 219

SEQ ID NO:6856

25 SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08086

SEQUENCE DESCRIPTION:

30 GATCTTNTCTC CATTTACAGT ACATTCTTAG GATGTATGTA GTAAATAAAG CTTTCTTTAA 60  
AGCAAA 66

SEQ ID NO:6857

35 SEQUENCE LENGTH:43

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08087

SEQUENCE DESCRIPTION:

40 GATCACCCCG TAGGAAATAA AGCAGGCATC TCTGGACCTC AAA 43

SEQ ID NO:6858

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS08088

SEQUENCE DESCRIPTION:

50 GATCAAAAGA CAGNTAAATN TTTCTTCTAG AACACAGTTA CCCCCTTGCT TCATCTATTG 60

EP 0 679 716 A1

CTAGAACTAT CTCATTGCTA TCTGTNATAG ACTAGTGATA CAAACTTTAA GAAAACAGGN 120  
 TAAAAAGATA CCCATTGCCT GTGTCTACTG ATAAAATTAT CCCAAAGGTA GGTGGTGTG 180  
 NTAGTTTCCG NGTAAGACCT TAAGGCCACA GCCAANCTCT TAAGTACTGT GTGNCCACTC 240  
 TTGTTGTTAT CACATAGTCA TNCTTGGTTG TACTATGTGA TGGTTAACCT GTAGCTNATN 300  
 ANTNTACTTA TTATTCTNTT CCTCCTTTAC CTCANCNN 338

SEQ ID NO:6859

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08089

SEQUENCE DESCRIPTION:

GATCGTTTGC AAGTAACTGA ATCCATTGCG NCATTGTGAA GGCTTAAATG AGTTTAGATG 60  
 GGAAATAGCG TTGTTATCGG NTTGGGTTTA AATTATTTGA TGAGTTCCAC TTGTATCATG 120  
 GCCTACCCGA GGAGANGNGG NGTTTGTTAA CTGGGCCTAT GTAGTAGCCT CATTNCCAT 180  
 CGTTTGATT ACTGACCACA TATGCTTGTC ACTGGGCANG AAGCCTNTTT CNGCTGCCTN 240  
 CACGCANTTT N 251

SEQ ID NO:6860

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08090

SEQUENCE DESCRIPTION:

GATCTTAATA TAAATNCACT TTCATTTTTN ATAGCTGTCC CATCTGGTCA TTTGGTTGGC 60  
 ACTAGACTGG TGGCAGGGGC TTCTAGCTGA CTCGCACAGG GNTTCTCACA ATAGCCGATA 120  
 TCAGAATTG TGTGAAGGA ACTTGCTCTT TCATCTAATA TGNTAGCGGA NAAAGGAGAG 180  
 GAAACTACTG CCTTAGAAA NTATAAGTAA AGTGATTAAA GTGCTCACGT TACCTTGNA 240  
 CATAGTTTTT CAGTCTATGG GTTTAGTTAC TTTAGNNGG NAGCNTGTNA CTTATATTAN 300  
 TAGTANTTTN GTAAAGTTGG NTGGATAAGC TATCCATGTT GCCAGGTTCA TGGATTNGN 359

SEQ ID NO:6861

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08091

SEQUENCE DESCRIPTION:

GATCCCCAAA CCACAAATAC ATATGTGTGC CTAAGTTTGT GCATGCATAC ATTAACAGG 60  
 ACATAAAGTG TAAA 75

SEQ ID NO:6862

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08092

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCATCATG GCAAAACCAG CTGGTGGGCC CAAGCCTCCA AGTGGGAAGA AAGACTGGGA 60  
 TGATGACCAA AATGATTGAA ATTGGCTTAA TTTTACTGT AGGTGAAGGC TGTATTTGTA 120  
 GTAGTACTCA AGAATCACCT GATGTNTTCT TATTCTCCTT AAATTAAGAG TTATTTTGTN 180  
 TTTGTNTTCT TGGCTGGATG TTATAATAAN CATATTGTNA CTGTCAAA 228

SEQ ID NO:6863

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08093

## SEQUENCE DESCRIPTION:

GATCATGCCT ACTTTCTTCT NTGTATCTCC CTCCTTCCCA GCCCACCCTGG GCAGCAGACT 60  
 CTNATGGAAG NAAGGTGCCG TAGTGGGNTT TTAGAACTA ACGGGACTGG TTTTCAAAGC 120  
 AGTTATCTTG GGAAGCTGTT TATTCCAGCG ATGTGACTTT TTTNAGAATA TTTCTTGGA 180  
 TCATATTCAG AGTCTGGGGC TGTGTGTTGA GCAGCCTTAA GGNTGCTAGA CACTCATTTA 240  
 GTGCCCAGGG AGTCCAGCGA ATGACGTCTG TGGCCAAGCG AGGTCTCAGG TGCAAAGCN 299

SEQ ID NO:6864

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08094

## SEQUENCE DESCRIPTION:

GATCCTCTGA ACCTGCAGAG GCCCNCTCCC CGAGCCTGGC CTGGCTCTGG CCCGGTCTTA 60  
 AGCTGGACTC CTCCTACACA ATTNATTNA CGTTTTATTT TGGTTTTCCC CACCCCCTCA 120  
 NGNNTGTCCG GGAGCCCCTG CCCTTNACCT AGCTCCCTTG GCCAGGAGCG AGCGAAGTGT 180  
 NGGCCCTGGT GAAGCTGCCC TCCTCTTCTC CCCTCACACT ACAGCCCTGG TGGGGGAGAA 240  
 GGGGGTGGGT GCTGCTTGTG GTTTAGTCTT TTTTTTTTTT TTTTNTTTN TNANAAAA 298

SEQ ID NO:6865

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08095

## SEQUENCE DESCRIPTION:

GATCTGCGGG GCAANTTCAA GCNNNCCCCA CTGCGGAGGG TGCGCATGTC GNCCGATGCC 60  
 ATGCTCAAGG CCCTGCTGGG CTCGAAGCAC AAGGTGTGCA TGGACCTGAG GGCCAACCTG 120  
 AAGCAGGTCA AGAAGGAGGA CACAGAGAAG GAGCGGGACC TGCAGACGT GGGTGACTGG 180  
 AGGAAGAAC TCGAGGAGAA GTCTGGCATG GAGGGCCGGA AGAAGATGTT TGANTCCGAG 240  
 TCCTAGGCCA CTCGCTGCCC CTACGNCTGC CCCGGTGCCC GGTTCACAGC AGAANN 296

SEQ ID NO:6866

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08096

SEQUENCE DESCRIPTION:

5 GATCCTGTTT TGTCAGCTGC ACCCTGAGCA AAAACTTGCC ACACCAGNGC TCCTAGAAAC 60  
AGCCAGGCT TTGGAGCGGA CCCTGAGGAA GCCTGGGAGG GGTGGGATG ACACGTATGT 120  
CTTGTCAGAT ATGCTCAAGA CGGTGAAAAT TGTGTGACTG CTTAGGCCAA GCAGCCCTCC 180  
TGCCTAGAAT GACCTTGGAC TCCCAGCCTG CCAGNGAATG NAGAAATACA ACGCACAGTA 240  
10 CTTTGAAGC TTCGTATTTT TCTGGTTTC ACACTCAGCT ACATGTGACC TCCAGCTTGG 300  
TGCGGTTAGN 310

SEQ ID NO:6867

SEQUENCE LENGTH:285

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08097

SEQUENCE DESCRIPTION:

20 GATCAGTTCA AGAAGGTAAT CCAAGGGCCT GATGACTCTT TTGGTAACCA GACACCAATC 60  
AAATAAGGGG AGGAGATGAA AATGGAATNA TTTCTTCCAT GCCACCTGTG CCTTTAGGAA 120  
CTGCCAGAA GAAATCCAA GGCTTTAGCC AGGAGCGGAA ACTGACTACC ATGTAATTAT 180  
CAAAGTAAAA TTGGGCATTG CATGCTATTT TTAATACCTG GNTTGCTGAT TTNCAAGAC 240  
AAAATACTTG GGGTTTCCA ATAAAGATTG TTGTAATATT GNAAA 285

25 SEQ ID NO:6868

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS08098

SEQUENCE DESCRIPTION:

GATCAGACTC TGTATCAAAA GTACCTTTGC CCTTAGGAAG AGTGAGTATT GGAGTCATCT 60  
TATCTATTAC TCCAAACCTC CCTTTNATT TCTTGAGCCT GGCTTGGACC TTGGCATTCC 120  
35 GTTTGANTTC CTTCTAAGTG GAACATTTGT GTTGATCTG TAACACTGGC ACTGAAATAA 180  
AGACCACACG GTTAAAGNAA A 201

SEQ ID NO:6869

SEQUENCE LENGTH:50

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08099

SEQUENCE DESCRIPTION:

45 GATCATGTGC TGCCTTTTAC TGCTGAATTA AAACAGATAT TTCACGNAAA 50

SEQ ID NO:6870

SEQUENCE LENGTH:43

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

55

# EP 0 679 716 A1

CLONE:HUMGS08100

SEQUENCE DESCRIPTION:

GATCTTCAGT GTAAATNACC ATGTATAAAC TGTAAGTGC AAA

43

SEQ ID NO:6871

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08101

SEQUENCE DESCRIPTION:

GATCATTAA TATATTCATA TTACCAAGAC TATTATACTG GAAGTGGTTT TTGTGTTATA 60  
AAGGTTTAAT TTTACATANG GCAGTTACTT AATGTGATTT TNAACCCTTA AAAAAGTGGG 120  
GATGTATACA TTTGTAAACA ATGCCATGAA AGCATTNCT TTCTCCTAAG GAAAAGTGAA 180  
TTTCTTATCA GAATATCTGG CTGGCCCTGT AATTAAATT AAAATAAANT TTGGCGNAN 240  
CAGCAAA 247

SEQ ID NO:6872

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08102

SEQUENCE DESCRIPTION:

GATCTATCTG AGAACAAAGA AGTCGACAGA ATAACATTGA TGACTTTTTA AATAATTAAT 60  
TTATTTGAAG AATGCTTGCA TACAAAAAGC TTCCTGCAGG AATTTTAAAC AAGCTGTCCT 120  
TGGTTATCCC AGGCAATGTC AGTTGATTTA NTAAGTTTA CATGCAAAAG NGAATACAAT 180  
TGTAACATTA ATTGGAACAT TAAGTTGGCT TATAAGCAGT ATTTCCACTG CTCCTACAAT 240  
TGNTTTNNGT TATTTGATAN TTNATTNAN ATTNNTNTT GGTGTGGN 288

SEQ ID NO:6873

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08103

SEQUENCE DESCRIPTION:

GATCGTACCT ATTGCACTCC ATCCTGGATG AAAGAGCCAG ACTCTGTCTC AAAACAAACA 60  
AAAAAGCGTG GGGACTTCTG GGGACAGACA AGGTGCCTGT AATATATTN CTCAGTCTTT 120  
GCCCTGAATG GTCTCAGCTT GANACCATNT CAACTGGAG AGAAGCAAGC CAGCCAATAG 180  
AATGGGGTGA TTTACAGGGA TTTCTGTTTA CTGTCAAAAT ATTTCTCATC TGCATATGT 240  
TTCCATTGT GGTCTGAAG GAAATTCTTA TAACTCAACA TTTGTCTGGT CTTN 294

SEQ ID NO:6874

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08104



# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCGACAC TCCAGGCAGA GCAGAGGGCA GGAGAGGCC AAAGAGCTAG GTCAAGCAGC 60  
TGGCTCCCCT GGAAGGGGAG CCGGGAGACA GGGAGGTCCT CACACTGCCC CCGTGGCCAC 120  
GCATGGCTGT CTGCACATC CATCAGGAGG AAGGGCAGGG GAGAAGTCAC ATGNGTACA 180  
GTGAACTNA TCAGTGTAC ACACGCCAG CAGGAGGGGA GAGCTCTGCT CCACACGCTG 240  
GCGGCCCTGG CTGCTCCANA GCAATCCGNT TGCTCCANCT TCAAGCCATT GGGGN 295

SEQ ID NO:6875

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08105

## SEQUENCE DESCRIPTION:

GATCCTGTAT TATCCATCTA CATCAGAACC AAATACTTC TCCAACACCC GGCAGCACTT 60  
GGCCCTGCAA GCTTAGGATG AGAACCATT AGTGTCCCAT TCTACTCTC TCATTCCCTC 120  
TTATCATCT GCAGGTGAAT CTTCAATAAA ATGCTTTTGT CATTCAA 168

SEQ ID NO:6876

SEQUENCE LENGTH:141

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08107

## SEQUENCE DESCRIPTION:

GATCCTTGAG ATGACTGTAG CCCTGGCTGA CAACTTNATT GCTGCCTGTN AAGGACCCTG 60  
AACCAGAGGA CTCAGCGAAA TTGTGCCAG ATTCTGACC TACAGCGCA GTGAGATAAT 120  
AAATGCTGTT GAGGTCACAA A 141

SEQ ID NO:6877

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08108

## SEQUENCE DESCRIPTION:

GATCTGCTCA CCCTCGGTNC ACANCAGTGT CAGCCATGCA AGCAGGACAG AATGGTGACT 60  
GGGTGCCCCT NGTGAGCTGT GTATTTCTA GGAGGTAGAA AACAATAAAA AATTGCATGC 120  
TAAA 124

SEQ ID NO:6878

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08109

## SEQUENCE DESCRIPTION:

GATCTCCTG CCTCAGCCTC CTGGGTGGCT GGGACTGCAG ATACATGCCA CCATGCCGGA 60  
CAAATTTNTT GTATTTNAG TAGAGATGGG GTTTTACCAT ATTGCTCGGA TTGGTCATGA 120

5 ACTCCTGGAT TCAAGCAATC TGCCACCTA GCCTCCCTAA GTGCCTGGCC AAATTTTGG 180  
TTTTAATAGT CGATTTGTGT ATATTTTGTG GTAGTATCTA CATATATTTA ATACATTTAT 240  
NTGTTGNTGN AAAAAGTANA ATTTGTAAAA NNTTTGNAAA 280

10 SEQ ID NO:6879  
SEQUENCE LENGTH:198  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08110  
SEQUENCE DESCRIPTION:  
15 GATCATTGTT GAACTTCAGC TCCAGTGTCT CTCCAGAATA AGACATTGGC ATTCAAATGT 60  
CTATATCTTG TTAATTACAA AATAAAAAAC AGATTAATTA GTGGCTTTTA AATTGTAGTT 120  
ATATCNGTGT ATATACACGC GGGGNACTGT ATAAAGACAT ACTAAAGGGC ACAGATTAAA 180  
ATAAGTATTA TTANTAAA 198

20 SEQ ID NO:6880  
SEQUENCE LENGTH:66  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08111  
25 SEQUENCE DESCRIPTION:  
GATCAAAGTT GTTAAAATTA TAAATNTATG ATGCAGNAAT AAAATTGATA TATTTTGATA 60  
TTCAAA 66

30 SEQ ID NO:6881  
SEQUENCE LENGTH:100  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08112  
35 SEQUENCE DESCRIPTION:  
GATCTCTTAC CTTTGGAAAA TAGGGGTTAG GCATGAAGGT GGTGTGATT AAGAAGATGG 60  
TTTTGTTATT AAATAGCATT AANCTGGAAT TGACAAGAAA 100

40 SEQ ID NO:6882  
SEQUENCE LENGTH:30  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08113  
45 SEQUENCE DESCRIPTION:  
GATCAAAGAA ATAATTCTTT TGCCACTAAA 30

50 SEQ ID NO:6883  
SEQUENCE LENGTH:172  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS08114

SEQUENCE DESCRIPTION:

GATCACTACA ACAATTTGNC TGCCTCCAAG GTCCTCTGAG GCAGAAGGCT CTGGGGNTTC 60  
 TGCTGTCCTT TGGNGGGTGT CTTCTGGGTA GAGGGATGGG AAGGAAGGGA CCCTCACCCC 120  
 NGGCNCTTCT TCTGACCCTG CCACTAAAAA ATTTATGGNC CAAGGGCNCA AA 172

SEQ ID NO:6884

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08115

SEQUENCE DESCRIPTION:

GATCAGCAAT NAGGGTGAGG AAAAAATCTT CTTAATCAAC AAGCTTCACT CCATCTACGA 60  
 GAGGAAGGAG AGGGAGGAGA GGAGCAGGGT TGGGACAACC GAGGAGGCTG CGGCACCCCC 120  
 TGCCCTGCTC ACAGATGAAC AGGATGCCTA GGGGGACGGC GATGGGCCTC ACGGGCCCGC 180  
 CCAGCACCTT GAGACCACAC TGTGCTCCTC CAGTGACCCT GCTGGGACAC CAGGACAAGG 240  
 AAGACAGTTT CGCCTCTNGA AAGCCGCAGC TGCCTTAGG CTGGAGCTGG N 291

SEQ ID NO:6885

SEQUENCE LENGTH:30

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08116

SEQUENCE DESCRIPTION:

GATCTGTAAA TAAAACTTAC ATTTTTCAAA 30

SEQ ID NO:6886

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08117

SEQUENCE DESCRIPTION:

GATCTGCCTG CCTCGGNCTC CCAAGTGCTG GGATTACAGG CGNGAGCAGC TGCACCCAGC 60  
 CTAGAATCTT GTATAATATG TAATTGTAGG GAAACTGCTC TCATAGGAAA GTTTTCTGCT 120  
 TTTTAAATAC AAAAATACAN AAAAATACAT AAANTCTGAT GATGAATATA AAAAAGTANC 180  
 CAACCTCATT GGNACAAGTA TTAACATTTT GGAATATGTT TTATTAGTTT TGTGATGTAC 240  
 TGTTTTACAA TTTTNACCAT TTTTTCAGT AATTACTGTA AANNGNNNNN N 291

SEQ ID NO:6887

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08118

SEQUENCE DESCRIPTION:

GATCCCAAGC TCAGTCCCCA CAAAGTTCAG GGCCGGTCTG AGGCAGGGGC AGGTCCGGGT 60

# EP 0 679 716 A1

CCAAAGCAAG GACACCACAG CTCTTCCGAC TCCAGCAGCA GCTCCAGCGA TTCGGACACG 120  
 GATGTGAAGT CCCACGCTGC TGGCTCCAAG CAGCACGAGA GCATCCCGGG CAAGGCCAAG 180  
 AAGCCCAAAG TGAAGAAGGA GAAGGGCAAG ANGGNGAAGG GCAAGANGAN GGAGGCTCCC 240  
 CACTGANGGG CCCTGGACAG GGCTCATTAA ACCTTCCTCT CTGCCAAA 288

SEQ ID NO:6888

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08119

SEQUENCE DESCRIPTION:

GATCCGCATT GAAGACCCAC CCCGCAGAAA GCACATGGAA TTCCTGGGTG GTGCAGTTCT 60  
 AGCGNTTATC ATGAAAGNCA AAGACAACCT TGGATGACC CGACAAGAGT ACCAAGAAAA 120  
 GGGTGTCCGT GTGCTAGAGA AACTTGGTGT GACTGTTCGA TAAACTCCAA AGCTTGTTC 180  
 CATCATACCC GTAATGCTTT CTTTTTCCT TTATTGCCAA TCTTTGAACT CATTCAACTC 240  
 CAGGACATGG AAGAGGCCTC TNTCTGCCCT TTGACTGGAA NGGTCAANGT TTTATTCTGG 300  
 TTGTCTGN 308

SEQ ID NO:6889

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08120

SEQUENCE DESCRIPTION:

GATCATGTCT TTTGCAGGAA CATGAATGGA GCTGGAGGCT ATTATCCTTA GCAAATAAT 60  
 GCAGGAACAG AAAACCAAAT ACTGCACGTN CTCACCTATA AGAGGGAGCT AAATNATGAG 120  
 AACTGATGAA CACAAAGAAG GAAACAACAC ACAATGGGGT CACTTGACA GTGGAAGGTG 180  
 GGAGGAGGGN GAGGAGCAGA AAACATAACT ATTGGATACT GGGCTTAGTA TCTGGGTGAT 240  
 GAAATAATCT GTACAACAAA CCCCATGNC ACAAGTTCAC CAATGTAACA NACCTTCACA 300  
 TGTACCCN 308

SEQ ID NO:6890

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08121

SEQUENCE DESCRIPTION:

GATCAATTCC CTTGAATAGG GAAGTAACAT TTGCCTTAAA TTTTTCGAC CTCGTCTTTC 60  
 TCCATATTGT CCTGCTCCCC TGTTTGACGA CAGTGCATTT GCCTTGTNAC CTGTGAGCTG 120  
 GAGAGAACCC AGATGTTGTT TATTGAATCT ACAACTCTGA AAGAGAAATC AATGAAGCAA 180  
 GTACAATGTT AACCCTAAAT TAATAAAGA GTTAACATCC CAAA 224

SEQ ID NO:6891

SEQUENCE LENGTH:28

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear  
CLONE:HUMGS08122  
SEQUENCE DESCRIPTION:  
GATCAAATAA AGTTATAAAA TTGCCAAA

28

SEQ ID NO:6892  
SEQUENCE LENGTH:140  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08123

SEQUENCE DESCRIPTION:  
GATCAGGCCT GGCCACTCCT CTTTGGAGGG CGGTTGAGGC CCACCTGCCT TGGGCTTCCC 60  
AATNCTGATT CCNNTACTAC ACCCTTCCCA GTTCTATTCC CCTCACCACA CTTGCTCCAA 120  
TAAAACTATT TATATACAAA 140

SEQ ID NO:6893  
SEQUENCE LENGTH:163  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08124

SEQUENCE DESCRIPTION:  
GATCGTCATC CCTTCCTGGA GTTCCTATCT TCCAAGATGT GACTGTCTGG AGTTCCTTGA 60  
CTAGGAAGAT GGATGAAAAC AGCAAGCCTG TGGATNGAGA CTACAGGGGA TATGGGAGGC 120  
AGGGAAGAGG GGTGTTTCT TTAATAAAT CATCATTGTT AAA 163

SEQ ID NO:6894  
SEQUENCE LENGTH:253  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08125

SEQUENCE DESCRIPTION:  
GATCACCTGA GGTGAGGAGT TTGAGACCAG CCTGGCCAAC ATGGTGAAAC GCCATCTCTA 60  
CTAAAATTGA AAAATTAGCT GGGCATGGTG GCAGGTGCCT GTAATCCCAG CTATTGGGGA 120  
GGCTGAAGCA GGAGAATCGC TTGAAACAGG AGGCAGAGAT TGCAGTGAGC CGAGNGGGGN 180  
GCCACTGCAC TCCAGCCTGG GCAACAGGAA CAAAACCTCTA TCTCAAAAAA TAAACAAGA 240  
TTTTTCTGCG AAA 253

SEQ ID NO:6895  
SEQUENCE LENGTH:99  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08126

SEQUENCE DESCRIPTION:  
GATCACTTGC AGCCCAGNAA GTTTGAGACC ACCCTGACCA ACACAGTGAA ACCCNCTCTC 60  
TAAAAAAGTT TGTTTTTAAA GTCTCCTGA AACATCAAA 99

SEQ ID NO:6896

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08127

SEQUENCE DESCRIPTION:

GATCAAGCTA TGCCTGATNC TGCCTTAAGC CTTATNAGGT CGCCACGGAA CCGCAGAAAC 60  
TCCTGGTGGG CAGAGCTGTG TGTGCCATCT TCATCATTGC ATTACCACCA CCAAGCACAG 120  
TGCCTGGCAC AAAAGAGTTG CTCAATAAAT AAATCAGGAT GANTGGNTAA ATACATGGNT 180  
AGGCACTTTG AGCTACAGAT GCGTTTAAAT ACTTTGTGTT TTTCTTAGTC AAACATGTGC 240  
ANTTANGCAT GTGATAAATG CTATGATGAC CACAANANTG CACAAA 286

SEQ ID NO:6897

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08128

SEQUENCE DESCRIPTION:

GATCATGGTG AAATATTTTN GATATATAAA TTCCTTAAGC TATTGTAACC ATGTTTTATT 60  
GCAAAGATGT AAAATATGCC AGATGTGTGT NAGTTGGAAA TCAAAAAAAG NAAAATAAAN 120  
TATGCAAAGA NTTCAA 137

SEQ ID NO:6898

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08129

SEQUENCE DESCRIPTION:

GATCCGCAAC AACTCAGCCA TCCACATCCG AGTCTTCAGG GTCACACCCA AGTAATTGAA 60  
AAGACACTCC TCCACTTATC CGNTCCGTGA TATGGCTCTT CGCATGCTGA GTACTGGACC 120  
TCGGACCAGA GCCATGTAAG AAAAGGCCTG TTCCCTGGAA GCCCAAAGNA CTCTGAATTG 180  
AGGGTGGGGG TAATTGTNTG TTGGTNGGCC CAGTTAGTGG GCTTTNNTAA GTGTGTGTAT 240  
GCGGTCTGTA NCTATTGCCA TATAAATAAA NAATCCTGTT GNACTNGTAN 290

SEQ ID NO:6899

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08130

SEQUENCE DESCRIPTION:

GATCATAAAA CGTTGTAAGT TTTCTAAAAC ACATAAGCTC TCAATAAACG TTAGCTTATC 60  
ATTGTCACAA A 71

SEQ ID NO:6900

# EP 0 679 716 A1

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08131

SEQUENCE DESCRIPTION:

GATCAAACAC TGTCAGAATT GCTGAAATCA ATACACAAAG AGATAAAGTT TAGCTTCTTT 60  
TTACTATTCA ATATTGAACA TAATATTGTT AAATATNGNG ATGAAATGCT GTTGGATNTG 120  
CTNCATTAAA TCTTAATGTA ATATTGTAAG NCTTTTGAGA ATATACTTGA TTAAAATGTG 180  
AAAGNNGGGN TTGTTANCTT ATTGCTATNC N 211

SEQ ID NO:6901

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08132

SEQUENCE DESCRIPTION:

GATCATCATC TNCTTGCGGA CTTCTCTGCC TGGTCTTGTG TGTTCTGTGA TTCAAACAAT 60  
AAAANGCTGG TNGAACTTAA A 81

SEQ ID NO:6902

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08133

SEQUENCE DESCRIPTION:

GATCAGACAC TGCCTTTTGT GTGTTTGCTG CCTNTGGATN CTTTTTAAA AAGACTGTGA 60  
CATATTAATAA NAGTGTACAT ATATAAATAT NACCTCTTTT GCTGTACAGT TGTGATAGAG 120  
ACTGAAGNTT TTATTTTNG TGTGCTTTT ATAAGNAAA ANTTAATACA CTAAN 175

SEQ ID NO:6903

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08134

SEQUENCE DESCRIPTION:

GATCATCTAA TTCTCTGTGG AATAAATACA CACATATATA TTACAAGGGA TAATTTAGAC 60  
CCCATACAAG TTTATAAAGA GTCATTGTGA AA 92

SEQ ID NO:6904

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08135

SEQUENCE DESCRIPTION:

GATCTGGAAT AACTGGAAT ATGTGATACT TAGAATACTT TGGCTGCTAA GGAAACTTCC 60

TCTCCATTGC AGAATAGCTG AGCCAAGTNA GTGAGTTTNC AGAAAGCAGG TGGTGAGCTC 120  
 NTGCCTGCTG GAGGTTGCCA TGGAGGGCCA TTCCTGCCCC GCAACAGCAC CGTCCTGCAG 180  
 5 GGAGCCACTT GGCAGAAGGG TGCAGGGCTG CTGGTGTGAG AGCAAGAGGG CTACAGGGAA 240  
 AGGGCCCTTT CTCAGGGGAT GTNGNTTTT TAAAAGGTTT GGGNACACTT GGCGGGTTTG 300  
 CTAAAATTGA GN 312

SEQ ID NO:6905

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08136

SEQUENCE DESCRIPTION:

GATCTCTCTT GCAGCTTGAG AATGTCCCAG TTAAGCCACT TAAAAANTCC TCTNTCCTGC 60  
 AGCCCAACAC TTTNCTAAGA GGTACAGAAA NGANAGGAAA TAAACACAC ATCATTATGG 120  
 AAA 123

SEQ ID NO:6906

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08137

SEQUENCE DESCRIPTION:

GATCTCAACA CAGACCCTNA CCAGCTGATN AATNCAGTNA ACACACTGGA CAGGGATGTC 60  
 CTCAACCAGC TACACGTACA GTCATGGAG CTGAGGAGCT GCAAGGNTTA CAAGCAGTGT 120  
 AACCCCGGA CTCGAAACAT GGACCTGGGG ACTTAAAGAT GGAGGAAGCT ATGAGCAATA 180  
 30 CAGGCAGTTT CAGCGTCGAA AGTGGCCAGA AN 212

SEQ ID NO:6907

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08138

SEQUENCE DESCRIPTION:

GATCAAGCCA AAAGAAATAT TTTNAAATA AGCCCTTTTC AAAAGTTTTT GAATTTATAG 60  
 40 AAAGCACCAA TGAATAACAT ATTTCTGTTT CGTTAATGTC AGCTGCCTGA ACATTCAGCA 120  
 GTTTATAAAT TGCTTAATTT GTGTNATCTA TTATCCAGTA AACCCATAGT TCCATGATAT 180  
 GTCACAGGNA TTGTNAGGTC CTATTTTAAA GGTACAGTCT TGTGGNATGT CATCN 235

SEQ ID NO:6908

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08139

SEQUENCE DESCRIPTION:

GATCCTTTGA-GCCCAGAAGT TGGAGACCAG CCTGGACAAC ATGACAAAAC CCCATCTCTA 60



EP 0 679 716 A1

CAGAAAATTT AAAAATTGGC CAGGCGTGGT CGCGCACGCT GTAGTCCCAG CTATTCAAAA 120  
GGCTGAGGTG GGAGGATTAT GTCCCTGGAG CCCAGGAAGT GGNGGTTGCA GNGATTGCAT 180  
CACTGCATTT NAGCCTGGGT GACAGNGTAC GCCNCTGTAT CAAA 224

SEQ ID NO:6909

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08140

SEQUENCE DESCRIPTION:

GATCCTGCTG GCCAGAAGCA AGCGGGNCG GCAATAAATC CAAGAAATTG TCCCAACAAC 60  
CACCAATTCT TACGGAGGAN TATTATTTAG CCAGCAGGAG TCGNGTTTGG TTTACTGCTT 120  
TTACTGTTTT GNGTTCATGN CTNTTATTT TAATGGCGTT AAAAGCACAG GCAAATGTCT 180  
TTGGTAATGC AGCTTAGTAT GANTTCTNTT ANAGN 215

SEQ ID NO:6910

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08141

SEQUENCE DESCRIPTION:

GATCACAGAC TCTGAAGNCA GACTGGCAAG ATTCAAATCC CGACTGCCAT TTTTAACTGA 60  
AAGACCTTAG GTAAGTTACC TAACCTCTCT GTACCTGTGT AAAATGGNGA TAACAGTAGT 120  
ATCCACTTCA CAGAGTTATG AGGNTGAAAT ACATTCATAT TTATAAAACG TTTGGACCCA 180  
GTACTTGGCA CATAGTAAGG CCATGTAAAGT GTTTGTAAAA TAAAACTGNA AATAAAGCCA 240  
TNTCCNAATN AAA 253

SEQ ID NO:6911

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08142

SEQUENCE DESCRIPTION:

GATCACACTG CTGCAAGACC TGACCAGTTG AGCTTCCGGC GTGGGGAAGT GCTGCGTGTC 60  
ATNACCACAN TGGATGAGGA CTGGCTCCGC TGTGGGCGGG ATGGCATGGA GGGTCTNGTG 120  
CCTGTGGGGT ATACCNACCT TGTTCTGTAG CCCTGGNGNC CTTTCTGCG TATGTGTCTC 180  
CTTCCTGTCA CCTGGGCATG GAATGGCCAG TGAACACCAT CCCAGAAGCA TTTTCCCTCT 240  
GCAAAATGAC GTTTCCTCCC ACGTCTGTTT CTGCTAATAT TTAAAATAAA CTTTCCTTCT 300  
TCCCTCCTAT ACCANCTGTA AGGGAAAATN TGCTCTTNTT CCAAATATAT AAAAAGGTN 359

SEQ ID NO:6912

SEQUENCE LENGTH:49

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08143

## SEQUENCE DESCRIPTION:

GATCTTTTAC ATTGCAAACA AAATGCTGTA TTGCTTAAAA GGGTTGAAA

49

SEQ ID NO:6913

SEQUENCE LENGTH:30

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08144

SEQUENCE DESCRIPTION:

GATCAGTTAA TAAACATGAG TAGCTTGAAA

30

SEQ ID NO:6914

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08145

SEQUENCE DESCRIPTION:

GATCTGAACT GTACAAAGTT CTCATAGCAC CNCTGGGAAG AGAAGGACGT AACAGAACC 60  
TGACACCAGC TCCTTTTCCT TNTATACATT ATTAAATACC TATTAAATAC AATTATTTTT 120  
GGAATAAA 128

SEQ ID NO:6915

SEQUENCE LENGTH:425

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08146

SEQUENCE DESCRIPTION:

GATCTACTTG TAACTTGTTG GCCTTCTTCC CACATCTGCC TCANACTGGG GGGGGCTCAG 60  
CTCCTCGGGT GATATCTAGC CTGCTTGTTA GCTCTAGCAG GGATAAGGAG AGCTGAGATT 120  
GGAGGGAATT GTGTTGCTCC TGGAGGGAGC CCAGGCATCA TTAAACAAGC CAGTAGGTCA 180  
CCTGGCTTCC GNGGGCCAAT TCATCTTTCA GACAATCTTT AGCAGAAATG GACTCAGGGA 240  
AGAGACTCAC ATGCTTTGGT TAGTATCTGT GTTCCGGTG GGTGTAATAG GGGNTTAGCC 300  
CCNGAAGGGN CTGAGCTAAA CAGTGTATT ATGGGAAAGG AATGGCATTN CTNGTTTCAA 360  
CNAGCGCTAN ATGCAACCAT TNCNCTNTTG TTATAGTATC TAAGGGTNNG NNAGTTAAAC 420  
GGTTN 425

SEQ ID NO:6916

SEQUENCE LENGTH:81

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08147

SEQUENCE DESCRIPTION:

GATCCACCAC CCAGCTTCAC CCCTCACCCC CAGCGGCTCA CCATGGGGAT GGCAGCAATA 60  
AAATACTTCT AATGGAACAA A 81

SEQ ID NO:6917

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08148

SEQUENCE DESCRIPTION:

GATCAACAAG CTTTNCACG AATTTAAGAG TTTTATCAAG ATATATCGAA TACTTCTACC 60  
 CATCTGTTCA TAGTTTATGG ACTGATGTTT CAAGNTTGTA TCATTCCTTT GCATATAATT 120  
 AAACCTGGAA CAACATGCAC TAGNTTTATG TCAGNAATAT CTGTTGGNTT TCCAAAGGNT 180  
 GTTAACAGAT GANGTTTATG TGCAAAAAAG GGTAAGATAT AAATNCAAGG AAGNAAAANN 240  
 GTTGNTAGCT AAAN 254

SEQ ID NO:6918

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08149

SEQUENCE DESCRIPTION:

GATCAGAGGA ACCTTAGAGG CCTGAAATTG TTGCTTCCAG TTAGCTGCC CCTCAAATTC 60  
 AAGTGAATAT TTTCCCTTCT CCCTTTACCC TTCTCCAGAA ATAAAGCAGG TGACAGGGTT 120  
 TTNAGAATCT TAAA 134

SEQ ID NO:6919

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08150

SEQUENCE DESCRIPTION:

GATCAAGAGT AATTACCAAC TTAATGTTTT TGCATTGGAC TTTGAGTTAA GNTTATTTTT 60  
 NAAATCCTGA GGACTAGCAT TAATTGACAG CTGACCCAGG TGCTACACAG AAGTGGCTTC 120  
 AGTGAATCTA GGAAGACAGC AGCAGACAGG ATTCCAGGAA CCAGTGTTTG NTGNGGCTAG 180  
 GNCTGAGGAG CAAGCGAGCA AGCAGAGNAA GAAAAGTTAA ATACCAGNTA AGCTTTTGAT 240  
 TTTTGTATTG TTTGCATCCC CTTGCCCTCA ATAAACN 277

SEQ ID NO:6920

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08151

SEQUENCE DESCRIPTION:

GATCTACCAC CAGAGAGTTC AACTGGNGA AAGNCCTCAT GAGTGCAATN AATGTGAAAA 60  
 ATCCTTTAGC CGAAGCTCCA GCCTCATTCA CCACCGGAGA CTTCACTG GAGAAAGACC 120  
 CTATGCGTGC AGTAAATGTG GGCAGTCATT TAAGCAAAGC TCCAGCTTCA GTTCACATCG 180  
 GAAAGTCCAC ACNGGGGANN GGCCTTATGT GTGTGGGNC TNTGGGNANT CCTTTAGCCA 240  
 TAGCTCCANC CTTAN 255

# EP 0 679 716 A1

SEQ ID NO:6921

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS08153

SEQUENCE DESCRIPTION:

10 GATCTGGCTT NTCCNGGAGG CTNCCATGGT TGGAAGATGG TATCAGAGGG CCTGCCTGGG 60  
CAGTCTGTCT CCGGGCCAGG GTCAGGGACC CTCTGCCTCT GGCAGCCTTA ACCTGTCCTC 120  
TGCTAGGACC AGGGTGATTT CAAGCCAGGG AAGCAACTGG GACCCTGAAA ACTGTCCCTC 180  
CCCAGCCCGG TCCNCGTGTA TGTGCCNTGG TCCCCTTGCT GCCATGTGGA TGCTGTTGTN 240  
ATTGCTGTTT GTATATTATC AAAATGTTTT TAN 273

15 SEQ ID NO:6922

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20 CLONE:HUMGS08154

SEQUENCE DESCRIPTION:

GATCTTCTTT ATAATATTT ATTGTTGAA TCACTTTTAG GATGTAACCT TATAAATAAA 60  
CATGAGCGCT GATGATTTGC AAA 83

25 SEQ ID NO:6923

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS08155

SEQUENCE DESCRIPTION:

GATCTCATC TCCATCTCA TCCTCTTCCT TCACAGCATT TACTTGGAGC TCTTTGTGAC 60  
ACACCATGTC AGTCATGATG AATCGGCCAA CAGCCAGCCC TTGCCAGCTG ACGTCACAGT 120  
CTAAGATGGG AAAGTGTGGT ACAGATAGAC ATGAAGAGAG CTTAGCAGTG ATTGAGGTGG 180  
35 TGAATAAATA TACAGTCATT GAATAAA 207

SEQ ID NO:6924

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS08156

SEQUENCE DESCRIPTION:

GATCACTGTG GGCTGGAGAG GAGAAGGAAA GGGTCTGCGC CANNCTGTCC GTCTTCACCC 60  
45 ATANCAAAGC ATACTAGAGC AAAAAACAG TTGTAATATA AAATGCACTG CCCTACTGTT 120  
GGTATGACTA CCGTTACCTA CTNTTGTGTCAT TGTATTACA GCTATGGCCA CTATTATTAA 180  
AGAGCTGTGT AACATCAAA 199

SEQ ID NO:6925

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55

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08157

SEQUENCE DESCRIPTION:

GATCATGCAG CAGAAGCAGA AAAAGGCAAA CNAGAAGAAG GAGGAACCCA AGTAGCTTTG 60  
 TGGCTTCGTG TCCAACCCTC TTNCCCTTCG CCTGTNTGCC TGGAGCCAGT CCCACCACGC 120  
 TCGCNITTCC TCCTGTAGTG CTCACAGGTC CCAGCACCGA TGGCATTCCC TTTNCCCTGA 180  
 GTCTGCAGCG GGTCCCTTTT GTNCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC 240  
 ACTCCCGGGG GTGAGGGGGT TACCCNTTCC CAGTGTTTTT AATTCCTGTG GGGCTCACCC 300  
 CAAAGTATTA AAAGTAGCTT TGTAATTCCA AAAAAAANGG NNNNNAGGGN GGGGGGGN 358

SEQ ID NO:6926

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08158

SEQUENCE DESCRIPTION:

GATCTGTACA TTTTACTATC TGTAATAAT TCTTCAAAGA ATAAATATAA AAAAAAGCA 60  
 AA 62

SEQ ID NO:6927

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08159

SEQUENCE DESCRIPTION:

GATCAGATAC AGCATTAAAC GTTTCTCAGT CTCCTNTCC TCATCTGTAA A 51

SEQ ID NO:6928

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08160

SEQUENCE DESCRIPTION:

GATCTTGCTA AAGTTAAAAT AAGGAACATT TCACCTTTTA AATATTTAAT TCTNATGTGG 60  
 ACTTATTTCC AGAAAACTTT GGTGATAATT CTTGAGACAA AAGGTGGTTA AGTAGCATTA 120  
 TTATGTAATG CTTATATACC ATAGAGTTTT TAATAGANGA GAAATCCATT TCCTCCGAGG 180  
 GTCACATTA ACAATGTACT TCCTTAAATT TNGTTAATG ATTGTGATGG GTGCTGCATT 240  
 TGCACATTGC ATTANGGAN 259

SEQ ID NO:6929

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS08161

SEQUENCE DESCRIPTION:

5 GATCGGATGC TGAATAAAAC TCACCGTGAA GCAAGTCCCA CTGAACGAAA AGTTGGTCGT 60  
AGCATTNTNC AGCAGCTGCT TCCGGCTCCC TGAGACCCAG CCATGGAAGG CATAGAAAGG 120  
CATGTGACAA GAAACTCATG GCTTTTAATC CTGGCAGGNC AAGGAAAACC CCGTCAAAGN 180  
TTTGACATAAN TTTGCTGCT CTCCTGCTGG GGGGGGNNNG NNNNNN 226

SEQ ID NO:6930

10 SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08162

15 SEQUENCE DESCRIPTION:

GATCGTTCTT GATTTTGTTC TCATTAGTGT CATTTCTTTG TCATTGAGGA CTTTCCCT 60  
TACAACAGTA ACACCATTTT TTGAAGAGCA AACTTATAA TACCTCCTGG GATTGTNAGC 120  
TAGTCATTCA GCCTGTGTAA CCATGTGGAA ATAAAAATTG ACGACCAATG TATTATATGG 180  
20 ACAACTTTTG CTTTGAGTAA TAAACTTGAT TGTAGGAAA 219

SEQ ID NO:6931

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS08163

SEQUENCE DESCRIPTION:

GATCCCACCC ATTCTTTCAC TTTAAGAAAA AACAAATAAT TGTTCAGAG GTGTCTGTAT 60  
30 TTTGCAGCTG CCCTTTTGTA AGANGCACTT TTCCCAAATA AAACAATTAA A 111

SEQ ID NO:6932

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS08164

SEQUENCE DESCRIPTION:

GATCATTTGA AATNTCTGGG AGTCTGAGGN GTACTGACAT AATNACCTGC TGGAGTCTGT 60  
40 AAATACACAT TTAAGACAGT GAGGATGTGA ATAAATATAT TAATGCAA 109

SEQ ID NO:6933

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS08165

SEQUENCE DESCRIPTION:

GATCAAATAG AGCCCTGTCC AGGTAGAAAA GAAATGGTAT GTAGAGCTTA GATGTCCCTA 60  
50 TTGTGACAGA GCCATGGTGT GTTTGTNNTA ATAAANCCAA AGAAACATAA A 111

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EP 0 679 716 A1

SEQ ID NO:6934  
SEQUENCE LENGTH:243  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS08166

SEQUENCE DESCRIPTION:

GATCCCAGCT GTTCTAGGCA GGGCCAGGCA GAGTGGGGCG CAGGCCCTNG AAGGGCGAGA 60  
CCCAGTGGCT GGGCTGCCCA GGGCTGAGGG GCCGCCTCTT GAGGGTACAC GCCTCTGGTC 120  
ACATGGCCAT GGAGCCTTGG GTACCCCTGA GTTAAGGGAG GACATTGGC CAGCTGGTGG 180  
CTGGGAGGGG AGCCTGGCTG CCCTGCTGCT TCTCCTGCCT AATAAACAGG CTTCTCCTGC 240  
AAA 243

SEQ ID NO:6935  
SEQUENCE LENGTH:124  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS08167

SEQUENCE DESCRIPTION:

GATCTATTTT NATAGTTCT TTTTCAGAAG TAAAATTTTG TACATATATA CATGTACATA 60  
TCTNTTTAGT TTGGGTTTCT TTCTATAACA TTTTGTAAGA AAATAAAAGT TTGAGCACCT 120  
GAAA 124

SEQ ID NO:6936  
SEQUENCE LENGTH:169  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS08168

SEQUENCE DESCRIPTION:

GATCAGTTGT ATGTAAATGT ACATTTTTGT NACTTTGGCT GTGCCCGTTA GAATTTATCT 60  
TCCATAAAGT ATTTCTCCCA TTGAGTCTAA TGATGTATAC TTTGCCTAGG TCTTTCCAAA 120  
ATTAAATTTA TGTAATGTC TATTTTATAT AAAATATGNT TAAAATAAA 169

SEQ ID NO:6937  
SEQUENCE LENGTH:314  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS08169

SEQUENCE DESCRIPTION:

GATCACATTT AGGAGCAAGC AGGTGAGGGC AGAGGTGCTG GAGTGAACGT CGGCTCTTTG 60  
GCTGGTAGCC TTACCCACTG AGGGAGAGGA GCTGAAACAT GAAATGGGGA TGCGTGANCA 120  
ATGTCTCCCT TTTGCAGAGC TGTATTGACT TGTCAAGAA TAACTGATAT GCCTTCACTC 180  
AGAAGAAAAG AAATGAATGT GAAAGAAAGC CAAGCATCNN TTTGCACTTA AATCANTTAC 240  
CACGGAAGNT ATATTTAGCT TCAACTTAG TTTAAATTA TGTGAATTAA ATATTTTGAT 300  
TTCCCTGGGN NAAA 314

# EP 0 679 716 A1

SEQ ID NO:6938  
 SEQUENCE LENGTH:46  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08170  
 SEQUENCE DESCRIPTION:  
 GATCAAGTGA CTGTTTAATA AATNAGTTGC TTGGGTAGAA TGGAAA 46

SEQ ID NO:6939  
 SEQUENCE LENGTH:21  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08172  
 SEQUENCE DESCRIPTION:  
 GATCTTGCTG AAAACCAGAA A 21

SEQ ID NO:6940  
 SEQUENCE LENGTH:85  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08173  
 SEQUENCE DESCRIPTION:  
 GATCAACAAT CATCACCTGC CTTTGTAGA AAAGAAAAAC AAAAAAGTA AATAAAATT 60  
 TTAAACAGTA AAATAAAAGT TAAAA 85

SEQ ID NO:6941  
 SEQUENCE LENGTH:274  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08174  
 SEQUENCE DESCRIPTION:  
 GATCACTACT GCAGCAGAAT GGTCTATGTN ATTTTCCTTC TTTGGTTTTT NCCTGACTTA 60  
 CATTGTAAT TTTAAGAAAA TTTCTTTACG GGTGGAAGCC AATTACATG GATTAACCCT 120  
 CTATGACACT GCACCTTGCC CTATTAACAA TGAACGAACA CGGCTACTTT CCAGAGATAT 180  
 TTNATGAAAG GATAAAATAT TTCTGTAATG ATTATGATTC TCAGGGATTG GGGNAAGGTT 240  
 CACAGNAGTT GCTTATTCTN CTCTGTAATT TTAN 274

SEQ ID NO:6942  
 SEQUENCE LENGTH:246  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08175  
 SEQUENCE DESCRIPTION:  
 GATCTAAGTT GGGCAAAAGA GAGTCATCCT GTTACCTTAA AAAGGAGTCT AGGGTGAGCC 60  
 CCAGTCTGCT GGTGGCCATC TTCACCACCT TTGGGGAGAG ATGGCCTCNG CAGACACACA 120



EP 0 679 716 A1

AAGCAAAGAG GTGGAGAGAA ACTGTGTCTT TGTGTCATTG TTTGAGTCCC TGGACCCAGC 180  
CCAGTCCCCC CGACTACGCT GANCTTTTCA ATTGTGGGGG GCAATAAATT CCATTTAGTT 240  
ANGAAA 246

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SEQ ID NO:6943  
SEQUENCE LENGTH:215  
SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS08176

SEQUENCE DESCRIPTION:

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GATCCACATN ATACCGGTGC TGAAGACCTG CAAGTNATTT TGGAAAAGGG CTGGTGCGGA 60  
TGGAAAGGGCC CAGATTTTGT GAACAAGGAT GCATACTATA ACTTATGTCT TCCTCAGCGA 120  
CCAAATATGA TTAAAAATAT CTGGAGTCA AAGACTGCAG TAGAGTGGTA TTATAAATTT 180  
NTGAATAAAG AATCAGTTTA NTTTTTCA TAAA 215

20

SEQ ID NO:6944  
SEQUENCE LENGTH:171  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08177

SEQUENCE DESCRIPTION:

25

GATCTGGACA CGAGCAGTCC CTGAGGGGCG GGGTCCCTGG CGTGAGGCCC CCGTNACAGC 60  
CCACCCTGGG GTGGGTATTG TGGGCACTGC TGCTCTGCTA GGGAGAAGCC TGTGTGGGGC 120  
ACACCTCTTC AAGGGAGCGT GAACTTTATA AATAAATCAG TTCTGTTTAA A 171

30

SEQ ID NO:6945  
SEQUENCE LENGTH:161  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08178

SEQUENCE DESCRIPTION:

35

GATCGGCCCC GGAAAAAGTC TGCCCCAGAA ACTCTCACAC TTCCAGACCC TGAGAAAAAA 60  
GCCACCCTGA ATTTACCCGG CATGCACTCT TCAGATAAGC CATGTCGGCC CAAATCTGAG 120  
TAACTTTATA TAANTATCTC ATGGGGTTTT ATATTTTCAA A 161

40

SEQ ID NO:6946  
SEQUENCE LENGTH:251  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08179

SEQUENCE DESCRIPTION:

45

GATCCTTGGG GAAGGTTTCA GTTGCACTGT ATGCTGTTGG ATTTGCCAAG TCTTTGTATA 60  
ACATAATCAT GTTTCCAAAG CACTTCTGGT GACACTGTGC ATCCAGTGTT AGTTTGCAGG 120  
TAATTTGCTT TCTGAGATAG AATATCTGGC AGAAGTGTGA AACTGTATTG CATGCTGCGG 180  
CCTGTGCAAG GAACACTTCC ACATGTGAGT TTTACACAAC AACAAATGAA AATAAATTTT 240

55

AATTTTATAA A

251

SEQ ID NO:6947

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08180

SEQUENCE DESCRIPTION:

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GATCCCTCTT GGTGTGAGTT TTCTGACCCA ACCAGCCTCT GGTTAGCATC ATTTGTACAT 60  
 TTAAACCTGT AAATAGTTGT TACAAAGCAA AGAGATTATT TATTTCATC CAAAGCTCTT 120  
 TTGAACACCC CCCNCACTTT ANTCCNTNGT TCAGGCCGAT GNGCTTGCTT TCCTTCANCC 180  
 TGTTTGTITT CTTATTTAGG NCTATTTATT ANTGGTTGGN CCAATGTACT CACAGCTGTT 240  
 GCGTCGAGCA GTCCTTNGTG AAANTNCTGT ATAANTN 277

SEQ ID NO:6948

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08181

SEQUENCE DESCRIPTION:

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GATCCAGCTT CAGCTGCACA CCTNTGTCCC CTTGGATGGG GNACTAAGGG NAAACGTCTG 60  
 TTGTATCACT GAAGTTTTTT GTTTTGTTC NATACGTGTC TGCATAAAAA TGCCAAAGTT 120  
 TTTTTTCAAA 130

SEQ ID NO:6949

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08182

SEQUENCE DESCRIPTION:

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GATCACCAAT NNTNNCTTTG AGCCAGCCAA CCAGATGGNG AAATATGACC CTCGCCATGG 60  
 TAAATACATG GCTTGCTGCC TGTAATACCG TGGTGACGTG N 101

SEQ ID NO:6950

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08184

SEQUENCE DESCRIPTION:

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GATCATGAAG ACCTGCTTTA GCCCCAACAG AGTGATTGGA CTCTCAAGTG ACTTGCAGCA 60  
 AGTAGGAGGG GCATCAGCTC GCATCCAGGA TGCCCTGAGT ACAGTGTTGC AATATGCAGA 120  
 GGATGTACTG TCTGGAAAGG TGTCAGCTGA CAATACTGTG GGCCGCTTCC TGATGAGCCT 180  
 GGTTAACCAA GTACCGAAAA TAGTTCCCGA TGACTTTNAG ACCATGCTCA ACAGCAACAT 240  
 CAATGACCTT TTGATGGTGA CCTACCTGGC CAACCTCACA CAGTCACAGA TTGCACTCAA 300  
 TGAN 304

55

SEQ ID NO:6951

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08185

SEQUENCE DESCRIPTION:

GATCCTATCT GTNCTGGCAG GACTGGCAGN CATGGTGGGC TACGCCTTGC TCAGNGGCAT 60  
 TGTCTCCATN CAGNGGGCAA CGCTGCTCGG GCGCCAGGCA CCCGGACCCT GGGCATGGCT 120  
 GAGGAGGATG AAGAGGAATN ATTTGTCCTC ACGCTCCCAA GACTGGTTTT TNTACTCTNA 180  
 TGCATTCCAG NGGCCCCCGT GCCTCCTCGT TGTGGGTACA GCGGACACG GGGTGCTGCC 240  
 ACCCAGAATA AAGCCACTCA CACTGAAA 268

SEQ ID NO:6952

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08186

SEQUENCE DESCRIPTION:

GATCCCACCG AAGCAGCGTG TCCTCCGTGG GAGCCCGAGG TGGGTCCAC CCGCATCTCC 60  
 TCTTCCACAC CCTCCTGGGA CCCCAGCCCT GGAGAAGTAG CTCTGGCTTG TTTCTTTTT 120  
 NATTAAGAT AATTTATGTA TCGACTAAGA AA 152

SEQ ID NO:6953

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08188

SEQUENCE DESCRIPTION:

GATCAGTGGG TCTAAGTNTC CGAGACTTAA CGAAAATAGT ATTCAGCTG CAATAAAGAT 60  
 TGAGTTTGCA AA 72

SEQ ID NO:6954

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08189

SEQUENCE DESCRIPTION:

GATCAGCATC CTNCGNTGCC CCTTAGCAAC TNAGGTGGTT GATTTGAAAC TGTGAAGGTG 60  
 TGATTTTTTC AGGAGCTGGA AGTCTTAGAA AAGCCTNGTA AATGCCTATA TTGTGGGCTT 120  
 TTAACGTATT TAAGGGACCA CTTAAGACGA GATTAGATGG GCTCTTCTGG ATTTGTNCCT 180  
 CATTTGTCAC AGGTGTCTTG TGATTGANAA TCATGAGCGA AGTGAAATTG CNTTGANTTT 240  
 CAAGGGAATT TAGTATGTNA ATCGTGCCTT NGAAACANGG GGGNAAAAAN ATN 293

SEQ ID NO:6955

# EP 0 679 716 A1

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08190

SEQUENCE DESCRIPTION:

GATCCTTCAA TAAAAAATCA ATGTGTGAAG GTTCCTAGGC ATAAAAGGAA GTTCAGAAGG 60  
NTATGTAGGA AATACTGTTG TCTCTCTGGG GATTGGGATT ACAGGGATT TTTCTCTTT 120  
NCTTTTGTGTT AAGTTTGTGT TTCCTAAAGT TTCTGCAATA AACGTACGAT GCTTGATATA 180  
TAAA 184

SEQ ID NO:6956

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08191

SEQUENCE DESCRIPTION:

GATCTTGAAT TTCTACATAA CTTTCTCAGT TTATATGCCC TGTGGCAAGT GCAGCAAGCA 60  
CTGTTTCTCTG TTTCTAAACT TGTAGAAAAT CATCCATACA TCTTACAGTT GTCAGTTTTA 120  
ACCAGATAAC AGTGGCACTT TGTTGCTGCT TTTTATCTT TAGCTTAGGT TAACAGGACC 180  
CTGGAAGTAA AGTTGTTGAT TTATTCAATA GAGTATTCTC AATTAATTTG GCTAGATTTC 240  
TACATGATTC AAANTCTAAA AANGTAGACA TGCATGCTTA CATGTCTAAG GCCTGAAAAA 300  
TTGGNGGGGN CATCCCAAAA TAAATGN 327

SEQ ID NO:6957

SEQUENCE LENGTH:22

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08192

SEQUENCE DESCRIPTION:

GATCTAAGTG GTGGTATGGA AA 22

SEQ ID NO:6958

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08193

SEQUENCE DESCRIPTION:

GATCTGTTGA CAATGGAGCA AGTGAAAGAC TTTGCTGCTA ATGTGTATGA AGCTTTTAGT 60  
ACCCCTCAGC AACTGGAGAA ATGATTTTCC CTTCAAGAAA AACTACAGTG GGATTCATTT 120  
ACTTTTAAA ATACACTGGG TAAATCACCT ATACTTAGAG TAACAGTTTG TTATCAAAAT 180  
GCCTGNTAAA ATATATNCTT AATAAANGTC TTCATTTTCAAT AAA 223

SEQ ID NO:6959

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08194

SEQUENCE DESCRIPTION:

5 GATCTTACTT GCGAAATGCG ATGGTTGCTG GGAATACCTG AAAGTGTGGA TTATATTGCT 60  
 TGACTTCTAC CTCAGAATCT NCTTTGTTTC ATGACTTAAT AGTGCTTTAA GTNNGGTATA 120  
 TNATTTNACC NCTAGGAATT CTNTGTTTTA CACAGAAATA AAAATTTTAA AATAGAAAAT 180  
 GCTTTTACTT TGTAAGGTAA GNGAGTATCC ATATGCTTAG ATGTGCTCGT TTCTAAAATN 240  
 10 CTAGNGGTTG CTATANTCAG CTCATGGAAT GCACAGCTAT TGCTTTTTGT GNTAGATTGT 300  
 ACATAAACAT CAGCAGNTGN AAGGGNAAAT N 331

SEQ ID NO:6960

SEQUENCE LENGTH:211

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08195

SEQUENCE DESCRIPTION:

20 GATCACCCAG ATGCAGTGAA GCTTTTNACC CGCCAGCTTT TGGAAGTCCA TCAGGGACAA 60  
 GGCCTAGATA TTTACTGGAG GGCTAATTAC ACTTGTCCTA CTGAAGAAGA ATATAAGCT 120  
 ATGGTGCTGC AGAAAACAGG TGGACTGTTT GGATTAGCAG TAGGTCTCAT GCAGTTGTTC 180  
 TCTGATTACA AAGAAGNTTT AAAACCGCAA A 211

25 SEQ ID NO:6961

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08196

30 SEQUENCE DESCRIPTION:

GATCATTGTA GATGAAGTGA AGCAAGAAGT TATCAGTACC AGCAGCAAGG CAGANCCNCC 60  
 CCAGTGCACC TCCCTGGCCT GGTCTGNTGA TGGCCAGACT CTGTTTGCTG GCTACACGGA 120  
 CAACCTGGTG CGAGTGTGGC AGGTGACCAT TGGCACACGC TCGAAGTTTN TGGCAGAGCT 180  
 35 TTNCAACTAA ANAANAANCT GGCATAAA 208

SEQ ID NO:6962

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS08197

SEQUENCE DESCRIPTION:

GATCCCAGCC CTTAGGTGGG CAGAGGCAGA CCCTCCCCAG AGCTCCTTAG GAAGAAGACA 60  
 45 GACTGGTTCA TTGAATGCCG CCTTATTAT TTCTGGTGAG GATGCATGCG TGGGGCTGCT 120  
 GGTGTTTAGA GTGGGGGCTA CCCTTNTAAA TCACTGCTAC TCAAA 165

SEQ ID NO:6963

SEQUENCE LENGTH:280

50 SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS08198

SEQUENCE DESCRIPTION:

5 GATCACTCTN GGTGAGCTNC TCTTTCTTTA TCTNTCTTTC TCCTTTTTTA AGAAAACGAG 60  
 TTAAGTTTAA CAGTTTGGCA TTACAGGCTT GTGATTCATG CTTACTGTAA AGTGGAAGTT 120  
 GANCTTATTT TAAAACTTCA AGCTCAGTAA TTTTGAACAC TGNAACATTC ATCTAGGNCA 180  
 TAATAACAAA GTTCAGTATT GACCATAACT GTTAAACAA TTTTAAGCTT TCCTCAAGTT 240  
 10 AGTTNTGTTG TAGGNGTGTA CCTAAGCAGG TAAGCGTANA 280

SEQ ID NO:6964

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08199

SEQUENCE DESCRIPTION:

20 GATCCATATA TGTGTGCATG TCATGAAATA AAAGNATCAC ACANCACAAA A 51

SEQ ID NO:6965

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS08200

SEQUENCE DESCRIPTION:

30 GATCTTGGAG CTTCCCTGTA GCCCACCTTC CCCGTGCTTC ATGTTTGTAG AGGAACCTTG 60  
 TGCCGGCCAG GCCCAGTTTC CTTGTGTGAT AACTAATGT ATTTGCTTTT TTTGGAAATA 120  
 GAGAAAATCA ATAAATTGCT AGTGTTTCTT TGAAA 155

SEQ ID NO:6966

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS08201

SEQUENCE DESCRIPTION:

40 GATCCAGCAT TGGGGCCACT AACTCCAGC CTGGACCACG GAGCGAGACT GTCTCAA 58

SEQ ID NO:6967

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS08202

SEQUENCE DESCRIPTION:

50 GATCAGGCTT CAGGATAGCC CAGCACTGAG GACATCTAAA ACAGTCTTCA TTTATTTATT 60  
 TATTGTTTAT AGTGTCCAAA AGTTGGAATT AAAGTGAATG GCTGAATCAA A 111

55 SEQ ID NO:6968

# EP 0 679 716 A1

SEQUENCE LENGTH:39  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
5 CLONE:HUMGS08203  
SEQUENCE DESCRIPTION:  
GATCATGACA AAGAAGATTA AAATTCATT AGCATGAAA 39

10 SEQ ID NO:6969  
SEQUENCE LENGTH:90  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08204  
15 SEQUENCE DESCRIPTION:  
GATCAATTGT ACCCCATACC TCAGCATCAT GCAATATAAC CATTAAGAGA CCTGCACATG 60  
TATTCCTGA ATTTAAAATA AAAGTTGAAA 90

20 SEQ ID NO:6970  
SEQUENCE LENGTH:315  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08205  
25 SEQUENCE DESCRIPTION:  
GATCATTGCA GTCTCTGGCT TTTNACTCC AGGCGGGCTC CGTGCCCTCC GGGGCCTCTT 60  
CTTCCTTGTN AGGCCAGTGG GAGCCACAGA GGCCTCATTG GCTTCCTATG AATATNAAAT 120  
GGGATTCTCT GTGGGGGAAG CTTCATAAG GCAGGAAGGG GTCCCCGGTT GTTGGCTATN 180  
30 AGTGTTATTT NCTTTTAAAT CATCTGTGCT CCTTCAAAGA CGACGTAAGA AGCTTGTGCC 240  
CTGGCGTTGC AGAAATCTCT GGCTGTAGGG ATTAAACCTA CATGTCTTCC TGATGGGGTG 300  
GTGAGGACGT AAACN 315

35 SEQ ID NO:6971  
SEQUENCE LENGTH:262  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08206  
40 SEQUENCE DESCRIPTION:  
GATCACCTGA GGTGAGGAGT TCACGACCAG CCTGGCCAAC ATGGTGAAAC CCTTCTCTAC 60  
TGAAAATACA AAAATTAGCC AGGTGTGGTG GCGCATACCT GTAGTCCCAG CTACTTGGGA 120  
GGCTGNGGCA GGNGAATCAC TTGAACTCGG GAGGCGAAGG TTGCAGTGAG CCGAGATTTC 180  
45 ACCAGTGCAC TCCAGCCTGG GTGACAGAGC AAGACTCCAT CTCAAAAAAA ANNTAATTAN 240  
AAAAAATTGC AGCTGCNGGA AA 262

50 SEQ ID NO:6972  
SEQUENCE LENGTH:118  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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# EP 0 679 716 A1

CLONE:HUMGS08207

SEQUENCE DESCRIPTION:

5 GATCTTGAG GTCTAGTATT TNAATAATGC ACTATTACCC AGGGCAGNTA TTATGAGAAA 60  
CTGTTTCTNC TCTAAGGGTT TATGGCAGAC TTTGCTTTT NAACATGTGA GANATGAN 118

SEQ ID NO:6973

SEQUENCE LENGTH:152

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08208

SEQUENCE DESCRIPTION:

15 GATCTGAGTA TTCCCAAGG GCACTCAGCC ACAGGGNTGA ACTAGTGTTC GTTGTATCC 60  
TTGCAGTTAT GTGACTTAAA GTGACTCAGA GATATCTATG TATGCNNGTG TACTCCGCTG 120  
GCAATGAAGT AAATATATCA ATTTGTGGNA AA 152

SEQ ID NO:6974

SEQUENCE LENGTH:297

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08209

SEQUENCE DESCRIPTION:

25 GATCCTCCTG CTTGGCCTC CAAAAATGCT GGGNTTATAG GCATGAGCCG CTGCACTTGG 60  
CCTGNTACTG ATTTTAATNN CTTGCGTTAT CACATAGTGT TGTATTTGAA ACATAGTTCA 120  
TGGTTTTATC AAAGAACTGA AGNTGAGAAT ACTGGTCATC TAACTTTGTA ATTTGATTTG 180  
ATTATACTGT AAAGTTTGAC AGTCTCATTT TATCACTGCG TTTGTATCTA TNACTAAANT 240  
GTATTTNTTG ACCTCTTACT GATTCATTGT TGGTNTGTNC AACTGTTGA CTNGNTN 297

SEQ ID NO:6975

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS08210

SEQUENCE DESCRIPTION:

40 GATCCTGTCA CCCAGGTAGT GAGTATAGCA CCCAGTGAAA CTGTAGTCTC ATNCCAGGCA 60  
CTGTGCTAGC CCACTCTGGG TCATTTAATC CTCTCCTAAG AAGAGAGGAG ACACAGCGTC 120  
CCCATTGAC AGATGCAGAA AGAGGTTCCA CAGGTGTGCN TTGATTCTNT CCTAAAACCG 180  
TTTCCCGGAA GCTTTTCCTG GTGTGGGCGC TTCTAACCTA ATCCTCAATC GNTTCCAGNA 240  
CTATTACTCT GTTCCACAG TGNTACTGTG TCTAGGTTTT ANGGGCGGCA AGTTCNATTT 300  
N 301

SEQ ID NO:6976

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS08211

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# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCTTCCG ACTTGGCCTC CCAAAGTGTT GGGATTACAG GCATTAGCTA CCACACCTGN 60  
 CCAAGGCCCA GGTTCGACA GAAAGGGAGA GAAAACCTGC CAGAGATGCC ATTCGGGAGC 120  
 CACTCTGCTT GGCAGGGACC TGTGTTCCCT TCATGCAGGT TCATCCTTAG AGGGCTGCCG 180  
 TCTTATCTGG TTGTGCAAAA GTCCCACAAC CTTTCTGGAT TGATAGTTTG TGGTGAANNT 240  
 AAACAATTTT AGTTTGTGTTG GAAA 264

SEQ ID NO:6977

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08212

## SEQUENCE DESCRIPTION:

GATCAGAACT ACAATTACAA CCAGCATGCG TATCCCACTG CCTATGGTGG GAAGTACTCA 60  
 GTCAAGACCC CTGCAAAGGG GGGAGTCTCA CTTTCTTCCT CGGCTTCCCG GGTGCAACCT 120  
 GGCCTGATGN AGTGGGTGAA GTTTTGGTAG GCAATTCTT GCAACCACCA CCGNGGCCCC 180  
 GNAAAGCACT GGTCGTNAGG GAGCTCCTNN CTTGGCCCN CACGCCTGTG CCAGCCCTGG 240  
 NCCCGNCTGC CACACCTCTG TTTCTTANGG CTGGGGACNC AGATTGTNTC TCCTTNTTTC 300  
 TTNCACTGC AATGTGCN 318

SEQ ID NO:6978

SEQUENCE LENGTH:166

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08213

## SEQUENCE DESCRIPTION:

GATCATNCTG CCCCATNTCC ACGCACCCAA AACCAGCCCT CTCGCTTCTA ACACAGGGCA 60  
 CCTGTGGGG CTCAGGGATG TTAGGGACGA GTTCCAGNCC TGCCACTNCC CTNGGGCGAC 120  
 CCCTCNCCTGT CCCTGCCTCC CTGCTCTGCC GCCCCTNTTN CTGGAN 166

SEQ ID NO:6979

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08214

## SEQUENCE DESCRIPTION:

GATCCGATAC AGATTACATT TCTTGCCAGA GAGTGTGCT GTTGTTTCTT TAGGTAAGTG 60  
 TGTATTGGTG ATTCCATAAT AAAAGCAGTA ACAATAACTA CCAA 105

SEQ ID NO:6980

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08215

## SEQUENCE DESCRIPTION:

GATCAGATAC ATGAACATGT CTTACATGGG TTGCTGTATT TAGAATTATA AACATTTTTC 60  
ATTATTGGAA AGTGTAACGN GGACCTTCTG CATACCTGTT TAGAACCAAA ACCACCATGA 120  
CACAGTTTTT ATAGTGTCTG TATATTTGTN ATGCAATGGT CTTGTAAAGG TTTTAAATGN 180  
AAACTACCAT TAGCCAGTCT TTCTTACTGA CANTAAATTA TTAATAAANT AAA 233

SEQ ID NO:6981

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08216

SEQUENCE DESCRIPTION:

GATCTTTCCA GAGGTCCATG GTGGAAGACG ATAACCCTGT GAAATACTTT ATAAAAATNC 60  
TTAATGTTCA AA 72

SEQ ID NO:6982

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08217

SEQUENCE DESCRIPTION:

GATCACCCAT CTGTGTGCTT CCATCCTGCA TTAAATTC A CTCAGTGTGG CCCAGAAA 58

SEQ ID NO:6983

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08218

SEQUENCE DESCRIPTION:

GATCTCCAAC AGCCAGTGTG TGTTTCCCAT CTCTTGTAGG TTCCATCAAT GGTGAGCACC 60  
AGCCTGAATG CAGAAGCGCT CCAGTATCTC CAAGGGTACC TTCAGGCAGC CAGTGTGACA 120  
CTGCTTTAAA CTGCATTTTT CTAATGGGCT AAACCCAGAT GGTTTCCTAG GAAATCACAG 180  
GCTTCTGAGC ACAGCTGCAT TAAANCAAAG GAAGTTCTCC TTTTGAACCTT GTCACGGATT 240  
CCATCTTGTA AAGGATATTA AATGTTGCTT TAACCTGAAA 280

SEQ ID NO:6984

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08219

SEQUENCE DESCRIPTION:

GATCCAGAGA CTCGTGCTGT CTCTTTGTCC CTTTCCTGAT GGTGTTACTT CGATTAACATA 60  
CTTCAGCTTG GTGTAAAAAT TGCCAAAGCA GTTGCCTGCC ACAACTTTGT AAAAGCCAAA 120  
AAGGAGGTTG AAAATTCACA GGCTGCCCGA AAAAAGANGA AACTTGCATG GGGGTTTGAA 180  
GCAAAGNNGN GATGGGAAAC CNAAGCAAC ATGGGNTACA TGTAACCTGC CAGAGTGCTT 240  
CAAGACATTT GTAGCCTCAA ATGCTCAAAT TTANTGNGAA TGTTTTCCTG CCTATGTTCA 300

TATGTCAGGT N

311

SEQ ID NO:6985

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08220

SEQUENCE DESCRIPTION:

GATCTGATGG TTTATAAAG GGGNGTTCTG CTGCATACAC TCTGTCTTGC CTGCTGNCAT 60  
 GCAAGATGTG ACTTAGCTCC TCCTTTACCT TCCACCATGN TTGTNAGGCC TCCCCAGCCA 120  
 TGTGGAAGCTG TGAGTTGANT AAACCTCTTT CCTTTATAAA 160

SEQ ID NO:6986

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08221

SEQUENCE DESCRIPTION:

GATCAAAAGA TAACTGCTTA TNATAGTAAG ATAACCTTGG AACAGAACTG TGATTAAAAA 60  
 CCTGAATAAT AAAAAACACA CAAGACCCAT TAAAACCTAT TCCTCACTTT TTAAA 115

SEQ ID NO:6987

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08222

SEQUENCE DESCRIPTION:

GATCCAGTTG GATATAGTAA CCACTGCCGA CTTNCTGGAT GTGCTAACTC ACACCAAGCC 60  
 CTCCGNAAAG AATCTGGCTC AGAGATACTC AGACTGGCAA AGAGAATTCG AGTCTGTCTG 120  
 AAACCACATT TACCCTGACC TGGCCACAAA GGCAACCACA AAGACCTCCT AGTTTATTAN 180  
 NGNNCGTGGG AGAACAAAAAT GATTGGAATG GAAAAGAGAA AATTATTTTT GANGACTGGA 240  
 TTAAGTTGAG CCACTGTATT GTTTGGNTA GCTGAGATAT ATTTNTTAAC TTTACCATTA 300  
 TCGATGTCAG CAAAATATTG AGAGTTTCTT N 331

SEQ ID NO:6988

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08223

SEQUENCE DESCRIPTION:

GATCTACTCC CAGTTTTTAA CTTTTNACAG AATATTGTTG CTTTCTTACA ACAATGTACA 60  
 TATATTTNCA GTTGATATATG CTTTTTTTTT TNCCAAATAA AGTTTGAGTT CTAAACTCAA 120  
 A 121

SEQ ID NO:6989

# EP 0 679 716 A1

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08224

SEQUENCE DESCRIPTION:

GATCCTTCCC TGGCTCTCAC CTGCTCCTTT AGGCTGTAAT TGCTTCCTAC ACACGAAGCC 60  
TCTGATTGGA GCCTCTGGTN CATCTCAGAA AAACCTTCCA AGAGCGCTGG GGTTCATGCT 120  
TTCTGAATAA AACTACTGT TTACATGGAA A 151

SEQ ID NO:6990

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08225

SEQUENCE DESCRIPTION:

GATCTCCATA ATTTAAGAT ACTCTATGTT AAACATTTT TNAAGTNCCT TTTTACATC 60  
ACGTCTGAAA TGCACGAGNG TGGCGGTTTC TGTTTCACTG GTTNNTTGT TCATTTTNN 119

SEQ ID NO:6991

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08226

SEQUENCE DESCRIPTION:

GATCCCGGGC CGTTATCCAT CTGGAGGCTG CAGGGTCCTT GGGGTAACAG GGACCACAGA 60  
CCCTCACCA CTCACAGATT CCTCACACTG GGGAAATAAA GCCATTTCAG AGGAAA 116

SEQ ID NO:6992

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08227

SEQUENCE DESCRIPTION:

GATCCGCTGG GACAGAGTGC CCACCGTCGT GTCTTTNATA TCTCTGTAAT AACCCACAGT 60  
TAAAAAGGGC AGGAAAAGGC ATCAGGGTAC CATGTTATCA GGCAAGTTCT TACATTCTAA 120  
GAAAATTCCT AGCTTTGTTG GGTGAGGCAA GTTTTAAAN GAANAATGTC ACTTCCCAT 180  
TTGATAANGA TTTCGTTATC ANTAAA 207

SEQ ID NO:6993

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08228

SEQUENCE DESCRIPTION:

GATCCTGATT GTAAGGTTTT CCACCTATTT CCCTGGATAT TTTNNTGGTC AGTACTGGCT 60

EP 0 679 716 A1

CTGGTGGGTG TTCCTTGTTT TAGGCTTTCT CCTGTTTCTN AGAGGATTTA TCAATTATGC 120  
 AAAAGTTCGG AAGATGCCAG AAACCTTCTC AAATCTCCCC AGGACCAGAG TTCTCTTTAT 180  
 TTATTAAAGA TGTTTTCTGG CAAAGGCCTT CCTGCATTTA TGAATTNTGG TCTCAAGCAG 240  
 CAAGNGAACA CCTGCAGGAN GTGAATCAAG CTGCAGAACA CAGAGGNNTA CTCACCTGCT 300  
 TTAAAAAAT ANAGTACTGT TGATN 325

SEQ ID NO:6994  
 SEQUENCE LENGTH:130  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08229

SEQUENCE DESCRIPTION:  
 GATCCCTCGG GNNTTAANTA CANGAAACCT AGAACTGACC AAAAGGCATT ATAACCTCTGA 60  
 CTCAAATACA AGGTACAGAA GATAAGCATC TTTGAGGAAA CTCCTACTTC AGTTCTTTTG 120  
 TTATNATGNN 130

SEQ ID NO:6995  
 SEQUENCE LENGTH:116  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08230

SEQUENCE DESCRIPTION:  
 GATCATATAA CATTCCAGGT ACTCAGGATG AATGGTTTGA GGACTGGTCT GAATTCTTCA 60  
 AAGGTTTCAG CTGTATTAAC ATTCTCCATC TAATAAACTT TATCTTGTC TGTAAA 116

SEQ ID NO:6996  
 SEQUENCE LENGTH:33  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08232

SEQUENCE DESCRIPTION:  
 GATCAGCAAA TAAATGAAAT TTATTAAG AAA 33

SEQ ID NO:6997  
 SEQUENCE LENGTH:246  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08233

SEQUENCE DESCRIPTION:  
 GATCTTTAGG CAGTTTTTAC TTGGCCAGAA AGCAGTGCTG AATACTTGNA ACTGTGTGCT 60  
 CTGTTCTACT TAATGTTCTG TCAGAAATGTT CTTTGTAGG CAGTATGTCA TGNTGTAATC 120  
 ATCTATCTCC TNGTCTGTTT CCAAGTTNNN CTGTGAAGTC TGCAGCCCTT TTGNGGTGGT 180  
 CATCANAGTC ACAGATTCCT TGTTTAACCA NGTGTCCNA AGCATGTACC TGNAGTTATA 240  
 TCATNN 246

SEQ ID NO:6998

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08234

SEQUENCE DESCRIPTION:

GATCATTATG CAATAAAGCT GCTAAAGTCA CATTGTGGT TGATACTCAA GCCTTGTTACA 60  
 AGCACATATC ATGTAGACAT TTTTAAATGT GAAGCTTTAA CAGGNATAGG ATAGCTGTTT 120  
 CAAACCTTGT GCAATTGTAA ATAANTTGT TAGCTGTGTT TCTTTCATTT TTAATANAAA 180  
 NTTAAA 186

SEQ ID NO:6999

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08235

SEQUENCE DESCRIPTION:

GATCTTCATA TTAATCTTAA AATTTTGTGA CGTGTCTTTT TCCTTTTTTT CCACAGTTTT 60  
 AATATATNAT TCTTCAACGA CATTITTTGT AACTTTACAC TTTTGTGGTT ATNTTATTTT 120  
 AAAAAAATGA AAAATTAATT TAAAAAATG CAAA 154

SEQ ID NO:7000

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08236

SEQUENCE DESCRIPTION:

GATCTGGTAC GNGGNGGACG NCATGGCCCG AGATGCCAC GGGAAACACAG CGCTGACCTA 60  
 CGCCCGNCAG GCCTCCAGCC AGGAGTGCAT CAACGTGCTT CTGCAGTACG GCTGCCCCGA 120  
 CGAGTGCCTG TAGTATCTGT TTTATTTNNC TGNAGTCTCC TTGGTGTAAG AACAAAATNG 180  
 GNAAAATAAG GATAN 195

SEQ ID NO:7001

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08237

SEQUENCE DESCRIPTION:

GATCAGGCCC TAAAACGTTG TTGTGATGAG GTTCTTTAG CAAGTTCTTG TTTAAATTAT 60  
 CATTTATTTG ATGAGTGAAG TTTTAAACAT GCTTTGCTGT GTGAAATTTA AAAAAGGGAT 120  
 GTTTTCCAG GCTGGAACAA TAAATGTGGC TGTGCAGTTT AAA 163

SEQ ID NO:7002

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08238

SEQUENCE DESCRIPTION:

5 GATCTTTGTG AAAGTAGTAC AGTATATNAC CTTTAATTNC TTTTTATTT TAAATATACT 60  
GTNACCNTGA AGCACTGGTT GGGCATTTTA ATTCATGTTA ATAAATCACA ATTATGTCAG 120  
TTTTAAA 127

SEQ ID NO:7003

10 SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08239

15 SEQUENCE DESCRIPTION:

GATCAGCCTC CTGTCTTATG TGGGCACGTT CCAAAGTTTA AATGCATTTT TTTGACTCTT 60  
GGCCAAAATT TAGAAGATGC TGTGAATATC ATTTTGAAC TGTGTAAATA CATGAAAGAG 120  
AAA 123

20 SEQ ID NO:7004

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS08240

SEQUENCE DESCRIPTION:

GATCTCAGCA TTACCTCTTT GGNAAGGAA GGTAGTTCAA GAAATGAAGA GCTGTTGATG 60  
GGATGATTGA AGAAACAGCT ATGAGAGGAT TGGCTCCCAT CTTTGTGNAC TCTTGGGNCA 120  
TCCTGTCATC TGAGAATGAA CAAAGACCAA TTTTGTGT GTGAAGCTTA AGGGTCATAT 180  
30 GTTGTCTTGT NTTTNTNAAT GCTAATCCTT GTGAAANTAA ATTGNCCAGG CGGAAGGAAA 240  
NCTCTATTTT AGGATNCAAA 260

35 SEQ ID NO:7005

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08241

SEQUENCE DESCRIPTION:

40 GATCTGTATT TNTATATACA CGTGTCCGNA CAAGTATAAC TAAATAAAAA TTAAAGNTTT 60  
TAATCATTTT AATTGAAAA 79

45 SEQ ID NO:7006

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08242

SEQUENCE DESCRIPTION:

50 GATCATATTT CTGCCAAGNA TGTGCCTTCA ACTTTATAAT TATAGTGTTG TAAAATAAA 59

55

EP 0 679 716 A1

SEQ ID NO:7007

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08243

SEQUENCE DESCRIPTION:

GATCTCACTT TTNCTTATTA GAATTTGTAC CTTTGTTGA TTAAGGAAAT AAAAGATGAA 60  
TGACAAA 67

SEQ ID NO:7008

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08244

SEQUENCE DESCRIPTION:

GATCAGTCTC TCAGTGCCTN CCTACTGGGC AGCTCATCTG TCCACTTATT CGTATTAAAT 60  
TTNCTTTTAA TTAAAA 76

SEQ ID NO:7009

SEQUENCE LENGTH:162

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08245

SEQUENCE DESCRIPTION:

GATCCACATC CCANATGCTG AACCAGAGAG CCCCTCATCC CTCCTCCCAG TACTTAGGCA 60  
GCGCCTTCTG TGTGCACTGC CTCTGCCGG GCACTGGGTA GGTGCACACG NGGACCGGGA 120  
CAGGGCCAGA NACTTTGGTN CCCGNGGTTT GTNTGNNGGG NN 162

SEQ ID NO:7010

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08246

SEQUENCE DESCRIPTION:

GATCGATTAA GTCTAGGAGT TTNAGACTTG CCTGGGCTTA GCAAGACCCT GTGGCAAA 58

SEQ ID NO:7011

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08247

SEQUENCE DESCRIPTION:

GATCCTTGAG TCTCCNCTCT GGATGGAATC CGCGAGCTGG CCACCTGGCC ACCCTCTACA 60  
CGACTCCACC CNNCCATGGC CGTGGGGCCC TTA CTCTCTG ACTTCTCAGG ACACAGGTCA 120



EP 0 679 716 A1

TGGAGGTTCT TCCCAAGCTG GCAGAGGCCA TTTGTGGAAA GTGGAGAGCT ACGTGGTGGN 180  
CATCTGCCAA CTCCAGCATC TCTGGNGGGG NTCCACGNTG AATGTNATTT TTGAAAACAG 240  
CTTATGTANT TAAAGTTGA ATGGCACATC ATAAA 275

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SEQ ID NO:7012  
SEQUENCE LENGTH:124  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS08248

SEQUENCE DESCRIPTION:

GATCAAGACC ACCCTGGCTA ACACGGTGAA ACCCTGTCTC TACTAAAAAT AAAAAANTT 60  
AGCCGGGCAT GGTGGCACAC GCCTGTACAT CCCAGCTACT CANGGNGGCT NGTGGCATGG 120  
NGNN 124

15

SEQ ID NO:7013  
SEQUENCE LENGTH:215  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS08249

SEQUENCE DESCRIPTION:

GATCANGAGC CCTTTTNCCTC CAGTAGTACA GGCTTTGAAA ACTACTTCTA TTAAGTTATT 60  
GATGCAATTT GATATTTTTT CATAATCTAT ATTTAAACAA AATTACATCA TTGCATCATC 120  
TTTTCTAAAT TCATCTCCAT TAAAACTTGC CTTAAGCTAC CAGNTTGCTT TTGCCANNGN 180  
NGGCCATACT GTGTGTTTGT TTGTTTAATN NNCTN 215

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SEQ ID NO:7014  
SEQUENCE LENGTH:373  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08250

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SEQUENCE DESCRIPTION:

GATCTCTCAG GGATAGAAGA TATTTCTCAT GAAGGCAGCC TAACTCTGAG GAAAACAATG 60  
CCAATTCAAG TACAGATTTC AACACATCTT CAACACTATG TGAAGGGTTC ACATCTTAAC 120  
CTGTGCAATT CAGATTGATA CTCAGAATAT GGGTTGATT GAATATCTGA AATATCAATG 180  
GAAAATCCCA CTNNGTTTTT GATGAACAGT TTGAACAGTT TTCTGTAATC AAGCAGCTTG 240  
CATAGAAATT GTATGATGAA ATTTTNCGNN GGTCTTGGT GCTGTTTTGT TCTTTTTTTG 300  
TTTTTTGTTG TTTTGTATT TACTTATATA CATATAANCT TTTNTTGAAA ATATGTTTTG 360  
GTTACTAANA GTN 373

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SEQ ID NO:7015  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08251

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SEQUENCE DESCRIPTION:

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# EP 0 679 716 A1

GATCCCAACC TGGACCCACT CATGAACCT CACATCCGCG TGGGCCCTC CTNAGCCCN 60  
 TTGCTTGTGG CTAGGCCAGC CTAGGATGTG GNTTCTGTGG AGGAGAGGCG GGGTAATGGG 120  
 GAGGCTGAGG GCACCTNTNC ACTGCCCTC TNCNTCAAGC CTAAGNCACT AAGACCCAG 180  
 ACCNAAAGCC AAGTCCACCA GAGTGGCTGC AGGNCAGGN 219

SEQ ID NO:7016

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08252

SEQUENCE DESCRIPTION:

GATCGCTTGA ACCCATAAGC TGGAGACCAG CCTGTGCACA TGGTGAGACC CTGTCCCTAC 60  
 CAAAAAAT AAAGTCATTA GAGTTTTTAA A 91

SEQ ID NO:7017

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08253

SEQUENCE DESCRIPTION:

GATCTGATGG TTTTATAAGG GGCTTCCCCC TTTACTCAGC TCTCATNTT CTCTCTCCTG 60  
 CCACCATGTA AAGAAGGATG TGTTTGGTTT CCCTTCCATC ACGATTGTAA GTTTCCTGAG 120  
 GCCTCCTAAG CCATGTGGAA CTGTGAGTCA NTTAAATCTC TTTACTNTAT NNNGNN 176

SEQ ID NO:7018

SEQUENCE LENGTH:174

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08254

SEQUENCE DESCRIPTION:

GATCATCACT TACCCACCCC CCAAGTTCAA GACCAAATCT TCCAGCTGCC CNNTTCGTGT 60  
 TTCCCTGTGT TTGCTGTAGC TGGGCATGTC TCCAGGAACC AAGAAGCCCT CAGCCTGGTG 120  
 TAGTCTCCCT GACCCTTNTN AATTCCTTAA GTCTAAAGAT GATGAACTTC TAAA 174

SEQ ID NO:7019

SEQUENCE LENGTH:45

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08255

SEQUENCE DESCRIPTION:

GATCCTCCCT TTCCTATAGN GNTAAAAGTG ATTTATCTTG GCAAA 45

SEQ ID NO:7020

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08256

SEQUENCE DESCRIPTION:

GATCATGTGA TGTTGGAGTA GGAGGGTTTA TTTGGTGAC TTTGGGATGC TGGTTTCATT 60  
GTAGGTATAA TNATGNGGNG CAAAGAATCC AGGNAAGAAT TGCCAGAGN 109

SEQ ID NO:7021

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08257

SEQUENCE DESCRIPTION:

GATCCCACTG AGGCCAGAGA ATAGGGTCTG GAGACAAAGG AGCATTCACT TCAGCCTCTG 60  
ACTGGTGGCA GGCCAAGTNT TTATTTACAT AGGGTGTAAC CAAATAGGAA ACCTCTAAAG 120  
GGTACTTAAA CCCAGATTT TNTACACAGG GCACTTGCTT GAGCCTCATC CCGCTTTCTG 180  
GAATGTACTT TTGCTTCAAT AAATCTGTGC TTTTGTTCCT TCAA 225

SEQ ID NO:7022

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08258

SEQUENCE DESCRIPTION:

GATCTGGAGG GCGTGGCTAC AGGACCCGGG ATGCCATTCA GTTACTCATC TTTNATGCTT 60  
TCGTCTGAC CTGTCTCAAC TAGACTTGCT CCTGCAACCA CCATGGGGGT TTTGCATTTA 120  
CATTTGTGGA CCATGTTACA GTTAAGAAAA ATCCTGTTTC AGTCCTTATA TGTAATAAAA 180  
TGTTTTATGA TGTAAA 196

SEQ ID NO:7023

SEQUENCE LENGTH:170

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08259

SEQUENCE DESCRIPTION:

GATCTNTCCT CCGCTTGAGA AGACCATGGA ACTGGATAGC TCACTTCCGG AATACAACAT 60  
GTTTCCCCGC AAAGGCCGGG GNCTCCCTAG NTCAAATTC CAATCTCATN AGCAGGTGNT 120  
AGAAAGGTNT TGTGGTAGCA ACTNCATGAT TTCTCTGTGA CCAAATNAN 170

SEQ ID NO:7024

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08260

SEQUENCE DESCRIPTION:

GATCAAATGT AAATNTTTTG AGGATATTTT NCTTGTTTT NAAAATCAAT TTTTAACCA 60

ATATTAAACC CTTTATTTGC CAAA

84

SEQ ID NO:7025

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08261

SEQUENCE DESCRIPTION:

GATCCACCAC TGGNCTCTCC CTCCCCCAGC CTGGAGCACG GGAGGGGAGG TGACGGCTGG 60  
 TGACTGATGG ATGGGTAGTG GGCTGAGAAG AGGGGACTAG GAAGGGCTAT TCCAGGCTCA 120  
 GCCCTGCTAC TGCAGCTTTG CCGCTGAGTG TAGGAAAAAC AGGCATGACA GACCAGGGTG 180  
 AGGGTTGTGC CCAGCTGGGC CACGGCCATG CGTGGGGTGG CCCAATAAAC ACCGTGGACT 240  
 CCCAAA 246

SEQ ID NO:7026

SEQUENCE LENGTH:45

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08262

SEQUENCE DESCRIPTION:

GATCAGTCTT TATNAATAAA ACCTGTTCTC TTTAATCAGC TTAAA 45

SEQ ID NO:7027

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08263

SEQUENCE DESCRIPTION:

GATCAGACTG NTAACCTTAA CACCATAGGT GCAAAAANGAG TTGTTCTNAG GTTTTTTTGA 60  
 AACATTAAAG TTCCAAAACA TGACATTTT AAGAATAAAT TTGAAATAGN GTATGATTGA 120  
 ATGCAGAGNA TTATGTACCT CTAATTGCTT AATTTTGTAG NGGTCTTNA TTGTAGAATT 180  
 GGNNCN 186

SEQ ID NO:7028

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08264

SEQUENCE DESCRIPTION:

GATCTCTTGG TAACAATTGA CATTGCACTA GNATTTGAAT GNTACTGTTG TTGGCATTTC 60  
 TGTTANTCTT TCAAGTAGTT GTAAATAATC TCTTTTCTC ATATAAACGG AATGCATAAT 120  
 GTCTTACTCT TGAGTCATT AGTAGCATTG ATATGGTACC AAGTTGTATA GCAGTGTAAC 180  
 AAAATCATGC TTTGACAATG NAATTTACAT ATGCCTCAC CTAGAGATGT TTTGTCTGTA 240  
 TGACTNNTNN CNTTNTAAAG TTNGNCNAAC N 271

SEQ ID NO:7029

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08265

SEQUENCE DESCRIPTION:

GATCAAATCA GGGTAATTGG GTATCCATCA CCTCAAACAT TTACCATTTC TTTGTGTTGG 60  
GAACATTCCA TATCTTTTTT TCTAGCTGTT CTGAAATTTG CTATACGTTT TTTTAACTAA 120  
AGGTCCCTTG CTGTGTTATG GAACACTGGA ATTTGTTCTT TCTGTTTAAC TGTATTTTGG 180  
TACCTATTAA CCAACTTCTC TTTATCCTCC CCCGTCCTCT ACCCTTCCCC AGCCTGTGGG 240  
AATCACCCAT NCTACTCTCT GCCTTTATGA GATTACTTN TTTNATCTCC CNATATAANA 300  
N 301

SEQ ID NO:7030

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08266

SEQUENCE DESCRIPTION:

GATCGTAGAA ACACAGAATG GGACTGGGGA AGCCCTTTGG AAATCCAGCT GCAGAAACAG 60  
ACACCCCAAT GCTATTTACA TACAGCTCTA TATATATAAA AAAAGNAAAT ATGNAAA 117

SEQ ID NO:7031

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08267

SEQUENCE DESCRIPTION:

GATCTCACCA GGGCCAGTC ATATATGCAC AGTTAGACCA CTCCGGCGGA CATCACAGTG 60  
ACAAGATTAA CAAGTCAGAG TCTGTGGTGT ATGCGGATAT CCGAAAGANT TAAGNGAATA 120  
CCTAGAACAT ATCCTCAGCA AGAAACAAAA CCAAACTGGA CTCTCGTGCA GAAAATGTAG 180  
CCCNTTACCA CATGTAGCCT TGGNGACCCA GGCAAGGACA AGTACACGTG TACTCACAGA 240  
GGGAGNGNAA GNTGTGTACA AAGGNTATGT ATAANTNTTC TNTTTAGTCA TCCTATN 297

SEQ ID NO:7032

SEQUENCE LENGTH:58

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08268

SEQUENCE DESCRIPTION:

GATCCTGGGG ACTCATATTC TTTCAGAATC ATGTAAATAA ATGGCATCAT GTTGTAAG 58

SEQ ID NO:7033

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS08269

SEQUENCE DESCRIPTION:

5 GATCTATTG GCCTCTCAAA TNAACTNAGA TTCCTGTAA AAAAGATTGA TGTTATTGTC 60  
TCTTGTAGAG GAAACTAATA AAGTGTGTGT ACCTNTGTGN AAA 103

SEQ ID NO:7034

SEQUENCE LENGTH:265

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08270

SEQUENCE DESCRIPTION:

15 GATCAAGAGT NATGGGCCTT GGAGCCCTTG CCAGCCCAGC CCACCTGTNA GGAGGCTGCC 60  
CATCCCCTCT TTNAGGCCAC CCTGTGTCCT CTCCCCTGCC TCTGCCCAGA GCTCCAGCCG 120  
GAGTGTCTTG CTGCTCAGAC CCCTCCGAGG TCCAAGTCCT GTCCTGCCAC TCAGCTCCCN 180  
CTGCACCCA GAAGAAACGC AGGGTGCGGT TGCATTTGAT TTCAGATAAA CAACAACCTC 240  
20 TTAGTAAAT NACCTNCCCA CTAAT 265

SEQ ID NO:7035

SEQUENCE LENGTH:46

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS08271

SEQUENCE DESCRIPTION:

GATCAATCTT GANGTGAAAT ATTTCCAAAA TAAAATTCTA CAGAAA 46

30 SEQ ID NO:7036

SEQUENCE LENGTH:254

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS08272

SEQUENCE DESCRIPTION:

GATCTTTGCA TAGAATGTCA AGCTAACCAG GCGTCCGNTA CTTCAGAAGA GTGTACTGTC 60  
GCATGGGGAG TCTGTAACCA TGCTTTTNAC TTCCACTGCA TCTCTCGCTG GCTCAAAACA 120  
CGACAGGTGT GTCCATTGGA CACAGAGAG TGGGAATTCC AAAAGTATGG GCACTAGGAA 180  
40 AAGNCTTCTT CCATCAGGNG TTAATTGTTT TGTATTTCAT TTAATGGCTT TCCCTGCTGT 240  
TACCTAATTA CATN 254

SEQ ID NO:7037

SEQUENCE LENGTH:222

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08273

SEQUENCE DESCRIPTION:

50 GATCATTGAG AAAGTGTGTTG AAACCTTCTC ATGAAGTGTA TATATAATGG CGTGAAAAAT 60

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# EP 0 679 716 A1

TCCTTTGGAA AAATNTATGT NCCTTTCATT TTGCCCAAAT TGCAAATTTT CAGCATGGNT 120  
GTGAAAAGCA TTAATAATTAT AACTTTGTGT ACANGATGAA AATAATTCAC TAAATTTGCC 180  
CTTTTTTACA CAAAATAAAA TGTTAANGTT ANNGCTGGNA AA 222

SEQ ID NO:7038  
SEQUENCE LENGTH:32  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08274  
SEQUENCE DESCRIPTION:  
GATCAAATGA CANTAAATCA TTCAAATCA AA 32

SEQ ID NO:7039  
SEQUENCE LENGTH:109  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08275  
SEQUENCE DESCRIPTION:  
GATCACCCAG GTACANCATG CTCTATATCC ATGCGGCCCT AGAAACCCAA GGAACATATA 60  
CAACCACTCT TGTGTCCCTC CTTATAACCN CAGNTTTATN CNAGAAGTN 109

SEQ ID NO:7040  
SEQUENCE LENGTH:301  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08276  
SEQUENCE DESCRIPTION:  
GATCACAAAT TGGTGCATTC TTAAGTGTGG ATAATTATGT ATGAAGCCAA ATTGTAATAA 60  
AACTGTTATT TGCCAAACAT AGAANCCTTG CTCGTGACT AGGCTGAGCC CAGAGTGTTA 120  
TTCTCTTCTT CTGCCTGTNA TGTATCTGGG CAATTTGTAG GGCTTTGCA GGTGAATCCA 180  
GTAGAGAACC ATGCTAAGAN TGNGCAGCAG TCATGCATGC CTGTATCATT GAAAGCCTTC 240  
CTNGCCATTT TNNCAGCTTC ACCTTNCGTG GTTTTTATTT TTTCCAGAGG GGGCCTGGGG 300  
N 301

SEQ ID NO:7041  
SEQUENCE LENGTH:151  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08277  
SEQUENCE DESCRIPTION:  
GATCCTCCTC CCTAAGCGCT TATCTGGTG CTTCAGCTC AGTCTGGCCA ATTCCACCTC 60  
TATGAGATAA GGAGGGTTCA GAGAACCCAG TCACTTTGCT GTTTTTCTGC NCACAGAGTT 120  
TCTCTAATAA ATCTTATTCT ATGTCTACAA A 151

SEQ ID NO:7042

# EP 0 679 716 A1

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08278

SEQUENCE DESCRIPTION:

GATCACATTG TTTGACCCAG TATGTCTTGT AGACACGTTA GTTATAATCA CCTTGTATCT 60  
CTAAATATGG TGTGATATGA ACCAGTCCAT TCACATTGGA AAAACTGATG GTTTTAAATA 120  
ANCTAATTCA CTAATAAA 138

SEQ ID NO:7043

SEQUENCE LENGTH:300

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08279

SEQUENCE DESCRIPTION:

GATCTGTCAA CAGGTAAAGT CAATCTGGGG CTTCCACTGC CTGCATTCCA GTCCCCAGAG 60  
CTTGGTGGTC CCGAAACGGG AAGTNCATAT TGGGGCATGG TGGCCTCCGT GAGCAAATNG 120  
TGTCTTGGGC AATCTNAGGC CAGGNCAGAT GTTGCCCCAC CCACTGGAGA TGGTGCTGAG 180  
GGAGGTGGGT GGGGCCTTCT GGGGAAGGTGA GTGGAGAGGG GCACCTGCCC CCCGCCCTCC 240  
CCATCCCCTA CTCCCCTGN TCAGCGCGGG NCATTANAAG GGTGCCANAN ATTTTTTTNN 300

SEQ ID NO:7044

SEQUENCE LENGTH:90

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08280

SEQUENCE DESCRIPTION:

GATCTCATTG CATGGGAAAA AAAAAATCC TGTCTTGTTT ATAAATTGAC AATGTCCTA 60  
AATAGAAATA AAGTGCACAN TAAATGNAAG 90

SEQ ID NO:7045

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08281

SEQUENCE DESCRIPTION:

GATCTNAGTT AGACATCACC ANTGGAAATC GATTGGAATA GAAACTTAAA GGAAATGGAA 60  
CCCTGACTAT TCTCCCATCA AATCATATAT GTTGACCTGT CTGAATTATA AACCAGCCTG 120  
ACCTTTCCTT TAGCATTAGA TGAATAAAAA TAACTTTGGA AATTTGTNAT TAAA 175

SEQ ID NO:7046

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08282



# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCCTCAGG ACTGACCAGT TAGCTGGCAG GTTGTNCAGC TTTTAATTCC AGTCATAATA 60  
GGTGACAGTG TTAACCGTGA AANTTTGNGA GGCACNTTTG NCCTCTTCCC TATAAAAATC 120  
ACACAAGCGT GNTTTTACAA AGGGTCCCCG TGGGAACCTT NGCTTAAGGA CCCTTTGNCC 180  
CNTCAGTTAN 190

SEQ ID NO:7047

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08283

## SEQUENCE DESCRIPTION:

GATCCTCAGG ACTGACCANT TAAGCTGGCA GGTGTGCCA GCTTTTAAAT CCCAGTCATA 60  
ATAAGGTGAC CAGTTTAAAC CCGTGNAAC TTNGAGGGGA CTTTTCCTT TTCCCTATNA 120  
AATNACACNG GGGGGTTTAA NAAGGTN 147

SEQ ID NO:7048

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08284

## SEQUENCE DESCRIPTION:

GATCCATCTG CCTCATAAA AGTGTTTCAGG TACAGCAGCT GAGGCTGCCC TGAGNAATCA 60  
AGGGGCCATT ACCAAGGGGC AGGAAAAGNA TATGTAAGAG GTGGCCTTCA TGGTAGAGCT 120  
TGACCCAAGA ACTACTCCAN ATTTCGGATGG CCCAGACTGG GNGCATCCCC TGACTTTCCC 180  
TTTGACTTCA CCCTGTTTGT AAATAAANCA AGGNAGATGC AAA 223

SEQ ID NO:7049

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08285

## SEQUENCE DESCRIPTION:

GATCTCCTCC CTNGTTTAAA TGCAATAAA TGCCCCAACT GCTTTGTAAG TGCAAA 56

SEQ ID NO:7050

SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08286

## SEQUENCE DESCRIPTION:

GATCACCTTA AAATTATTN ACGNACTGNA GNCAATNAAG TCCGTTATGT TTAGAGTAGA 60  
AAATGTTTAG GTTAAAGAGC ATCTGTCAAC AGAATCTACA AAAAAGN 107

SEQ ID NO:7051

# EP 0 679 716 A1

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08287

SEQUENCE DESCRIPTION:

GATCCAATTN CATNNGCGGC TGCATCTNCT GCTCATGCCG CCCAAACACC ACCCAGATGT 60  
CACTTACGTC AAGAAGGTCC GGACCCTCCG TATGCACCTG TTCACGGCCC TGCAGCTGCT 120  
NTGNN 125

SEQ ID NO:7052

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08288

SEQUENCE DESCRIPTION:

GATCCAAGAA ACGNANGACA CAACAACAAC GATGCCGTGT GTCTGCTCTA CCTGGGCAAG 60  
CTCAAGNACT CCCTGCGGCA GCTNGAGGCC ATGGTCCAGC AGGACCCAG GCACTACCTG 120  
CACGAGAGCG TGCTCTTCAA CCTGACCACC ATGTACGAGC TGGAGTCCTC ACGGNGCATG 180  
CAGAAGAAAC AGGCCCTGCT GGNGGCTGTC GNCGGCAAGG NGGGGGCCAG CTTTAACACA 240  
CAGTGCCTCA AGCTGGCCTA GCTGNNTNNN ACACAN 276

SEQ ID NO:7053

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08289

SEQUENCE DESCRIPTION:

GATCGAGTTT ACAGTTGTGN NNTCTTGAAG GTATTACTTA ACTTCACTAC AGCTTGTCTA 60  
GAAGACCTTT CTAGGNGTTA TCTGGTTCTA GAAGGGTCTA TACTTGTCTT TGTCTTTAAG 120  
CTATTGACA ACTCTACGNG TTGTAGNAAA CTGCTAATAA TACAAATNCT TGTTGTCCAT 180  
GGNAAGGCAA ATAAATTTNC TACAGTGNN 209

SEQ ID NO:7054

SEQUENCE LENGTH:126

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08290

SEQUENCE DESCRIPTION:

GATCTCATTT TCAGTTTAAG TAACTGCTGT TACTTAAGTG ATTACACTTT TGCTCAAATT 60  
GAAGCTTAAT GGAATTATNG CCCTCAGGAT AGTATTTTGT AAATAAAGNT GATTTAAATA 120  
TGNAAA 126

SEQ ID NO:7055

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08291

SEQUENCE DESCRIPTION:

5 GATCGCACCA TTGCACTCCC ACCTGGGCAA CAAAGAGTGA AACTTGGTCT CAGAAACGAA 60  
 AAAAAACACA AAAACCTTTC TNAGTCCCAG CATATGTGGA GCAGCCTCAT TCTTCATAGC 120  
 TGTGTGTCAT TCCGTTGCGT GATGGGGTCA CAGAGCACAG ACCTGGTGCC CTTTTCCTTT 180  
 TTAATATGTG GAAACCCCTC CATGCTTTCC AAAGCCTACA AGTACAGCAG CCCCNAGTTT 240  
 10 AGGGTGNGCA GCAGTGGTCA GAGCTCTTTN CTANTN 276

SEQ ID NO:7056

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08292

SEQUENCE DESCRIPTION:

GATCTCCAGG AGTCCCCTGC ACATACCTTC TCCATCGTGT CAGCTGTGTT TCTCTTGATT 60  
 20 CCGTGACACC CGGTTTATTA GTTCAAAAGT GTGACACCTT TTCTGGGCAA GGAACAGCCC 120  
 CTTTAAGGAG CAAATCACTT CTGNNNNAGT TATTATGGTA ATATGAGGCA ATCTGATTAG 180  
 CTTACAGAC TGAGTCTCCA CAACACCAAA ATATCCAGAT GTAAACCCCA AACTGTGTACA 240  
 CAAANGNAAG CACAGATTGT TTACCTGTTG TGGAGN 276

25 SEQ ID NO:7057

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS08293

SEQUENCE DESCRIPTION:

GATCCCTGTT ACCCAGAGAA TANNTACATT CTTTATCTTG ACATTCAAGG CATTTCTATC 60  
 ACATATTTGA TAGTTGGTGT TCAAAAAAAC ACTAGTTTGT TGCCAGCCGT GATGCTCAGG 120  
 35 CTTGAAATGC ATTATTNNGA ATGTGAAGTA AATACTGTAC CTTTAAA 167

SEQ ID NO:7058

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS08294

SEQUENCE DESCRIPTION:

GATCACATAC CCTTCTTTTA AGTGAATTTT TTTCATTTGA TTTGTCAATA AACGAATCAA 60  
 ACTGGNAAA 69

45 SEQ ID NO:7059

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS08295

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# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCTCCCTG CCTGGGCTGG CTGTGAGGCC ACCTTTGTCC CAGGCCCAGC CTCAAGGCAA 60  
 GGAGGGCGCT TCACTGAGGT GTGAATTGTA CGTACAGGCT TTTTATATAC CAAAAGTATT 120  
 TTTTGACTAG ACCATTCAAA GCTACCCGAA CTATGTTGGA AATTTTTTTT TTCTCATTAA 180  
 AATACAGGCC CTTAGGCTCT ATTTTAAATG TATNAGTCGC AN 222

SEQ ID NO:7060

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08296

## SEQUENCE DESCRIPTION:

GATCAAAATA CCTGTTTATA TATCTGTTAT TTAAAGAAAA ATTTTCCACA GTGTTTTGTT 60  
 ATTTTCCAGC GTTCTTAGN ACATTTGGGN ATTNCACTAA AATATAGCTG GGTGGATTGA 120  
 AGTAAAGGGC AANTGCGTTT GCAAA 145

SEQ ID NO:7061

SEQUENCE LENGTH:20

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08297

## SEQUENCE DESCRIPTION:

GATCTTCCAA AACACACAAA 20

SEQ ID NO:7062

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08298

## SEQUENCE DESCRIPTION:

GATCAATCAA GAATAATTTT AATTTTCTTT TGTATTTGAA ATGTAAATAG TTTTCTTTTC 60  
 GATTAAAAAA ATTTCTTATA ACTGCTAAAC AGTTAAANNC TTAAAGTAG TAAATGAGTT 120  
 TATAGAAAGC ATGTATTCTT GATTTTNGTG CCTTGGTAAA GTTGATAACT ATTTATGAAT 180  
 ATTTGACCAA ATTATTCCAG CATCAGAATA ATAAGCAAAA TAACCNN 227

SEQ ID NO:7063

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08299

## SEQUENCE DESCRIPTION:

GATCACACCA CTGCATGCCA GCCTGGGCGA CAGAGTGAGA CCCTGTCTCA GAAAAGAAAA 60  
 AAAAAAGTAAA AATTGCATGT AAGTTGACCC GCACTATTCA AATTTGTGGT GTTCAAGGTT 120  
 CAACTGTAAT TTCTAGCAG CATTTTGTGT GTTTGAGAAT CTCTTGACAC TCTTCAAGTA 180  
 AATCCCTAAA TTACAACTTT GACATCAAA 209

EP 0 679 716 A1

SEQ ID NO:7064

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08300

SEQUENCE DESCRIPTION:

GATCGACTGA GCTCAAATTT CAGTTGGGGC CCTATTAGTC TGCCTTTCCA AAAAGGGCGT 60  
TGGGACTTTA ATTTAAACT TAACCAGTTG AAAAATAAAG GTGGCGTGGA AATGCTTTTT 120  
GATTTGCAAA 130

SEQ ID NO:7065

SEQUENCE LENGTH:223

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08301

SEQUENCE DESCRIPTION:

GATCTGGGCT TTAAAGCAGA GGCCATGTCC TTGTCTGGTC CTGCTTNTGG CTACAGCCAC 60  
CCTGGAACGG AGAAGGCAGC TGACGGGGAT TGCCTTCCTC AGCCGCAGCA GCACCTGGGG 120  
CTCCAGCTGC TGGAATCCTA CCATCCCAGG AGGCAGGNAC AGCCAGGNNG AGGGGAGGAG 180  
TGGGCAGTGA AGATGAAGCC CCATGCTCAG TCCCCTCCNA TNN 223

SEQ ID NO:7066

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08302

SEQUENCE DESCRIPTION:

GATCGGAGAC ATCTGCTGT TCGGNACGTT GCTGATGAAT GCCGNGGCGG TGCTGAACTT 60  
TAAGCTGAAA AAGAAGGACA CGCAGGGCTT TGGGGAGGAG TCCAGGGAGC CCAGCACAGG 120  
TGACAACATC CGGGAATTCT TGCTGAGCCT CAGATACTTT CGAATCTTCA TCGCCCTGTG 180  
GNACATCTTC ATGATGTTCT NCATGATTGT NCTGTTCGGC TCTTGAATCC CAGCGATGAA 240  
ACCAGGAACT CACTTTCCAN 260

SEQ ID NO:7067

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08303

SEQUENCE DESCRIPTION:

GATCGAAAGA AGNACATCAT GAAAAATAAA TGAACCTTGC TTAGTGGATT GACTCCTTTG 60  
CTGAAGTCAG TTATTCATCA AGAATGCAAT TAGNCTAATT GTGAATAAAT GATTGNNTGA 120  
AGNTATAATA AATAAAACCG TAAACTCTGG CAAA 154

SEQ ID NO:7068

EP 0 679 716 A1

SEQUENCE LENGTH:29  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
5 CLONE:HUMGS08304  
SEQUENCE DESCRIPTION:  
GATCAATAAA ATGTGATTTT NCTGATAAA 29

10 SEQ ID NO:7069  
SEQUENCE LENGTH:74  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08305  
15 SEQUENCE DESCRIPTION:  
GATCGTCCCA TCACAGTGTT GTTAATGTTT GCTGTATTTA TTAATTNCT TAAAGTGAAA 60  
TCTGAAAAAT GAAA 74

20 SEQ ID NO:7070  
SEQUENCE LENGTH:264  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08306  
25 SEQUENCE DESCRIPTION:  
GATCTGGCTT CACAGACAGT TGACACATCT AAAAGAATCT TTGTTTCAA CTGGACTGAC 60  
TCATTGAGAG GAAACCTTCA CTGCACCTCA CCAGTGCAGA CAGAAGACCT GGAGGCAGGA 120  
CGGGAGGCAT TTTATACTTC AGCACGATAT GGGCCCTGAC TTTTCATTTT CTACATGGAG 180  
ACATATTGCT GGAGGCTCAT CATCCTGAGG GGAGAAACAT GGATTCATG GTTTGGCCAT 240  
30 AAAAGTATGC AACAAAGAGT TCCN 264

35 SEQ ID NO:7071  
SEQUENCE LENGTH:27  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08307  
SEQUENCE DESCRIPTION:  
40 GATCANTAAA AAAAATAAAT AATTAAA 27

45 SEQ ID NO:7072  
SEQUENCE LENGTH:175  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08308  
SEQUENCE DESCRIPTION:  
GATCTNTTTT NTCTGGAGTC CTGGAGTTNC TTCCTAAGG TTAAATATAA GCAAGCNCCA 60  
50 GAAAGAAATGC TGACAGAAAA GGGACCCTAG CTGTGGTAGG AAGTGGCCCT CAGAGTCAAG 120  
GAGGCAGGAT GANTTTAAAT NCTNCATGTA GGGCATATTT TGGGGAGTNA TGGGN 175

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SEQ ID NO:7073  
SEQUENCE LENGTH:281  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08309  
SEQUENCE DESCRIPTION:  
GATCGACTTT AAGTTGCTTC GGGTCTAGTA GAAATCCGGT TATTTCCAAG CCTGTNAAAT 60  
GTGAAGTTCA AGAAAATTGA ATCCGTGTAT AGCAAAACCA TTTTNTCTCA CAATTTTSTA 120  
ACCAATGAAC ATTGTGTGGG AAATTNATTC CATATGTTTT CAAGTCATTT ATGCAACTTG 180  
AATAATTAAA ATATTCATTG GTAAGAGCTG CCTGATGTCT TTAAAGTCAG GAAATTGTCT 240  
TATGCCAAAA GTAGACAANC TCAAAACACCA AAAGGTCANN N 281

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SEQ ID NO:7074  
SEQUENCE LENGTH:106  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08310  
SEQUENCE DESCRIPTION:  
GATCATTTTT CTTGGAGGNT GGAGATTGGC TAGTACCTCT GGCCTAACTG TGTAGGTCAA 60  
TACTCTTTTA CATTGCCTTC TAATAAAAGC AGNATGATNC AGCAA 106

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SEQ ID NO:7075  
SEQUENCE LENGTH:69  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08311  
SEQUENCE DESCRIPTION:  
GATCTTGTGT CTGTTGTGCC TGAATTTGGC GTGTCTAATA AAGGCCCATG CACACTATAG 60  
GCACTCAA 69

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SEQ ID NO:7076  
SEQUENCE LENGTH:292  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08312  
SEQUENCE DESCRIPTION:  
GATCAGTGAA ATNTTAAACT CCCACGGTAA CATCATGCCT ATGGACATTA AAGGAATAGC 60  
AAGGACTTGC TCCCACGACT TCACATTTGC TCCCACTGGC CAGGAATGTG GGCTCTTAGT 120  
GATTCCAGAT AAGGGCAAAG CTGGGGCCCA ATGTATGTAG CCAAATTGNA GNAATCATGG 180  
NGCACAGGCA AATGGTGACA TGAATTTGTA ANCTGTGTTT ATGTGTTNTT ATATTTATAT 240  
TTCTGANCTC AGTACATGTT AATATTTAAN TAATTATGCA GTAACTTTCA AA 292

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SEQ ID NO:7077  
SEQUENCE LENGTH:29

SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08313  
SEQUENCE DESCRIPTION:  
GATCCTGCAC TCTAGCACAT GACTCCAAA

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SEQ ID NO:7078  
SEQUENCE LENGTH:334  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08314  
SEQUENCE DESCRIPTION:

GATCCCCTGT CCCCTGGGGC TGGTGGATAG GGCAGAATCC TGGGCCCCCA GAGACCTTTG 60  
CCCACACACA CTCCTCCCC TTGTCCCTGG GGNACTCCCC CAGGATTGTG CAATAGTCAG 120  
AGTGTCCCTT TTTGCAGGGG ACTGGGCCAT GGGTCCTAGG CCCATCTGTC CATCCTCCTC 180  
TCCATGCAAG TGCTGTTTGG GCAGNAGTCA CCATGCAAGG GTGNCATCGN CANCCACGTA 240  
CCAAGNCACC GCAGCTGCTG CCACTCTGCT GCCTGTACAG AAGGAANCTG NATCTTTTNN 300  
ATATTCTAAT AAAATNACTG TGGGNTTNA NAAA 334

SEQ ID NO:7079  
SEQUENCE LENGTH:245  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08315  
SEQUENCE DESCRIPTION:

GATCCCGTAA ATTGAAGGCA ACAAGGTCTT GGTCTNCAG TAAGGGGGGC ATGGAGCCCT 60  
GGTGGGAAGG AAAGAAGNGA AATTTGTGTT CCTGATTCCT TAATCCCCAN GAAAGGTCCC 120  
TCTGCTAACA TTCACATATC TTTTCTAGC CAAAGTCTGT CCATTTNAAC CCTNTAGCAT 180  
CTGAGCTATC TGCATCCAGN TTTCAAANAT ATTTGNTGT TTACTAACAT GTNTGTNAGC 240  
CTNTN 245

SEQ ID NO:7080  
SEQUENCE LENGTH:88  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08316  
SEQUENCE DESCRIPTION:

GATCACAAAT NACTTGTTGA AATGTAAGGC AGTCCCCCTC CTCCTCTTTA TCTACATTAC 60  
TTCCCGAAAA TAAATGCANA TTAATAAA 88

SEQ ID NO:7081  
SEQUENCE LENGTH:149  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08317



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## SEQUENCE DESCRIPTION:

GATCAGGTCA CAGTGTGTAC GTAAGAGTCA GCTNCTTATG GNTATTGTCA TCTAGGTAAC 60  
 TTTGTAAAAA AACAAACAAA ACTGGCATTG TTAATTCCAA AAAGAAAAAA AAAAGCAGTA 120  
 AAAANAAANG GNCATTTGNA CCNCCGGCN 149

SEQ ID NO:7082

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08318

## SEQUENCE DESCRIPTION:

GATCTCAGCC TCGGGTGGTC AGGGTGGGAA ATGATAGGAA GAAGCTGTCA TCTGCATCCT 60  
 AGTTTGCCTG AAATGAACCC AAATAATACC CATTATTATT AGTCCTGAAT TATGAGTAGT 120  
 GAATGATACC CATCATCTG GCATCATGAT GAGTAGTGTC CACTTCCATT CTGAAAAGTG 180  
 CCCTGCTGTG AAAAATAAAT TATATAGTCC TCCTAGGTAA ATGAAGGAGG AGGGAGAAGT 240  
 GTGAAAGAGT ATGGCTTAAA TCAGACAAGA TATACAAGAA GATACTTTAT ATAGGGCAGG 300  
 AGCGGTGGCT TN 312

SEQ ID NO:7083

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08319

## SEQUENCE DESCRIPTION:

GATCTGGGAA ACTGATTGAA TAATACACTT TTCTTGCTTT GGTGCTCAA GTGGTTTTTT 60  
 TCCCCAATA AAATTATTTA ATTGAAA 87

SEQ ID NO:7084

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08320

## SEQUENCE DESCRIPTION:

GATCAGGAAA TGCATCTNCG CAGATGGTAT TTCCTTCAGA AAAGACTTTN CTACTTTAAA 60  
 TATAAATNAN GCCATAACAG TTTCATGCTG TGGAAAGAGG GTGAAAAGGT TCATTTTAAG 120  
 AGATTATATA ATANGACCTT NCACATTTCC TGTGAAATGT CTAACCTTNC CAGTNCTTCA 180  
 GCAAGTTTTT TTGGGGGGTG ATGGGGGAGN GGTAGTATTG GTTTTAGAGG TTTCAAATCT 240  
 GTGANCTTTG GAGAGGGGAC AGTTGTTGGC TCTGGTATTT CCTAGTTTTG TAGTAACGTT 300  
 TTGCTAGCCN NN 312

SEQ ID NO:7085

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08321

## SEQUENCE DESCRIPTION:

5 GATCTGATGG TTTTAAAAAG GGGTGTCTCC CTGCACAAAC TCATTCTCTG TTGCCTACC 60  
 GCCATCCGCT TAAGATGTGA CCTGCTCCTC CTTGCCTTCC GCCGCGATTG TNAGGCCTCC 120  
 TCAGCTATGT GGAAGTGTAA ATCGAATTAA ACCTCTTTCT TTTGTAAA 168

SEQ ID NO:7086

SEQUENCE LENGTH:146

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08322

## SEQUENCE DESCRIPTION:

15 GATCCATGTG TTTTACTCTA AAGTGCTAAA TATGGGAGTT TCCTTTTTTT ACTCTTTGTC 60  
 ACTGATGACA CAACAGAAAA GAAACTGTAG ACCTTGGGAC AATCAACATT TAAATAAACT 120  
 TTATAATTAT TTTTCAAAC TTAAAA 146

SEQ ID NO:7087

SEQUENCE LENGTH:314

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08323

## SEQUENCE DESCRIPTION:

25 GATCAATAAA GCTGTCTAC ACTTGTGCTA GGNAGGCACC GCTGTGACTG GGCTCCGGGC 60  
 CTTTCCACTA CGTTGAAGAA GAAAACCTAT TTTTAAATGT AAATAAAATA TCTGGTAGCC 120  
 TGTGTGGAAA GCTGACCGTT TTAAGAAGTG GCATGTGCCT TGAAAGGGGG CAGAATGTTC 180  
 AGTCGGTCGT GTTTTAAACA CAGAGTCTCT AGAAGAGGTG CAGACATCCC GTCTGACTGT 240  
 CCCTGTGGAC TCTCTCAGTT GTATGTTGCT ATAATCCTCC AAATCAAAGC TCTTCTGCT 300  
 30 TGTGCAAGAT TNNN 314

SEQ ID NO:7088

SEQUENCE LENGTH:71

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08324

## SEQUENCE DESCRIPTION:

40 GATCTTACTG AATTTATTTT GTAAATGCCT AATGAGGCAG ATTTTGAAT TAAAGAAATG 60  
 CTACATGTAA A 71

SEQ ID NO:7089

SEQUENCE LENGTH:412

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08325

## SEQUENCE DESCRIPTION:

50 GATCCTAACA TATCAGGACA TGGACTCAGG ACCTGCCCCG TGATGCTGTT GATTCTCAA 60  
 AGGTCTTCCA AAATCAACA GAGCCAGAAG TAGCCGCCG CTCAGCGGCT CAGGTGCCAG 120

55

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CTCTGTTCTG ATTCAACCAGG GGTCCGTCAG TAGTCATTGC CACCCGCGGG GCACCTCCCT 180  
GGCCACACGC CTGTTCCAG CAAGTGCTGA AACTCACTAG ACCGTCTGCC TGTTCGAAA 240  
TGGGGAAAGC GTGCGTGCGC GTTATTTATT TAAGTGCGCC TGTGTGCGCG GGTGTGGGAG 300  
CACACTTTGC AAAGCCACAG CGTTTCTGGT TTTGGGTGTA CAGTCTTTGT GTGCCTGGCG 360  
AGAAGAATAT TTTCTATTTN TTTTAAGTCA TTTATGGTT TCCTGGTCCT GN 412

SEQ ID NO:7090

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08326

SEQUENCE DESCRIPTION:

GATCTATTTT TGGCTTATGT CTTTAAATAC TACTCTCTTT CTCTGAATTT TGAAATATGA 60  
AGTAAATCT AGCCCATTTG TTTTATGCAA A 91

SEQ ID NO:7091

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08327

SEQUENCE DESCRIPTION:

GATCTCAAGA GTTCAAGACC AGCCTGGGCA ATATGGTGAA ACCCGTTTGT ATTAAAAATA 60  
CAAAAATTAG CTGTGCATGG TGGCCACGG CTGTAATCCC AGCTACTCAG GAAGCTGAGG 120  
TCCGAGAATC ACTTGAATGC TTGAACTCGG GAGGCAGAAG TTGCTGTGAG CCGAGATGGC 180  
ATCACTGCGC TCCAGCCTGG GCAACAGAGA GAGACTGTCT CCACTGTCTC CAAAAAATA 240  
NGAAAAAATA AAGGTTGTTN GATTCTGTC CCTCAAGGAA ATTNTGGAAA ANAN 294

SEQ ID NO:7092

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08328

SEQUENCE DESCRIPTION:

GATCATGTTT TGAAGCAGCA GGTCCAGGTC ACTTTGTATA TAGAATTTTG CTGTATTCAA 60  
TAAATCTGTT TGGAGGAAA 79

SEQ ID NO:7093

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08329

SEQUENCE DESCRIPTION:

GATCTTTCCC TAGAGAATGT AACATACGTT TTTATTCATT TAATCACTTC ATTATGCCGG 60  
GGTTAATNAT GTTTATTTTA TAATTGGTAA TAAAGGCCAC ATTTATTTT GTAACGTGTA 120  
AA 122

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SEQ ID NO:7094

SEQUENCE LENGTH:50

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08330

SEQUENCE DESCRIPTION:

GATCTTAAAC TCTTTGATTA AAAATAATAA ATGGAAATGT GTTAAGCAAA

50

SEQ ID NO:7095

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08331

SEQUENCE DESCRIPTION:

GATCCAGGGA TTGGGGAAA AGGAAGGAAT TTGATGTTTT TTGGGGTGGG AGGGGAGGGT

60

GTGTTTTTTT CACCAA

77

SEQ ID NO:7096

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08332

SEQUENCE DESCRIPTION:

GATCGCTGGC CTTCTGACT TAACATTNAT GCATGCCAAG GTGTTGATGT TCCCAGCCAC

60

GTTAACACCT TCCACAAGNT CTCAAGAAAA AGCAGACGGA TAACTGATGT GAATTGGACA

120

GTTTCTATTG CTTTTCTTT TTTCCATCCC TTCCCTACCA TCAAAAGCAT ACCTGCTCTA

180

ATTAAA

186

SEQ ID NO:7097

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08333

SEQUENCE DESCRIPTION:

GATCATATAC TCTGCTGTGG TCATGCCAC TCTTTGGGAG TATATCCCT TTATATATAT

60

TGAGTATTGT ACCACTTGAG AAATTCCTTT GTTCTGTTAT ACAAATTA TCTTTCTGCT

120

CATAATGATT GATGATACCA CCAGTAAAA TAGGATGTTT ACCCAAAC AAGTGTCAAT

180

TAAGAATTG AACACAACCA CATTTTTTAA AATGAACTT CTATCGGAAG TAAATTAATT

240

TGNGGTAATA AAGTCCAGTA TTNGGNAAA TGTACAATGT TAAATCTCAA A

291

SEQ ID NO:7098

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS08334

SEQUENCE DESCRIPTION:

GATCAGACTT TTGTNTCTTG GGTCCCAGAT GGCACAGGAG CACTGCATGC TTGTTTTCTA 60  
 GAGCCCAGCC AGTCATGGGT GCTAGCCTAG TCTCCACACA CCAGCAAGTA GAACCCAAGT 120  
 GTANNNNNAT AAATATTTCC TGAGTACCAG TAAGAGAATG CATTCTTTTC TCATCTAGGC 180  
 CAGGAATGTT GAAAATGCTC AGCCTTACAT AGAAACTCCT AGATTTTCAC TAACGCATTT 240  
 CACAAAAGTA AATAAGTATT TCATATAATT CAGAGGATGT TTAAATTGTC AGCATTTTAA 300  
 TAAATAN 307

SEQ ID NO:7099

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08335

SEQUENCE DESCRIPTION:

GATCTGTACT TTGAACAAAG AAAGTGTGTA GAGACCCCTG GGAGTGAGGG GTAGGGGATA 60  
 CAATACTCTG AAGCAGAAGA GGACCCTTGC AGTGATGGTT AGGGACTCTT CTGAGTAGGA 120  
 GACGTAATCG GCTTTTGGTC CATGGAACCTT TTACCACATG TATTCAGCAT ATATACACGA 180  
 TTAAAGTGCT GCAAATAAA 199

SEQ ID NO:7100

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08336

SEQUENCE DESCRIPTION:

GATCTGGGAG TGGCTTCCTA ACGGAAATGG AACAGGATTA CCAACTAGTN GACGAAAGTA 60  
 ATGCTTTCCA TGACAACCTT AGGTCTCTTG ACAGNAATCT GCCCTCAGAC AGCCAGGACT 120  
 TGGGTCAACA TGGATTAGAA GAGGATTNA TGTATAAAA GAGGATTTTC CCACCTTGAC 180  
 ACCAGGCAAT GTAGTTAGCA TATTTANNGT ACCATGGTTA TATGATTAAT CTTGGGACAA 240  
 AGAATTTNAT AGAAATTTTT AAACATCTGA AAAAGAAGCT TAAGTTTTAT CATCCTN 297

SEQ ID NO:7101

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08337

SEQUENCE DESCRIPTION:

GATCTTTGTC TGTGAAGAAG AAAATTATCT CCCTAGTTCA ATCTGTAGTG AAATAAGGCT 60  
 ACAGAAGGCA TTGTTTTTTC CTTTTTNATT TTTTGATTA TATATTTNCC TTAAATATGT 120  
 TTTATTGTCT TCTCTANGCA AAAAGTTCTT AATAANCATA GTATTTCTCT CTGCGTCCTA 180  
 TTTCATTAGT GAAGACATAG TTCACCTAAA ATGGCATCCT GCTCTGAATC TAGNCTTTTT 240  
 AGAAATGGCA TATGGTTTTG ATGATATGNC CACCATCCAA AATGTCCGAN TNAATN 296

SEQ ID NO:7102

# EP 0 679 716 A1

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08338

SEQUENCE DESCRIPTION:

GATCAACTTT AAGAAGATTT AAAAAACGCT CAAGAAAGAN GAGGATATCC NACTNTTCCC 60  
CGTGCAGACA AAATACATGG ATGTGGTCAA NGAGTGAATC CGTTTAGCTC GACAGATTGA 120  
GAAATCTGAG TATCGGAACT TCCAGGCTTG CCTNCACAAC TCTTGGATTG AGCAGGCAGC 180  
AGCTGCCCTG GAGATTGAGC TGGAAGANGA CATGTATAAG GNAGGAAAAG CTNNCCAGCA 240  
AGAAGAACGT CGGNGACAAA AGCAGATGGN GGTCTNGAA GAAGGAGCTG CGNCNCCTGC 300  
TTNTN 305

SEQ ID NO:7103

SEQUENCE LENGTH:414

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08339

SEQUENCE DESCRIPTION:

GATCCACAAG TCCTTGTTCC ACTGTGCCTT GGTTCCTCCT TTATTTCTAA GTGGAAAAAG 60  
TATTAGCCAC CATCTNACCT CACAGTGATG TTGTGAGGAC ATGTGGAAGC ACTTTAAGTT 120  
TTTTCATCAT AACATAAATN ATTTTCAAGT GTAACCTATT AACCTATTTA TTATTTATGT 180  
ATTTATTTAA GCATCAAATA TTTGTGCAAG AATTTGGAAA AATAGANGAT GAATCATTGA 240  
TTGANTAGTT ATAAAGATGT TATAGTAAAT TNATTTTATT TTAGATATTA AATGATGTTT 300  
TATTAGGATA AATTTCAATC AGGGTTTTTN GGATTAANCA ACCANCCAAT TGGGTCCCCA 360  
GTTAANTTTC CATTTCAGAT ANCCACCANN TAGTTTCNNN GTNTAGGTCC ATTN 414

SEQ ID NO:7104

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08340

SEQUENCE DESCRIPTION:

GATCCCCTGA CTGGCTGGGG GCAGCTCCCA GGATATCCTG CCTTCCAACCT GTTCTGAAG 60  
CGCTCCTCC TAACATGGCG ATTCCGGAGG TCAAGNNCNT GGGCTCTCCC CAGGGTCTAA 120  
CGGTTAAGGT GACCACATAC CAGTGCCAAG GGGNTNTAA AGTGGTGATG TAGTTNTGCT 180  
CCCCTCCCCA AGAGCGGGTG GNGGGGGGTT NAANATGTTT GGCCTGNNTA AGTGGGCCTT 240  
CCCATTNAAG TN 252

SEQ ID NO:7105

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08341

SEQUENCE DESCRIPTION:

GATCTTATTT TTTAATTTTA AGTGCCACTA TTAATGTAAA AAGGGGGGGG CTCTACAGCA 60

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GTCGTGATGA AACTTAAATA TATATCCTTT GTCCTCGAGA TTTTAGGAAG GGTGTAGGGT 120  
 GAGTAGGCCA TTTTNAATTN CTGAAGTGCT AAGTGTTTTT ATACAGCAA CAAAAAGTCA 180  
 ATTTTCCTTT CCACCAGTGC GAGAGAGGAT GTATACTTN CAAGAGAGAT GATTGCCTAT 240  
 TTNCCGTTTG ACAGAGTCCC GTAGATGAGC AATGGGGAAC TGGTTGCCAG GGTCTAANTT 300  
 TGGATTGATT TATGCACN 318

SEQ ID NO:7106  
 SEQUENCE LENGTH:299  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08342

SEQUENCE DESCRIPTION:  
 GATCTGTGAC CCCAGCCATG AGGACCCTCG CCATCCTTGC TGCCATTCTC CTGGTGGCCC 60  
 TGCAGGCCCA GGCTGAGCCA CTCCAGGCAA GAGCTGATGA GGTGCTGCA GCCCGGAGC 120  
 AGATTGCAGC GGACATCCCA GAAGTGGTTG TTTCCCTTGC ATGGGACGAA AGCTTGGCTC 180  
 CAAAGCATCC AGGCTCAAGG AAAACATGG CCTGCTATTG CAGAATACCA GCGTGCATTG 240  
 CAGGAGAACG TCGCTATGGA ACCTGCATCT ACCAGGGAAG ACTCTGGGCA TTCTGCTTN 299

SEQ ID NO:7107  
 SEQUENCE LENGTH:302  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08343

SEQUENCE DESCRIPTION:  
 GATCTTAGAG GTTGAAGCCC ACCTTCTCTT TTCACATAGG AGGGAACAGA CCATGGAAAT 60  
 TTAAACGACT TCCTCAGGCT CACAGAACTA GTTTTTTAAT CCTCAGGCAG TGNATCCCCC 120  
 CACCCTACAA CTGTGCACAA CCTCTTTCCC CACAGTGCAA TTCAGAATAT GCTCAGGGAA 180  
 TGCCAGGCAC CTGTGAAAAC TGCTGGGAGA AAAGCATGNT TCCACAAGG ACTAAGTATC 240  
 AGTGATTGT AATTTTCTG TTTTGTATTA TCTGCTTGC TGATGTAGAC AAGAGTTAAC 300  
 TN 302

SEQ ID NO:7108  
 SEQUENCE LENGTH:110  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08344

SEQUENCE DESCRIPTION:  
 GATCNAACTG TCTCACTGCT TTTCCAATA TAATCATNTC GCTCTNACTT TAACAAAAGG 60  
 CGATGGCACA GTAATTTAGT AAATTTNTGT AATAACATNT AAAAAAAGN 110

SEQ ID NO:7109  
 SEQUENCE LENGTH:121  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08345

## SEQUENCE DESCRIPTION:

GATCCTGTCT AAAAAAGAAA AGAAAAGAAA AGAAAAGAAA AGAAAATCAG CATTGTATCC 60  
CCAGAACCTG CTACAGTGTA CTGTACACTT AATAAATATT GGTGGAATGA ATGAACTGAA 120  
A 121

SEQ ID NO:7110

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08346

## SEQUENCE DESCRIPTION:

GATCATCAGT AAATTTGTCA TGTTATATAT TTATTTTTTT ATAAATCAAG ACTTCTGTGT 60  
GCTCTTAAAT ATATTAAAA CAATTTACAT TTCAGGAAA 99

SEQ ID NO:7111

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08347

## SEQUENCE DESCRIPTION:

GATCCCAGNA GGAGGGAAGA AAATTTGCAG TGACTGAAAA CAGTAAAAAA AAAAAAATA 60  
ATGTATAAAA AAGTTGCATT ACACAGTNCA AA 92

SEQ ID NO:7112

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08348

## SEQUENCE DESCRIPTION:

GATCATTCTN GTTGATACCC TTCTTTGAAT ATTCTAGTGT ATTAATATAC CATTGGTTAT 60  
TNAATCATGT CTNATTAATG GACTGGCTGT TTTCACATAT TNGATATATC AAGTGTCTTC 120  
ACAACTTGTG CTTGCATATT CTTTCCCAA ATATTGAAAG TCCATATATT TCCTTGATCA 180  
TNTTTAAAGT TGATATCTNA ATNTNTCATT GTAGTNGCAA AGCATGTAAT TNCTTGGGGG 240  
AGGGGGGCTG TAAATATTGA CATTTTAAAA TAAACTTTT AAATCAGCCT TAAATGTATC 300  
AGGN 304

SEQ ID NO:7113

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08349

## SEQUENCE DESCRIPTION:

GATCAAATTT CAGTCGTCT TCTGTATACT GTGGAGGTAC ACTCTNTAG AAAGTNCAAA 60  
AAGTCTACGC TCTNCTTCT TTCTAACTCC AGTGAAGTAA TGGGGTCCTG CTCAAGTTGA 120  
AAGAGTCCTA TTTGCACTGT AGCCTCGCCG TCTGTGAATT GGACCATCCT ATTTAACTGG 180



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CTTCAGCCTC CCNACCTTCT TCAGCCACCT CTCTTTTCA GTTGGCTGAC TTCCACACCT 240  
AGCATCTCAT GAGTGCCAAG CAAAAGGAGA GAAGAGAGAA ATAGCCTGCG CTGTTTTTTT 300  
AGTTTGNNN 309

SEQ ID NO:7114  
SEQUENCE LENGTH:282  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08350

SEQUENCE DESCRIPTION:  
GATCTTCCCC AGCTATGAAG CCTATCTTGG AATGGGAAAC CATGAAATTT GTCTTTTAAA 60  
AGAAAGGGAA GAAATAGCCT TACAGCCCCT GTTCCTCCAA GTGCACATTT AGCCTTAAAA 120  
TCCTGGGAGT CGGGAGACAC CGTGGAGTCC TTACATCCAC AGTGTCTGCT GGTCTGTGGTC 180  
AGAAGGCAGT AATGCAAGAG TCCTTTTGTG AAGAGTGTTC CTATGTAGAG ATGTTTATAT 240  
TTAAGTAGTT CTTTATAAAA TAAAAGCATT TCTAATGGCA AA 282

SEQ ID NO:7115  
SEQUENCE LENGTH:27  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08351  
SEQUENCE DESCRIPTION:  
GATCTGTTTT CTGTAACTTT TGCTAAA 27

SEQ ID NO:7116  
SEQUENCE LENGTH:251  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08352  
SEQUENCE DESCRIPTION:  
GATCTTAGGC TTCAGCTCTT TATCTTACAC CTTGAGACCC CAAGAGAGTC CCAAATTCCT 60  
GGAAAGGCAG CATCACAGAG TGGGGAAATA CAGGACTTGG CTTAGGTTC TAGTCCTTAA 120  
CACAGCTTCT TCCTTGCTGT GTGTTCTTTG GTAGGTCACT AAATCTCTCT GAGCCTCAAA 180  
TTTCTTATCT CTAGGTTGAA AAATAAAATA AAGTCCCCAT GCCAATCAGT GCAAGGAATC 240  
TGTGAGATAA A 251

SEQ ID NO:7117  
SEQUENCE LENGTH:123  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08353  
SEQUENCE DESCRIPTION:  
GATCACGCCA CGGCACTCCA CCCTGGGCGA CAGAGCGAGA CCTTGTCTCA GAAAAATCT 60  
GTGAGGTAA AAGGCTGTGT GTGTGAAAT ATCTTGGAAA TTGTAAAGAA CTACACAANT 120  
AAA 123

SEQ ID NO:7118  
SEQUENCE LENGTH:295  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08354

## SEQUENCE DESCRIPTION:

GATCATT CAT CAACATGTGT CTCTNAATTT AATTCAGTAG TTGTAATTAT TCTTTGGTTT 60  
AGACCAAGAA AAAGGAAATC CCCCTTTNA ATGTATTCTT TGGTTTNAGG ACATGACTCC 120  
TGTAAGGNAG AGGAAAGGGA GATGCTTCCT GTTTGANCTG CAGTGAATTC ACGGTTCTCTG 180  
TTTCACTACT CCAAACCTTA TGGCGACTCA CACACACATT CCTCTTNTCT GTTACTGCCA 240  
AAGGTTCTGGG TTTAGTACAC TTCAGTTCCA CTCAAGCATT GAAAAGGTTC TCGTN 295

SEQ ID NO:7119  
SEQUENCE LENGTH:203  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08355

## SEQUENCE DESCRIPTION:

GATCCCCAGG ATGCCCACTT CCCTCCACCC CCACACCCCA GCCGTGTCCC TAACCCCTGG 60  
CAACCAGGAA TCCACTCTCC ATTTCTATAA TGTTGNNATT TCAAGAATGT TATTCAATGG 120  
AATCATATAG TATGTAACCT GTTTTGAGCT TAAAAAATAA GTATACATGA CTTTAATGAG 180  
GAAANTAAAA NTGGATATTG AAA 203

SEQ ID NO:7120  
SEQUENCE LENGTH:82  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08356

## SEQUENCE DESCRIPTION:

GATCCGTTAG TGTCTGTTTA GAAAAGATGT TATAAACTTA CAGAAACAAA TATAATAAAC 60  
TGAAGCAGAT TTGAAAAGCA AA 82

SEQ ID NO:7121  
SEQUENCE LENGTH:79  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08357

## SEQUENCE DESCRIPTION:

GATCTTTTGC ATTGCAGAGA TTTTATATAT ATTTTGTTTG TAATGAGCCA TTCTCAATAA 60  
ACATTATTCT CACTGCAAA 79

SEQ ID NO:7122  
SEQUENCE LENGTH:299  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08358

SEQUENCE DESCRIPTION:

5 GATCCCTAGT AACTCCTTC TTCACITTTTA CTGTCAGATT TACAAAGGTC CTCCCATTGC 60  
AAAGCAGTGN NNNTCCTAAT TTATATATTG TTTTNCCTAGT TCATTTTGTG TTTCCAACCT 120  
TTCATGTAAA ATTTTAATTA TTTTGAATG TGTGGATGTG AGACTGAGGT GCCTTTTGGT 180  
ACTGAAATNC TTTTCCATG TACCTGAAGT GTTACTTTTG TGATATAGGA AATCCTTGTA 240  
10 TATATACTTN ATTGGTCCCT AGGCTTCCTA TTTNGTNACC TTGCTTNNNN NGTGGCANN 299

SEQ ID NO:7123

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08359

SEQUENCE DESCRIPTION:

GATCATGTGC CAAGGCTGCG GTGCGTTCTG TCACGATGAC TGTATTGGAC CCTCAAAGCT 60  
20 CTGTGTATTG TNCCTTGTGG TGAGATAATA AATTATGGCC ATGGGAAA 108

SEQ ID NO:7124

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS08360

SEQUENCE DESCRIPTION:

GATCAGACTG TGCTTTCTAA TTCTAAAAAA TTGAGCAGTG TTGGTATTCT TNCAGTATTT 60  
30 TTNCTCTCAC CTGGAAAACCT ACCTGGAAGT TGTCAGGCAT TTNCTTACTG NNN 113

SEQ ID NO:7125

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS08361

SEQUENCE DESCRIPTION:

GATCTCTAAG TAATTNTNCA AAATCCGGTA TTACTATGTC AAGTTATTGC TTTTGGTAAA 60  
40 TTCATCTGAC CCAGTTATAA ATGAAAGANT ATGGANTTAA AAATTTTAAA NCTAAATAAT 120  
TTGNN 125

SEQ ID NO:7126

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS08362

SEQUENCE DESCRIPTION:

GATCATGCTC CATCCAGCCC CACCCAATGG CCTTTTGTGC TTGTTTCCTA TAACTTCAGT 60  
50 ATTGTAAACT AGTTTTTGGT TTGCAGTTTT TGTTGTTGTT TATAGACACT CTTGGGTGTA 120

55

AA

122

5

SEQ ID NO:7127  
 SEQUENCE LENGTH:256  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08363

10

SEQUENCE DESCRIPTION:

15

GATCGGCACT CACGATTGTN ATGTTGGCTA CATCCTTGAC AAAGCCGATG GCCTTTCCAG 60  
 GTTGGAACCT GCAATAACCA TCCTGTTGAG GATGCAAAGG GCATGAAATA CAGGTTATGG 120  
 ACCCGAAGTC TCAGCCTCCC CACGCAGTTC AATAACATTT ACTAAACAAA ACAAGATGTG 180  
 CCAGGGCCTG GGGGATGGGA TAATTCAGA GAGAATTAAA GCATCCTTGT CCTCAAGGAG 240  
 CTTAGGGTCT GGTAAA 256

20

SEQ ID NO:7128  
 SEQUENCE LENGTH:346  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08364

25

SEQUENCE DESCRIPTION:

30

GATCAACAGG GGTGAAAAGA ACCACCCTGA GGTTCATG CCTCTCCAN NTTAGTGGT 60  
 AGNATTTTGT GTCTTTACTC CACCCTTCAC CTTAGTTCCA CCAAGGTCA CACACCAGAT 120  
 GTAACGTGTT TNAGCTGAG TTGTATGGAT TAACTTCAGT CCACTGTAAA TACACCTGGG 180  
 ATGGGGTGGG GTTGGGGTTG TTTAGGGAGA AGCAGCCAGA CTTGCTTTGT GAACTGAATG 240  
 TATTTTATG CAATTTTGA TGGCCTTTCA ACCCTAAGAT GAATGGTTT GTTTTACTGG 300  
 TTGTTGTTAT ATAGTTTGA GTATTCTGTG TTTGAAAGTT TGGGTN 346

35

SEQ ID NO:7129  
 SEQUENCE LENGTH:42  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08365

40

SEQUENCE DESCRIPTION:

GATCGTGTCT CTGATAAAG AATAAAGCT GTTTATTGCA AA 42

45

SEQ ID NO:7130  
 SEQUENCE LENGTH:338  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08366

50

SEQUENCE DESCRIPTION:

GATCTTAGGT CCCACTCANG GTCCTAACTG GCTATGGCCA CAGCTGGAAC TACCCGAGAA 60  
 GNCTTTTGTA CATGTTTGGT AGCCGTAGCA CAAGTGATTG GAGTAGAACA TGCTACTGCT 120  
 GTACATTTT AACTCCCCTA ATGGTGTGTC TATAATTNTN AAATCTAAGG GGGGGGGCTC 180  
 AGTAAAGCCT CCTGGCACCA GGCCTTCCTG CTCGACTGAA AAAAATTCN TCTTTGAAAA 240

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TCCCCTTTTA CTCATGGCCC ACAGTAGAAT ATCCAAAACG CCTTGGCTTT CAGGCCTGGC 300  
CTTTCCTACA GGGAGCTCAG TAACCTGGAC GGCTCTAN 338

5 SEQ ID NO:7131  
SEQUENCE LENGTH:294  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08367  
10 SEQUENCE DESCRIPTION:  
GATCTTTTCA AGATGCATTC CAGATGAACT GCTAGGTGAG GGGGAAGCTT CATTTTTGTT 60  
ACCTGATAGA ATAGCTTNC TNATGAGATA TATATAATGT GATACTATGT TTGGATATTT 120  
TTGGTCTTAA AGCAAGACTC AGTGGTGTAT CTNCATTAAG AGCTTCCTTT AAAAAAGNTA 180  
15 CAGGGNTACT AAAAAACAA GNACCCAAAC AATCAAGNTG GGCCACCTT GGNACCNTGT 240  
TTTGATNAC CTTCCATGGT TTGGTTGGCG GTATGGNAAA AGGATTGNNT GGTN 294

SEQ ID NO:7132  
SEQUENCE LENGTH:107  
20 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08368  
SEQUENCE DESCRIPTION:  
GATCATGCTG TGTGGAGGAC AAATCTTTAA AATCCAGCA TTGTATTGTC TATTGACACA 60  
25 CAAAGTTTGA AAATAAAGGG GCAAAAAATT TTAATGCAAA AATGAAA 107

SEQ ID NO:7133  
SEQUENCE LENGTH:328  
30 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08369  
SEQUENCE DESCRIPTION:  
GATCTGCGAT GGCTGACATN AATAGGTCAC CATGTTGGCA GCTGTATAAT CAGCAATGAA 60  
35 AGCTGAATAT TATCACCAGA TAACCAAATT ATGAAATATC TATATNANCT TCANGATTCA 120  
GGNCCANTGA ACCAGTATCT GCCCTTACGA GATTTAGCTG AANGTGAANT GCAAGGTGGT 180  
GAACGGCATT CTAACAAGAG TGTGAAGAAA GAGATNGANG GCTGTCCGCT GCTGGAGGGG 240  
AAGAANGGTG GGGCGGCTTT TNCAAGGCTC TGTGGCTCAG TGGACCTTCA ATANATTGGA 300  
40 CCTTCAATAA ATTAATTGNA AANCANGN 328

SEQ ID NO:7134  
SEQUENCE LENGTH:244  
45 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08371  
SEQUENCE DESCRIPTION:  
GATCTGAGGG ATTTGCTCGT CATTTGCTGT GGCAGAGATG ATGTTGACAC CCTGGGATGC 60  
50 TGTGGGAGGG ACAAAGACT CACGTATATG TTCTGTCAAA TCGGAGAAGT AAATAATCCG 120

55

TTGGGATGCC AGGATACTTT ATTCTACAGC GAAGTTAATT TTGTATCCGT CGAGGCTACA 180  
GTAGAGGTAA AAATGACATT GAGTTGTACT TTGCTTTGAA TTAAAGTTGA TGGGTAGCAG 240  
5 CAAA 244

SEQ ID NO:7135  
SEQUENCE LENGTH:48  
SEQUENCE TYPE:nucleic acid  
10 TOPOLOGY:linear  
CLONE:HUMGS08372  
SEQUENCE DESCRIPTION:  
GATCTTGACT CCAAAAATTA ATAAATAAAT AAAAATAAAT AAAATAAA 48

15 SEQ ID NO:7136  
SEQUENCE LENGTH:48  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS08373  
SEQUENCE DESCRIPTION:  
GATCATGGTA TAATTAATTG AAATTTATTA AAATCTGTTT TTATTAAA 48

25 SEQ ID NO:7137  
SEQUENCE LENGTH:267  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08374  
30 SEQUENCE DESCRIPTION:  
GATCTGTGAC TTCAAGTTTG GACCGTGGA GAACAGCACT TTCAAACCCA CAACTGAGAA 60  
TNATGACACA GGGACAAGTA GCAGTGATAC ATCAGATGAC GACGATGTNT GAAGGATTTC 120  
CTAACAGCTT TNGAAATCTT AGTGTGATAC ATCTCTCATA CAGTTTGGGG NGAATTGTNA 180  
35 AAATGAAAGG ACTATANTTT ATGTAGTGGA ATACCCCN AGAAGAGGNN TTTTGGGG 240  
GCTTCAACTT GNTGGAACC NAGANTN 267

40 SEQ ID NO:7138  
SEQUENCE LENGTH:314  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08375  
SEQUENCE DESCRIPTION:  
45 GATCATTGAA ATTCTGAGAA AACTTCTTTT AAACCTCACC TTTGTGGGGT TTTTGGAGAA 60  
GGTTATCAAA AATTTTCATGG AAGGACCACA TTTTATATTT ATTGTGCTTC GAGTGACTGA 120  
CCCCAGTGGT ATCCTGTGAC ATGTAACAGC CAGGAGTGTT AAGCGTTCAG TGATGTGGGG 180  
TGAAAAGTTA CTACCTGTCA AGGTTTGTGT TACCCTCCTA TAAATGGTGT ACATAATGTA 240  
TTGTTGGTAA TTATTTGGT ACTTTTATGA TGTATATTTA TTAAACAGAT TTTTACAAAT 300  
50 GGAANAAAGA NAAA 314

SEQ ID NO:7139

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08376

SEQUENCE DESCRIPTION:

GATCCAGAGT AAATGAGAAG TCTCTATCTG AGCTGGTCAG TTAGTGGAGT ACATGTNACT 60  
 AATCTGGGTT TAAAGTTTAC TTCATTATCT GCTAGTGTC TCCACAGCAG TTCATCCTCA 120  
 TCCACACTAA GCCATCCTGT NAGCTTTTAA AGGAAGTTAA TTTAATTAAC ATTAATATAC 180  
 TCTATGGGCT CCCTCTCCCA CCTGTCTGCA TAGAAAGGCA GAATTAGACA TAGCATGCTT 240  
 TGGAAAAGCA AATAGGAATT GTTGGGAATG ATTTANTCTT GTTGTGTGTG TTGTTGTTGT 300  
 TCACTTGTGG TTCTACATTC CTGGTGNATG NTGAATGTNG CTGTCAAGN 349

SEQ ID NO:7140

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08377

SEQUENCE DESCRIPTION:

GATCTTGTGC TTCCATTTAA GAAATTCTTC CATTTAAAGA AGAAAAAAAA TCTCTCTAAT 60  
 TGAATATCTG AAGATATATG AAAAAGCCTA TGCTTTTAAA TTAANCTGTT AAGACAGTCC 120  
 ATTGAAAGAT TGTGGAAGTN CACATCTATT TTNCACCTTA ATTTTTCCTA TTGTCCCTAC 180  
 TCATGACTCT AAAAAGTGCA TGGCTTGGGG CTATACCTTG TTTTGCAGTT TGTGTTGATC 240  
 GTGCCTTTCC TTATCTACAT TAGCTTAGAC TATACCTTNT TTTNAGAAG GGAAGTGGN 300  
 AATTAAGTGT GGCAAAACCT ATTTNGGCAC ACCNCCTTTG TTCAATN 347

SEQ ID NO:7141

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08378

SEQUENCE DESCRIPTION:

GATCTTAATT CTTTGCAATT ATANATGAAA AATGACTGAT TTTTCTNAAA ATATGTAAGT 60  
 TATNTAAATA TATCTGTTTG TACAGATTTT AACCATAAAA ACATTTTGG AAAACCATAA 120  
 A 121

SEQ ID NO:7142

SEQUENCE LENGTH:409

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08379

SEQUENCE DESCRIPTION:

GATCTGGAAA CTATTTGGGT TTTGTTTTCA ACTTTTCATT NGGATGTTTG NCNTTGCACA 60  
 CACACATCCA CCGGTGGAAG AGACGCCCGG TGAAAACACC TGTCTGCTTT CTAAGCCAGT 120  
 NAGGTTGAGG TGAGAGGTTT GCCAGAGTTT GTCTACCTCT GGGTATCCCT NNTGTCTGGG 180

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5 ATAAAAGATN TCAAGCCAGT TGGCGGGATG GAATGGNTGC ACCGCAAATA ATGCATTTNC 240  
 TGAGTTTTCT TGTAAAAAA AAATTTTTTT AAGTAAGNAA AAAANAGGTA ATAACATGGC 300  
 CAATTTTNTT ACATAAAATG GCCTTTCTGG NGTNTAAATT ATTCCTAAAA AAATCCNGTT 360  
 TTATATANAC NATCCAGTTG NTGGAAAAAA NTTTTCCAAA NGTTTTTGN 409

10 SEQ ID NO:7143  
 SEQUENCE LENGTH:89  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08380  
 SEQUENCE DESCRIPTION:  
 15 GATCTAGAAA ACTTTGGATT TTTGAAGTAA ATTTTAATGT TTCATATTAA TTTCTTGAAA 60  
 ATGTATTAAA TGTCATTGAA AGCCTTAAA 89

20 SEQ ID NO:7144  
 SEQUENCE LENGTH:375  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08381  
 SEQUENCE DESCRIPTION:  
 25 GATCACTGTG GACCATCTTA GCAGTTGACC TAACACATCT TCTTTTCANN ATCTAAGAAC 60  
 TTTTGCCACT GTGACTAATG GTCCTAATAT TAAGCATGTT GTTATATTT ATCATATATC 120  
 TATGGCTACA TGGTTATATT ATGCTGTGGT TGC GTTCGGT TTTATTTACA GTTGCNANTA 180  
 CAAATATTTG CTGTAAACATT TGA CTCTTCTAA GGTTTAGATG CCATTTAAGA ACTGAGATGG 240  
 ATAGCTTTTA AAGCATCTTT TACTTCTTAC CATTTTTTAA AAGTATGCAG CTAAATTCGA 300  
 30 AGCTTTTGGT CTATATTGTT AATTGCCATT GCTGTAAATC TAAAATGAA TGAATAAAAA 360  
 TGNITTCATN NTAAA 375

35 SEQ ID NO:7145  
 SEQUENCE LENGTH:513  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08382  
 SEQUENCE DESCRIPTION:  
 40 GATCTCGCTC CTTTGAGAGG TCCCATAAAA GCAAGCACCA TGGTGGCAGT CGCTCAGGAC 60  
 ATGGCAGGCA CAGGCGCTGA CTTTCTCTTC CTTTGAGNCT GCATCAGTTC TTGGTNTTGC 120  
 CTATCTACAG TGTGATGTAT GGA CTCAATC AAAACATTA AACGCAAAC GATTNGGATT 180  
 TGATTTCTTG AAACCCTCTA GGTCTCTAGA ACACTGAGGA CAGTTTCTTT TGAAGAAGAAC 240  
 TATGTTAATT TTTTGCACA TAAAATGCC CTAGCAGTAT CTAATTA AAA ACCATGGTCA 300  
 45 GGTTCAATTG TACTTTATTA TAGTTGTGTA TTGTTTATTG CTATAAAGAC CTGGAGNGTG 360  
 AATTCTGTAA AAATGTATCT TATTTTATA CAGTTAAAAT TTGCAGACAC TGTTCTATTT 420  
 AAGNGGTTAT TTTGTTTAAAN TGGATGGGNG ATNCCTTNTT AANCACTGGN TTGGNCTGGA 480  
 TNGTGTAAGG TTTTNCAGG GNNTAGTTCC TGN 513

50 SEQ ID NO:7146

55



SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08383

SEQUENCE DESCRIPTION:

GATCTGAGAA TCTTTATTGA GAAAGAGCAC TTAAGAGAAT ATTTAAGTA TTGCATCTGT 60  
ATAAGTAAGA AAATATTTTG TCTAAAATGC CTCAGTGTAT TTGTATTTT TTGCAAGTGA 120  
AGGTTTACAA TTTACAAAGT GTGTATTAAA AAAAACAAAA AGAACAAAA AATCTGCAAA 180

SEQ ID NO:7147

SEQUENCE LENGTH:187

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08384

SEQUENCE DESCRIPTION:

GATCAAGAAA CTGGAAAATG TGAAGCAATC TCTATTGAGA TAGCATCTTA GTGTTTTAGA 60  
GAAATCAAGA ATTTTAAAA ACAAGAATAT CAACATTGG TTTGTGTAT AAGTGGTGTT 120  
TGTATTAAAA TACTTTTCA ATGAACTGTA TAACTATGT TTTATTAAAC TACAATATAT 180  
CAGTAAA 187

SEQ ID NO:7148

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08385

SEQUENCE DESCRIPTION:

GATCCAGAGG CGAGAAGCCA CCCTGTTAGA NCTCCTGTCC ATCATCCAGG TAAGTCAACT 60  
CTCTCCTTTC AGGGCCAATC CCCAGACCTT TTGTTGAGCC AGGNCNNTAT CACCTNTCCT 120  
ACTNACTTAA AGN 133

SEQ ID NO:7149

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08386

SEQUENCE DESCRIPTION:

GATCCTTGTC AAAATGAGAT TCCAGGTCCT AGAGAGCTGC TTNAGGGAG TTCCAGGAGT 60  
ACTTACTATT GGTCAATGCAA TAGGAGAACA GAGACCCGNG GGCTGCTTTG GGGGAGGGGG 120  
GAACTCGAGA ATGTATGGAT TTACCTGAAA ACAAATTATT CATTTAATCA AA 172

SEQ ID NO:7150

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08387

## SEQUENCE DESCRIPTION:

GATCACCATT CAATTTGAGT TTCCAGGGGG AAGTGCATGT ATAATGAAAT GATAATGGAC 60  
TTCAATGAAG AATGTCATCA ATTATGTACA TATGTATTTN CTTTAAATAC AAAGTGTAAT 120  
TTTGTGCCAG TGAAATGGAG TCTGAATAGT TATGTGTTTC TTTTATCCCT GGAAATATTT 180  
ATTAAACTTT ATAGTTTATC CGAGTATGTT GTATGCTTTG ACAATAAATG ACTATTTTCT 240  
TCAAAGCAAA 250

SEQ ID NO:7151

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08388

## SEQUENCE DESCRIPTION:

GATCATCACC ACCACGGTTC CTGAGGACAT CATGTCCAAC CGAGGCAATN ACCTCCTGCT 60  
GAAGCTCCTG CAGNATCGGT ATCCCCGGGT GATGGCAGAG GAGGGTCTTC GAGTGGTGAG 120  
GCAGTGGTTG GAGGCCTCCT CACAGCTGGA GGAAGCCTCA NTTTATAGCC GATGGGAGGT 180  
GGAAGAGGAC TGGTGTCTGT NTGTCCTCCG CTCCTACCAG GCAGAACACG GGCCCGACTT 240  
CCCCTGGAGC GTGGGGGAGG ACATGAGTGC AGATGGACGG TN 282

SEQ ID NO:7152

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08389

## SEQUENCE DESCRIPTION:

GATCAAAGTA GAAGCNTTTG AATAATGAAT TTAAGGCCAC GCAAAANCTT TCCTCACCTA 60  
TTGACATGAC ATCTAAAAGA CATTTGGAAC TCGAAAAGCA TAGTGCCCA AGTATGGTAC 120  
ATTCTNCTCT NACTCCTTTC TCAGTGCAAG TANCTAACAT TCAAGATTGG NCTCTCAAAT 180  
CGGAGCACTG GCATCAAAAA GANCTGAGTG GCAAAANTCA GAATAGTTTC AAAACTGGAG 240  
TTGTTGAAAT GAAAGACAGT GGCTACAAAG TTTCTGACCC AGAGAACTTG TATTTGACGC 300  
AGGGGNTAGC AAACCTTATCT GCAGNGGTTG TCTCACTCAA GAGNCTTNTA GNCACACAAC 360  
CAGTCTCTGT TTCAGACTCT GGGTAANTTN N 391

SEQ ID NO:7153

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08390

## SEQUENCE DESCRIPTION:

GATCTAAAAA TAATTCTTAA TCATGAATTT AATTCACGAC TTCCTTGTTT TCAGTCTTAT 60  
TCAGCTTACT GTAGGAGATT TTAATANACT AAAGCTTTTG TTGATTATG AGTTAGAAA 119

SEQ ID NO:7154

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08391

SEQUENCE DESCRIPTION:

5 GATCTTGAC CAAGCCAACG GGTNTCCTGG CTCTCCTGCC CACAGGATGA ACATTTTCGG 60  
CTTCCTTAGG AGTTTGGCC TACCGTATTC CAAAGCGTGT GCTGGTTTCT CATATTGTCT 120  
GTAGGCTCAC TCAGCCCGCA GTTTATGTGT GTGCTTTTT CTATGAAAA TGATGTATTT 180  
TGCTACTTCC TGTGTACAAA GTTTTATTGT AAATGTTTT TGTGCTTTGC ATGAACAGGG 240  
10 GCCACGTTGT TGCAATTGTT TCAGTAGAAC TGGTTTGATT TCTN 284

SEQ ID NO:7155

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08392

SEQUENCE DESCRIPTION:

20 GATCGAGACC ATCCTGGCTA ACACAGTGAA CCCCGTCTCT ACTAAAAATA TAAAAAATTA 60  
GTGGGCGCATG GTGGCGGGCG CCTGTAGTCC CAACTACTCG GGAGACTGAG GCAGAAGAAT 120  
GGCGTGAAC CAGGAGGCGG ANTTGCAGTG AGCCAAGGCG ACAGAGCAGG ACTCTGTCTC 180  
AAAAAATAAA AAATAGTGCA CTGTCCCTCG AGAAAGTTT CTAACATCTA GTAATTTGTA 240  
ACTTAGAAGT GGAGTTGCCT TGTGGATGTC TTTTTGTCAT TCTGTAGGN 289

25 SEQ ID NO:7156

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08393

SEQUENCE DESCRIPTION:

30 GATCCAAC TGAGATGGC AGCTGAGTCA TTGCCAGTNT CCTTCGGGAC ACTGTCCAGC 60  
TGGGAGCTGG AAGCCTGGTA TGAGGACCTG CAAGAGGTCC TGTNTTCAGA TGAAAATGGG 120  
GGTACCTATG TTTCACCTCC TGGAAATNAA GAGGANGNNT CAAAAATCTT CACCACTCTT 180  
35 GACCCTGCTT NTTTGGCTTG GCTGACTGAG GAGGAGCCAG NACCAGCAGA GGTCACAAGC 240  
ACCTCCCAGA GCCCTCACTC TCCAGATTCC AGTCAGGGCT CCCTGGCTCA TGN 293

40 SEQ ID NO:7157

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08394

SEQUENCE DESCRIPTION:

45 GATCACGATG TAAATAATNA AGCATTTTGG TAGGATGTCT ANNGTAATAA ACAATTTTGG 60  
TACCATAAA 69

50 SEQ ID NO:7158

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS08395

SEQUENCE DESCRIPTION:

5 GATCTTGGCC TCCCAAACCC CTTATTTTAA AAATACTTTG CGCCTTGCTT TGATAATTG 60  
TATTATGTAT CCAAAGTGAA ATNATCTGCT TTCTGCATTA GAATGTAAGC CCCCTGAGGG 120  
TTGAGTCAGT CTGTCTTGTT TGCTGTGCCA CGCCTGATGC CCAGCCCAGC AGCATGCTTT 180  
GTACACTGAT ATATTGGGTA AATTTTGTG AATAAATTAA GCTCAACTAT TTGTATTTC 240  
10 ATAGNTTGAG TTGTATTGCT TCCTGTTCTT CAAGCTTAAA TTTGACCTGT CTAATAAAAA 300  
GGAGNAATTA AA 312

SEQ ID NO:7159

SEQUENCE LENGTH:92

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08396

SEQUENCE DESCRIPTION:

20 GATCTTTTGT GGTCTGTGTA AAGATACTGA GGAATGTNTT TCAGCCAAGC CAAGAGGATG 60  
GTTTCAATAA ACCTAATAAT CTGAAGTTCA AA 92

SEQ ID NO:7160

SEQUENCE LENGTH:61

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08397

SEQUENCE DESCRIPTION:

30 GATCTTGCAA TATATACTCA GGAAATTACC ATGGGCAGAA TAAAATGCTT TAAAAAATAA 60  
A 61

SEQ ID NO:7161

SEQUENCE LENGTH:319

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08398

SEQUENCE DESCRIPTION:

40 GATCCAAACT GNAGAACTTC TCATTCATCC CCAAGGCCTC CAGGCAGTAT CCAATGGGGA 60  
ATCAGCTCTA AAAGGAACCA GACCAACGTT TTCCAGCCCC TTNATTCTGC TTCCNTCTGT 120  
NTNAGGAAAAG GNTAGAAATN TTCAGGGCAT CATCATACAG GCTCCTCATC TACAAAGTTC 180  
CAGTAGCAGT GACGCCTACA CGGAAGANTT GGAAGTCAA ACAGGCTGGG GTCACCTCAN 240  
TNGCATCTGA CGCTGTCCAA CCAGAAGTTC GATTTTNNNTN CTGGGGGTGA AGGTGGAAAC 300  
45 AGACTGTACT TAAAGGNTN 319

SEQ ID NO:7162

SEQUENCE LENGTH:134

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS08399

SEQUENCE DESCRIPTION:

5 GATCCANAAA TAAGTTTAAC TTACGGAGGC TTCTAGTTCT AAAGATGCAA NGTAAGATGC 60  
CAAAGCAGTG GAAAGATTGA AGTCAAACAG TCGGGCCCAT GTGTGTGTCN TACNTCAACC 120  
NTTNGTGTGT TATN 134

SEQ ID NO:7163

SEQUENCE LENGTH:147

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08400

SEQUENCE DESCRIPTION:

15 GATCTATGTG TCTGTNTGTG TGTCCATCCC GCCGACCCCC CAGACTAACC TCCAGGCATG 60  
GACTGAATCT GGTTCCTCTC TTGTACACCC CTCAACCCTA TGCAGCCTGG AGTGGGCATC 120  
AATAAAATGA ACTGTCGACT GAACAAA 147

SEQ ID NO:7164

20 SEQUENCE LENGTH:320

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08402

SEQUENCE DESCRIPTION:

25 GATCTAGNAA CTAGNAAATA CTATTTGTCC CAGCAATCCC ATTACTGGGT ATATACCCAA 60  
AGGAATATAA ACCATTTAAT TATAAAGATA CATGCAGATT TTTATTCATT GCAGCACTCT 120  
NNACAATAGC AAAGACACAA TAGCAAATGC CCATCAAAGA TAGACTGGAT AAAGAAAATG 180  
TGGTACATAT ACACCATGGA ATACTGTGCA GTGCAGCCAT TACAGCTTTT GGTGATACAG 240  
30 TGAATCAGAT TTTNNATTAA TTCTTTTAAT TGGTTATTAC TGNNGTGGA NNAGTAATGG 300  
TTTGTATTGG NATCCTTGNN 320

SEQ ID NO:7165

35 SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08403

SEQUENCE DESCRIPTION:

40 GATCCATATT TTAAATTGCA ACCCTGTTCC CTATGATACC TATCTGTCTA TGAATGAAAC 60  
AAAGGTTTTA CAAA 74

SEQ ID NO:7166

45 SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08404

SEQUENCE DESCRIPTION:

50 GATCCAAAGA ACTTCTGTTA TATGGGTTAT AGCTGTTAAT ATTTGTCATA TTCGAAATTG 60

55

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AAATAAGATT TTAAGGTATT TTAAAATAAC AGTNCAAAAC CATTGTATNT TGACATGAAT 120  
AACACTTTTA TGAATAAAC TATATTCCAA AACAATAAAA TTACCAAAAA GTTGCAAA 178

5 SEQ ID NO:7167  
SEQUENCE LENGTH:98  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS08405  
SEQUENCE DESCRIPTION:  
GATCACAGAT TTCATCAGGA TTGAGCTGCG TGGTAAGCTC GCCACTCTGG ACAAGTCACA 60  
GGGTACCCAT TATTAGCAA TAAAAGCTTT AACTCAAA 98

15 SEQ ID NO:7168  
SEQUENCE LENGTH:110  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08406

20 SEQUENCE DESCRIPTION:  
GATCTCTGTG GCCTAGGTTT TGTACATACA GAAACTGCAT GGTATTTAAA TTATTGTTTG 60  
TCTCTGATGA TGTATGCAGT TTCTTAAAA ACAACCAAAA AAAAAGTAAA 110

25 SEQ ID NO:7169  
SEQUENCE LENGTH:298  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08407

30 SEQUENCE DESCRIPTION:  
GATCCTGAAG AGCGCTGAGG GACGGGTGCT TCGNCGANCA GCACCAGCGA NACGTCAAAC 60  
TCATGAGACA GATGCTAATG GATGCCGNCC TCCCTANTTG TCCACTGCCC CAGCCACATC 120  
ATCCCTGTGC GGGTTGCAGA TGCTGCTAAA AACACAGAAG TCTGTGGATG AGCTAATGAG 180  
CAGCCATAAC ATCTACGTGC AAGCAATCAN TTACCCTACG GTGCCCCGGG NAGAAGAGCT 240  
35 CCTTCGGGNT TGCCNCNACC CTTNNGGGGG GACCCCAGGA TTGNTGGAAC TAANTTCN 298

40 SEQ ID NO:7170  
SEQUENCE LENGTH:329  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08408

SEQUENCE DESCRIPTION:  
GATCCACCCG CCTCGGCCTC CCAAAGTGCT GGGATTATAG GCGTGACCNC TGCACCCGGC 60  
45 CAAAAGTTGA TTTTAAATTA CATAAAATC GTAAAACTT CTAGTAAAAA CTGATTNNG 120  
NGANTACAGT TATATTTTAA AACCTTAAGG TGACAAGCAT TTTCTATGCC TAAATCTTCA 180  
TTGGTTTGCC TGGAAGAGT CTCTGTTAAA AGATTTTCCA TATTCAAAGT AAAAGGAAAG 240  
ATTTCTTGCT TTCTAATTGT CTTTGGACA CATGCCTATT TTCTTTGAGG TATAANCCTT 300  
50 TAGATGTGAA ANATGTAATT TCCATTCCNN 329

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SEQ ID NO:7171

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08409

SEQUENCE DESCRIPTION:

GATCCAGATT TTTCTGTTG TGTCTGAAGA GAACCATGAC ATTTAGAAGT ATATTGGTAA 60  
TCTATTAGGT CCATTGGCAA AGTATATTGG TCCATATTCA AACCTATTCC AAAAGGTTAG 120  
AAGTGTTTAA GATTCCTTTA TTGTGGTACC ATGTCTGTTT ACCTATGCTT ATGAGCAACA 180  
ATAANTTACT AGTTTACCTT CTGGAATTTT AAA 213

SEQ ID NO:7172

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08410

SEQUENCE DESCRIPTION:

GATCTGGTGG GCAGTCGAAC CATGGTGAAC TCCACCTCCG TGGAATAAAC GGAGATTCAG 60  
CGTGGGCGAC TGAATCCAGC ACGTCTGTGT GAGTANCGGG ACAGTAAACA CTCCACATNN 120  
NNTCAGTTTT TCACTTCTAC CTACATATTT GTATGTTTNN NTGTATAACA GCCTTTTCCT 180  
TCTGGTTCTA ACTGCTGTTA AAATTAATAT ATCATTATCT TTGCTGTTAT TGACAGCGAT 240  
ATAATTTTAT TACATATGAT TAGAGGGATG AGACAGACAT TCNNCGGGNT ATTNCTTTTA 300  
ATGGGCACAA AATGGGCCCT TGCCTCTAAN GN 332

SEQ ID NO:7173

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08411

SEQUENCE DESCRIPTION:

GATCCAGAGG CTCAGTGAAC CCCATCAACT TGGTGGCCCT GGTGTCTCAC ACTTGATATCC 60  
TTCTGCCCTC GAGACCTGGC ACAGCAGTAT CCCTTGAAGA AATCCTGAGG CTTTGTAGAG 120  
TGCTCCTTGA CCATGTTTAA TAATTCTTCC CTCCCCTGCT TGTNTATTTT TTTCTCTTCA 180  
CGGCTCTTCC TATACCTTAG GCCAGTCTCA AGCACTCACT GGAGACCCTT GGGCCTTGGG 240  
CGACCATTGA GTCCTAGTCT CCCTTGTTTG TGCCCCTGTA GGAGGTAGGT CCTTTTNTCC 300  
TCCGGCCTAG TAGGGGACCT TGGGTAACAT TN 332

SEQ ID NO:7174

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08412

SEQUENCE DESCRIPTION:

GATCTGCTTT GCAGAGGAAA TAACTTGTTT TTTCTCATGT TTCATCTTCT TTTTATGTAA 60

ATATGTAATA CTTTCCTATA TTGCCCTTTG AAATNTTTGG ATAAAAGATG ATGTTTAAAG 120  
TTCCAAA 127

5 SEQ ID NO:7175  
SEQUENCE LENGTH:144  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS08413  
SEQUENCE DESCRIPTION:  
GATCTGCCCG CCTCAGCCTC CCATTGTTGA CCATTTTAT ATGTTTATTT ACCTATGTGG 60  
TTTTCTTTTC TCATAAAATG CTTGTTTCATA TATTNCCCC ATTTCTACTT ATCTNGTTCT 120  
TATTAAATNG CCAAAGTGCA TAAA 144

15 SEQ ID NO:7176  
SEQUENCE LENGTH:347  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS08414  
SEQUENCE DESCRIPTION:  
GATCATCTCT AAAATTAAAA AAATTAATAT TAAATGTTGG ACCAAGGATT TCAACCATGC 60  
AGTATGTTGC TTCTGGGGTC TGCTGTCCTA TTCCAGCCCT AGTGAATAGT TAATGCCTTG 120  
25 AACTATTCTC ATCACACAG GTTGCCAGGC CACCAAATAA CGAAGCCAAT CCAGGATTTG 180  
TCCATACAGA AAATGTGTGC GCTCCCAGCT AAATCTCAGT TAAGGAGGTT GTTCTATATA 240  
CAGCCAAGTA GCAGAAATAT TCATAAATGT CATTTGCAA TATAATAAAC ANTGTAATGA 300  
ATGGGTATTT CCTTCTTGT TAATTCTATG TGCTCAATTA AAAGGNN 347

30 SEQ ID NO:7177  
SEQUENCE LENGTH:213  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS08415  
SEQUENCE DESCRIPTION:  
GATCATACTA ATAATTTAAT ATTTGAATTG TATGGAAGTA CAATTCAGTA TCATTTTACA 60  
TATGGTATAT TGTGATGCTG TATCATATTT TATGTTACGG TTTATAAGAA AAGCTCCTAG 120  
GTATAAAATG CTACATAGCA GGAACCTGGT TTTCAATGT TATTATTTCC TACTGTTTTT 180  
40 GACGTAACGG CAATAAAATT TGTTTGAACC AAA 213

45 SEQ ID NO:7178  
SEQUENCE LENGTH:161  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08416  
SEQUENCE DESCRIPTION:  
GATCTTAAGA AGAGAATAGA ATCTTTAATT GACCGGGACT ACATGGAAAG AGATAAAGAA 60  
50 AATCCAAACC AGTACAATA TATTGCATAG AATGTTGGCC TTGCAGCATT TGGTGTCTATA 120

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TGCAGTAGCC AGTGGATAAA CTAACCTGTT GATTCAATAA A 161

5 SEQ ID NO:7179  
SEQUENCE LENGTH:69  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08417  
10 SEQUENCE DESCRIPTION:  
GATCATGTGC AATATTTCTT ACTGTGCCGA GAAGCCACAA TGAGCGAGAT TAAAGCTGTT 60  
TAACACAAA 69

15 SEQ ID NO:7180  
SEQUENCE LENGTH:348  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08418  
20 SEQUENCE DESCRIPTION:  
GATCTCTGTT CCTTTTGGCT CTAATATGCT ACAACTGTAG GCCAATTATC ACTTTACCAA 60  
TTAAGAGTTA GGCCAGATAA GTGAAATTTA ACTTAAGGGC ACACAGCTAA TAAGTAATAG 120  
GCCTAAACTG GATTTCCCTTA TTCCAAATCC TGTCTTTTCC CCACTATTCC ATTAGACCCC 180  
ACAAATGTTA GTTGTGTGTG TGTGTGTGTG TGTTTTTAAT CACTGTAACC GGGTGCATTT 240  
25 TTTTAAGGCA AAATTTCTCC CTTATCTACT GTGATGACTT CAGAAGATAC ANTGGTCCCA 300  
GGGGCCAAGT AGAAAGCATT TTTAAAGNTT AATCTGAATT AAGCTGAN 348

30 SEQ ID NO:7181  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08419  
35 SEQUENCE DESCRIPTION:  
GATCCACTTC TGTAATTAAG TACNTGGTTG TCTCGTGATG CGTCTACAGT TATTTATAGT 60  
TACAACCATT ACCNGNCACT GTAGATACAC ATATAAAAAT AGNTGTTNGG TATCCATAGT 120  
TNCGCTTGTT CN 132

40 SEQ ID NO:7182  
SEQUENCE LENGTH:85  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08420  
45 SEQUENCE DESCRIPTION:  
GATCTCATCA CTGCACTCTA GCCTAGGTGA CGGAGCGAGA CCCTGCCGCT AAATAAATAA 60  
ATAAATAAAT AACATAGTAG TGAAA 85

50 SEQ ID NO:7183  
SEQUENCE LENGTH:224

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# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08421

SEQUENCE DESCRIPTION:

GATCATGGAC TGGTGCCTTT GCATTTCAGAA GGAGAGCTGT CAGCGTANAC CGAATTCAAG 60  
ACCAAGGCGT GCTACCTGAG CTGACAGCTT TTTGAAAGCC GAGCTGTTTC TGAACCATGT 120  
ACATACATGT TCTGAAACTT TCTCATCATT TTATGAGTAC TGTTCATTGA GAGATGACAA 180  
TGAAGATTAG ATGAAATTGG AAATAAACCA ACATTGTTTA CAAA 224

SEQ ID NO:7184

SEQUENCE LENGTH:38

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08422

SEQUENCE DESCRIPTION:

GATCTCTGCA GTATTAAAAA GATGTACTCC CAATTAAA 38

SEQ ID NO:7185

SEQUENCE LENGTH:67

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08423

SEQUENCE DESCRIPTION:

GATCTTTGGC AGTGCCAGCA GGTTAAATTT TGACCTGCTC AATTAAAAAT AAACACTGGC 60  
GTTTAAA 67

SEQ ID NO:7186

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08424

SEQUENCE DESCRIPTION:

GATCTTCAAA GAAGAGAATG TAATTTATAC CATGAATATG TTATTTTTTC ATGTTGGAGC 60  
ACTGAAATAC TTTCAGTTTG TTTTCTTATT GTTTAAATAA AATTTTAAAT TCTTAAA 117

SEQ ID NO:7187

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08425

SEQUENCE DESCRIPTION:

GATCTTTGTT ATTTTAGGGG GGAAATCACA TGGTATCTAG CATGGGACAA AGCAGCAAAA 60  
TAAACCAAAA GGACAATCTC TATTTTATAT AGAAAATAAA CATACTTNC TGCATCCTGT 120  
GTACTTTAAG TATATCTATA TTTNTNANGG GTTCATACTG TGTTGANTTT NCCTNATGAN 180  
ATAGTCACTT CCCAGTGTA TTTTAATGCA AATGCATATN CTATAANNTA N 231

EP 0 679 716 A1

SEQ ID NO:7188

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08426

SEQUENCE DESCRIPTION:

GATCTCTGTT CTAAGAAAAG GAGTGTGCCT TGCATTTAAA AGGAAATATT GGTTCCTAGG 60  
 GAAGGGAGGA GGCTAAATAA TTGATACGGA ATTTTCCTCT TTTGTCTTCT TTTTCTCAC 120  
 TTAAGAATCC GATACTGGAA GACTGATTGA GAAAAGTTT TAACATGACA TTAAATGTGA 180  
 AATTTTAAAA ATTGAAA 197

SEQ ID NO:7189

SEQUENCE LENGTH:115

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08427

SEQUENCE DESCRIPTION:

GATCAGGAGA CAGGGAGGCC CCGCACATCA CACAGATAAA GTCAGACAAT TGTAATTAAT 60  
 ACTTTTGCTG CCTCAAGTTG TTTTAAAT AAAGTACTTT GAAATGCATG AGAAA 115

SEQ ID NO:7190

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08428

SEQUENCE DESCRIPTION:

GATCCTTGTT GGCATTATTC TAACTGATAC GTAGACACTT ACTTGGAAN NNNNGGACAT 60  
 TATATTAAAT GAGTGCTATC TGTGAAATTG GTTATATTAG GTGGCTTGAC TAATGTTTTT 120  
 CCTATAATTG TATATGGACT GCATTTTAA AAAAAACCGC ATTTGCCTTT ATGCTAGATT 180  
 GTAAAAAATT ATATTAGAAT GCATAAGACA TGTTTTNCCN TCATATGCTA GACTTNCCT 240  
 AGCATTTTCGT ATTTCTGTGT TGTCAGTGTG TGATTTTNA ACCGGAATTT GGTTTAAAAA 300  
 AAATCTGGTG GTAATATATG TGAGAANTN 329

SEQ ID NO:7191

SEQUENCE LENGTH:353

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08429

SEQUENCE DESCRIPTION:

GATCTTCATT CCAAATTTTA CTGCATGGAA ATGACTAATA ATGTGCATAA AAAGTAACT 60  
 ATAAGGATGC TCACTGCAGG GTGGCTTATA TTAACACAAA TTCACAAACA ACTCCACTGT 120  
 TCCAGCACAG CAGTGTGTTG TAAATCATGA CATGTTTCTA TGCTCAATTA CTATCCAAC 180  
 TTTGAGAAAT AGGTTGGAGA TATGTAATTN CCAATATGAA AATAAATTC CTATATNCTA 240  
 TTTAGTAAAA NTAATTCATA AATNTCCATT TTNCAACAA CTTTCATGAAT TTNTTCCAAA 300

ATACANATGT TATCTATCCA TTTNGGAATT AGGANTGGTT NNNATCATTT TGN 353

5 SEQ ID NO:7192  
SEQUENCE LENGTH:352  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08430

10 SEQUENCE DESCRIPTION:  
GATCTCAGTT TTTCCATCAA AATTATAATA TGCTCATGAA AATAATATTA ATTTGCCTTC 60  
CCTTTGCAAA CACCGGCAGT TGAAAGGAAA AGGACGGGGA ATGTGANNNN AAAGAGACCG 120  
CCTGGAATAA ATGTCCCCCT ATGATTCTTT AAGGCAGTGG TTCTCGAGCT TGAATTTTCA 180  
15 TTAGGAAATT CTGTGAGGNG NTTGTAACCA GATTCTGGG TCTGCCACAT GCACCTATCT 240  
NTNGCTGAAT TGCTTTAATA GAATAATGAG AGCAAGTTTG TCTAACTAAT ACCAACCTGN 300  
CANCTTGAAT ANCAATAAAA TGCAATTTGG TACATAAATT ATAATGCTGC NN 352

20 SEQ ID NO:7193  
SEQUENCE LENGTH:348  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08431

25 SEQUENCE DESCRIPTION:  
GATCCTGGAG AGGAGAAATC CTGGCCTCTG CTCATGCGCA GGTCACAACC GGGCTGGAAG 60  
TGCGGTTNAG CTCTCTGCCA CTTTCTTCAA TGTA AAAAGT AGGCATCAAA GATACGACTT 120  
CTACTATATA CATTTNTNTG TCCCTGAGAA CAGAGAAACG TAACCCTGTA GGGGACTGGT 180  
TACAGAGGAC CTCCTGGAGC ATCTGCCCCA TTCCTCCAAG TCCAAGCACA GCCATGCTGA 240  
30 GTGGAAGCNA GGCCACCATC TGAGTGGATT GGTCCCAAGT NTGTAATGAG GAAAGTGGCC 300  
AGGTGCCGGC ACAGTGCCTC TCCAGAGCC TCAAGAAGGG CCATTNGN 348

35 SEQ ID NO:7194  
SEQUENCE LENGTH:349  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08432

40 SEQUENCE DESCRIPTION:  
GATCACAACT CTCAGTCTAC CTGGAACACC CCACCCAACA TGCTGCTGC CTGGGGACAT 60  
GCCAGTTTCA TCAGCTCTCC GCCCTACCTC ACAAGCACCC GAAGCTTGTN TCCAATGTCT 120  
GGACTTTTTG GTTCCATCTG GGCCCCGCAA AGCGATGTGT ATGAAAATTG CTGCCCCATC 180  
AACCCACCA CGGAACATTC GACCCACATG GAAAACCAAG CGGGTCGTGT GCAAGGAATA 240  
CTACCCGGGG TTCAACCCGT TTCGCGCTA TATGAACCTG GACATATGGA CTACCACAGC 300  
45 GAATAGGAAT GCAAATTTCC CACTGTCTAG AGACTCGAGT TACTTGTNN 349

50 SEQ ID NO:7195  
SEQUENCE LENGTH:342  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS08434

SEQUENCE DESCRIPTION:

5 GATCTGCCTG CCTCGGCCTC CCAAAGTGCT GGGATTACAG GCCTGAGCCA CTGCGCCCAG 60  
 ACCAAAAGTT TTTTAAATG GATGTTTAC AGATAGAACT AAATCTTCA TTTACCTCAC 120  
 TTAATTTCTG AAAACACTGT GTCCTCCAAC TGCTCTGTAT TCCCAAAGAT TAAAATTAGC 180  
 CTTGGGGAGC AGAGCTGGTT CCTCGTAAAC CCCTGTGAGT GCCCAGACCC TTTGGAGGAG 240  
 GTTCTCAGTG GGCTTTTGCC TGCTCCACA GATGTAACCC ACCCTTCCTG CTGCTCCTAA 300  
 10 GACCACCATG AGGAAGGCTG GGAATTGGCT CTTGAATTAA NN 342

SEQ ID NO:7196

SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08435

SEQUENCE DESCRIPTION:

20 GATCTGCATT TNNAGGTTCC GAGCCTGACC CCTGGAAGT ACCAGCGCTC GATTGTNAGC 60  
 CTTGGCCTGG GGTTTTAACC TTGCCAGTGA AGTTTCGGTT TTAAAGTGAT TAAATGTCAC 120  
 TTCCTCATCA GTTTCACCTC TGGAGGTTTT CTTATCCTAC TCCCTGGTGC CAGGGACGTA 180  
 CCTGGGAGTT TGAATCAGGC CCATTTGAGC GTGGCAGCCG TGTGGGTGA AGGTCCGGGG 240  
 CTCGGTGAGG CACTGGGGGG GTTTTCGGGA GGAAAATGAA AATGCTTCTA GAATGAGTGA 300  
 25 ACCACATCAT AGCTCTCACT GTTTTTTCAA TAGCTACTTT TTTAGCAGA CANCAGAGCC 360  
 ACAN 364

SEQ ID NO:7197

SEQUENCE LENGTH:30

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS08436

SEQUENCE DESCRIPTION:

35 GATCTCAAAA TAAATTCAGA AAGAAATAAA 30

SEQ ID NO:7198

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS08437

SEQUENCE DESCRIPTION:

45 GATCTGCCTA GCCAACTTTC TTAACCCAAG CCCAACTGA AAGTCTAAAA GATGTATTTT 60  
 TGGGGAATTA CCCACCTCA ACATTCTCAG GTTNCCAGT GTNCTCTGTC TGTNTCAGTA 120  
 TTTTAAAAAC ACTAACTCAA TAATNCTCAA AAATCAAAGT CTGCTTTNAT NATCTGGTAA 180  
 TAAAATAATA GGCAAA 196

SEQ ID NO:7199

SEQUENCE LENGTH:102

50 SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS08438

SEQUENCE DESCRIPTION:

5 GATCCGCCCA TCTCCGTCTC CCAAAGTGCT GCGAATNACA GCGGTGACAN CCAAACCCGG 60  
CCTGATTAAA GTTAAATAAA TACTAGTTCC CTTCTCGTCA AA 102

SEQ ID NO:7200

SEQUENCE LENGTH:341

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08439

SEQUENCE DESCRIPTION:

15 GATCAGTGCA TTTAGACATC CAGAAGTTAC TTCCACTATT GAGGAACTAT GTAGACATGA 60  
ATTTAAGCTT GTACATGTGC CAATCTTGTT AATGTCACCT GACCACTGAT TCACATAGAC 120  
AGACATTAACT GTCTGATGCC TCAGGTTGAT GCGGAACTTN CTTCTAGTG TCTTAACATT 180  
TATGANCTTA TGTGTTGACTT GAGGGGCATT TCAGCAAAGC TGTGNAGGAA AAGTAGGTTC 240  
20 TGGNCTGATG TCTGCTTTGT NCCATAGACA TTTTGGAGCA TAAGGNAGTA TCTNCTTCTG 300  
CTATATGTNC AGGGCTTGTC CCCAAATNAA TTCCTGATTT N 341

SEQ ID NO:7201

SEQUENCE LENGTH:110

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08440

SEQUENCE DESCRIPTION:

30 GATCTNCTAC AGTTCCTNCA AGCCTAGACA ACCTAAGAAA CTTTACTATC AGCAGCTTAA 60  
GATGAAAATC ACAGACTTTA AGAACAGGCG AAGTTTTAAN TGTATATNNN 110

SEQ ID NO:7202

SEQUENCE LENGTH:45

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08441

SEQUENCE DESCRIPTION:

40 GATCCAAAGA AATAATCCAA AATAAAAAGT TATATCCAAG ATAAA 45

SEQ ID NO:7203

SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08442

SEQUENCE DESCRIPTION:

45 GATCCACAGT GGAGTTTTAG TAATTATATT TTNTTGATTT CTTCAATTTG TTTTCTGGTA 60  
TAAAAGTAGA GATAATGTGT AGTCACTTCT AATTTAGTGA AACCAATTGT AATAATTNTG 120  
50 GAAATATTTT GTCTTTAAGT GTAAATATTT AAAAATTTGG CATACCCTAA TGTNAATAAT 180

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AAAAAGAACT ATTTGCAGAA AA

202

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SEQ ID NO:7204  
 SEQUENCE LENGTH:337  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08443

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SEQUENCE DESCRIPTION:  
 GATCGGAAAA CTCTGATTGA ACCATTCACT TTATTAGCCA GTAACTTTC TCAACCCCAG 60  
 AGCAAATCAA GCTTTCCTTT GCCTGGGAGG AAAANCATAG GGAAGTCTAA TTCTGAGAAC 120  
 TAAAAATCAG TAATTTCCAC AATTGTATGT TGAATAGTGA TTGCCTTTAN GNGNCTGTGN 180  
 NCATGGAGTA ATATTACTAT TAAAAATAGG CCATTTGTAT CTACCTTTGG TCCTTAGGAA 240  
 AATTCCTAAG GAAGTCAATT AATGCACITT NAGATGTTAA AAGTATTTGG GCTAAGGTTA 300  
 TTATTGCCTG ATATGGAAAT AATTATNNTT CTGNTTN 337

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SEQ ID NO:7205  
 SEQUENCE LENGTH:351  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08444

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SEQUENCE DESCRIPTION:  
 GATCAGTGAC AATTACAGG AATGTAGCAG CGATGGAATT CCCTGGAACA GTTTTTTGTT 60  
 TTTNTTTTGT TTTTGTGTTT TGTGGGGGGG GGCAACTAAA CAAACACAAA GTATTCTGTG 120  
 TCAGGTATTG GGCTGGACAG GGAAGTTGTG TGTGGGGGTG GTTTTTTCT CTATTTTTTT 180  
 GTTTGTTTCT TGTTTTNAA TAATGTTTAC AATCTGCCTC AATCACTTTG TCTTTTANAA 240  
 NGNTTCCACC TCCAGTCCTN TCTCCTCCCC CCTACTCAGG CCCTTGAGGC TATAGGGGGT 300  
 TNCTTNGAGG ACCTCANCAA AATCCCAATC CAAGTNAACC TTTTGCACAN N 351

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SEQ ID NO:7206  
 SEQUENCE LENGTH:273  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08445

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SEQUENCE DESCRIPTION:  
 GATCTATTTT TTTAAAAGAT ATTTGTGCAG AACTGTCATG TAACTCTAAG TTTTACTCCT 60  
 AACATACATA TGTTTGGGGA AGTATTCTAT TCTATACTTG CCAATGTGGA GAACAAAATA 120  
 GTTTTTTTAA GAATGAAGAA GTATATATAT CCATTCTGTA TTTTACGTGC AGCAGAATTA 180  
 TCTTCCGTAG GATTTTTTTG TGTATTCACA AGGTGATATT TGTATTGTAA AACAATAATG 240  
 GTGAAGGAAA TAAAAGGCT TTTAAATTT AAA 273

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SEQ ID NO:7207  
 SEQUENCE LENGTH:328  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08446

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## SEQUENCE DESCRIPTION:

5 GATCAGATTT TTAATAAATG GATTTCTCAT ATAAATAATA TTATCAAAAA AGGATTTCTC 60  
ATATAAATAA TATTATCAAA AAAGCTGATT TTAAGAAGTTT CTCCCAAAGT CTTATTCTAG 120  
TAATTATAGA GACCTAGGTA ATGAGTGGCA GATATATCTG CCTTTCAGAT ATGCCGTAAT 180  
GTGAAAAATA ACACAGTCAT GTGATATTCT TNATTAATA AACTGTGTT GTTTTTATTT 240  
TGGAGTAGTT CTCATAATTC ATTGGTAGGG AACTATCCAG TATTATATT CCTATGTATG 300  
10 TNTATCAGNT TAATTTTGAG GCTTGGAN 328

SEQ ID NO:7208

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08447

## SEQUENCE DESCRIPTION:

20 GATCTGTACA TACAGTGTTA AGAATGTAGA TATTAATAAT GTTATATTTA GCTGTTACAT 60  
AATATTAAGA CTCAGAGTTA AGTAATTCA CTGAAATTGA TTGCTTTTGT TGTCTTGGAG 120  
TCAAAATAAA TAACTGAAAT CTAAT 145

SEQ ID NO:7209

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS08448

## SEQUENCE DESCRIPTION:

30 GATCTGTTNA CATAAGCACT AGTCACAGGA CTACTCGTGA ATTTTCATCAA TTTATTCTAT 60  
TGTGTTTATT CATGATATCA CCTTAGTAAT TTTTGAAAAA AAAAANGTAC CACACTTGGC 120  
CAAANGCTCA TCAGGCTGAT TGTTTANCTG TNGCTGATTG CTTATCTTTA TATTGTATGA 180  
CCCGGGGNT NGNTTTGAAN GTTATATTAG GTTTGAAATG ANTTATN 227

SEQ ID NO:7210

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS08449

## SEQUENCE DESCRIPTION:

40 GATCTTTGAA CTCTGCAATA TGAAGCATAT ATGTGAGTGC TTAGCTTTCA CTCTCTTTCT 60  
GTGTGTGTGT GTGTGTATAC AGATACTAAG ACACAGATAC ATTCACATAT ATACATCTAA 120  
ATATATATAC AGTACAGTCC ATATTCAGAT TTCTTCAAGG TTATGGGTCT ATTGTTTAAA 180  
45 TTCGGAATCC AGTCAAGGAC AACACATTAA AATTGATTGT TTTGCCTCTA CAGTGTGTTT 240  
TTTTGGTTTT CATGACATTG ACTTTGATTT GAATAGGTCA GACCATTTC TGTACTTTAT 300  
ANAGGCACTT TGTAGATTG TCTGATGATT TGN 333

SEQ ID NO:7211

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid



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TOPOLOGY:linear

CLONE:HUMGS08450

SEQUENCE DESCRIPTION:

5 GATCAAGAGA GTTCGATTGG CCAAAGAACA GGAATCCCGG GCAGATTGTA TCAGTGAGTT 60  
TATAGAATGG CAGTATAATG ACAATAACAC TTCTCATTGT TTTAACAAAA TGACCAATCT 120  
GAAATTAGAG GATGCAAGGA GAGAAAAGAA A 151

SEQ ID NO:7212

10 SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08451

15 SEQUENCE DESCRIPTION:

GATCTGACAG ACGTCAATAC CTGCAGGCGT CTACAGAGAG GAAATTTGAT AAAAATATTT 60  
TAGTCACTGA CTACACTACC ATTATCTGAA GCATTCAGAT AAGACTTAGC AGAGAATGTC 120  
AGATTTTGTT TTCAATTATA ATTTTAGAAA TGCAAAATCT TATTTTTTCT AAGTTGCTTA 180  
TTGTCTATAT AAATGTTTAA TATCATTTAA AAACATGCAG AATAATACAC CTGCAGAATA 240  
20 AAAGAGCTGA AATTAAAATA TCTTTTCAA TNAAA 275

SEQ ID NO:7213

SEQUENCE LENGTH:103

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08452

SEQUENCE DESCRIPTION:

30 GATCACTTGA GTCCAGGAGT TTGGTGTTAC AGTGAGCTAT GATGGCACCA CTGCACTCCA 60  
GCCTGGGCCA CAGAGTAAGA ACATGTCTTT AAGAAAAAAA AAN 103

SEQ ID NO:7214

SEQUENCE LENGTH:144

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08453

SEQUENCE DESCRIPTION:

40 GATCTGTAGA CATGAAGGCA AAGCTCTTGT ATTTTTTTTT CATCCAAACA CCTCAATTTA 60  
TTTTATAAAT TCGTTCATTT TTCCTGTTAT GTTTTATATA ATATATGGAC TAAACAAAAT 120  
AAAATAACAG TGCAAAAGAG GAAA 144

SEQ ID NO:7215

SEQUENCE LENGTH:164

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08454

SEQUENCE DESCRIPTION:

50 GATCAGAAGA GGATGACAAT GGCAACAAGT GTTTGGAAGT TCCAAGGTGT GTTCAAAGAG 60

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# EP 0 679 716 A1

GCTTGCCTTG AGGGAGGGCT GGAATCTGTC TTCCCTGACT CGGCTCCTCA GGTCTTTAGC 120  
CTCCACCTTG TCTAAGCTTT GGTCTATAAA GTGCGCTACA GAAA 164

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SEQ ID NO:7216  
SEQUENCE LENGTH:332  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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CLONE:HUMGS08455

SEQUENCE DESCRIPTION:

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GATCTGAAGT CCCCCCAACC CTCTCCAAGT AAAGTAGTTT ATTAGAAGCT CTTAAGTCTT 60  
TAATAGACCT GCATATTTC TTCCCTTATG ATTCCTATA AAATATAGTT TATGGTGTTA 120  
TATTTTAAAC TGAAATACTG TACATATGTA AATAACTCTT GACAGGAAGA AAATATATTA 180  
ATGTAGTATT TGCCCCCTAT CAGTGAGCTG AACAAATACA TCATTTAAAT CTATGCTGCA 240  
CTTTGAGTTG CTACAAATAT GGTTCGNTTT GTTTATTTT GAAAAATGTG ATAAAGAAAT 300  
CTAAAGANTG NNNAANTAA NNNNNNNNG NN 332

20

SEQ ID NO:7217  
SEQUENCE LENGTH:277  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

25

CLONE:HUMGS08456

SEQUENCE DESCRIPTION:

30

GATCTGTACC ATCTGTGTGC TGCTGTATGC GTTCCATTGA TGGGACATCT TCAGGGACTC 60  
TTGACAGCCA CCGCTTTCAC ACCCTGGTCT GGAATAAGGA AACATCGGAG GGAGAAGTTG 120  
ACTGTCTTGA TAATTAGCCT GACCAGCAGG ATGAATGCAA GACTGACAGT GATGGACTCT 180  
GTGACATGGT CAGGTTGAGC TGAAGCCACA GTTCTCTGT GCTGTGTTT CTAACACATT 240  
TTTCTGTTTT TAATTAATAA AANNNNNNNA GGGTAAA 277

35

SEQ ID NO:7218  
SEQUENCE LENGTH:198  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS08457

SEQUENCE DESCRIPTION:

40

GATCTTAAAC TCCTGACCTC AAGCAGTCTA CCCCCGTTGG CCTCCCAAAG TGCTGGGATT 60  
ACAGGTGTGA GCCACTGCAC CCAGCCAAGT TTATGTATTT TNATTCTTTT TCATGAATGT 120  
GATTTGTAA ATNAGTGATT AAATATAATT TTNATATATT TGTATGACTT TNCTGTAAAT 180  
AAAAATTTAA ATCAGAAA 198

45

SEQ ID NO:7219  
SEQUENCE LENGTH:409  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

50

CLONE:HUMGS08458

SEQUENCE DESCRIPTION:

55

GATCTGCATC TNACGCCAC TGCACACCGT TCCTCTCCAT CTGCCCTTCC CTCCCAGGCC 60  
CCCGGTCGGG GGAGCAGGTG TGGCAAGTGT TAGGAACTCC CTTCTGGTGA CAGCTGGTCT 120  
TCCTAGAGTG TTGCTGGTAA CTATCGCCTC TTGGTCTTCT GACATCATTG CCAGGAACGG 180  
GGCACTTTTT CGTCTTGTAG TTTGGCCCTC GGGTTTCCTC ACTAGGTATT GTGTAACCTC 240  
CTCAAAAAA GGTTTATGAA ATGCTGAACC TCAGGTTTCA TAGACGTCTT TGTACACTAA 300  
AAATTCTGCA GCAGGAATAT TTTTAAACAT TCGCAGTTTT TTGTAAGCTA TATTTTTTGG 360  
ATATTTAAAT TGCTATNTNA AAANTTTTAA ANTNAATTTT GCTAATNNN 409

SEQ ID NO:7220

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08459

SEQUENCE DESCRIPTION:

GATCTCCTGT TCCGTTAGAA ATACGGTTAT GTTGACATTA TGGTACTGT GCTTGTGGTT 60  
TTGCAATAAA CATGTATTGA AAGCAAA 87

SEQ ID NO:7221

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08460

SEQUENCE DESCRIPTION:

GATCAGATAA AATAACTCCT GACAGAACT GTNNGGAAAC CAGCTGAATG TTTGACCTGA 60  
TGACTGATGT TGTATGGTTT ATGTTAAATG TATATTCTTT TAATCAATGA ATAAAGCATT 120  
AAAAATGAAA 130

SEQ ID NO:7222

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08461

SEQUENCE DESCRIPTION:

GATCAGAAAC ATTTACAATC TATTCTCTTT GAAGCCTGGC ACCTGGAGGC GTCATCTGTA 60  
TGAGANNNNN GGACTCCACA ACCTTTTATC ATAACCAGA CATTCCTTTC TATTGATAAT 120  
AACCAATTGC CAATCAGAAA AATTAAAAAT CTACTTATAA CCCAGAAGCA CTACCCGCA 180  
ACCCTTGCTT GCTTCAAATT GTTCCAACCT TCTGGACCGA ACCAATGTAT AGCTTAAATG 240  
TATTTGATTG N 251

SEQ ID NO:7223

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08462

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

5 GATCGGTGCC ATGGCAAGCA CACCCTCAGT CATCATCCTC ATCAGGACAG NCAGCCNNGA 60  
 ACTCAAGTCT TACGCTTTGG GAGTTCTTTT TCTCNTCCTT CGTTGTTGG GCTTCATCCC 120  
 NCCACCCCTC ATCTTCGGGG CTGGCATCGA CTCCACCTGC CTGTTCTGGA GCACGNNNTG 180  
 TGGGNGAGN 189

10 SEQ ID NO:7224  
 SEQUENCE LENGTH:97  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08463  
 SEQUENCE DESCRIPTION:  
 15 GATCTGATTT GGCCTGGGAC CAGTGTTCAG GTTGTTTGG TCTTTATTAA AAATCACAAT 60  
 ATTCGAAAA CAAAAAACC TAGGAGATAA ATGTAAA 97

20 SEQ ID NO:7225  
 SEQUENCE LENGTH:255  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08464  
 SEQUENCE DESCRIPTION:  
 25 GATCTGAAAT NAGAGGTTTT GGTTCACCT ATCTATGGTA TGTCTTAAAA ATCAACGAAG 60  
 ATGTCCTTGT CTTTTTNAA TTNCCGAGT GTGTTGCAGT TCCACAGCTC ACTGTTAGGT 120  
 GGCACATACC CCAAACCTGAA AACCTGACCT CGTAGGGCAT GAGTCAAAAG ACAGGTAGGC 180  
 ACAGGACAGG GCAGTGGTGA CACTACAGCT TTCAGGGTTC CCAGCCTGTC AAGAATGAGC 240  
 ATGTCTTAGC AGGGN 255

30 SEQ ID NO:7226  
 SEQUENCE LENGTH:63  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 35 CLONE:HUMGS08465  
 SEQUENCE DESCRIPTION:  
 GATCAAATTT GAAAAACCTA ACATTGAGAC AATACTATAT TAAAGTATCT CTGGTACCCG 60  
 AAA 63

40 SEQ ID NO:7227  
 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 45 CLONE:HUMGS08466  
 SEQUENCE DESCRIPTION:  
 GATCCAGCAA TCTCACTGAG TATCTAACCA AAGGAAAATA AATCACTATA CAAA 55

50 SEQ ID NO:7228  
 SEQUENCE LENGTH:220

55

# EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08467

SEQUENCE DESCRIPTION:

GATCCAAGAA CCCTCTCTTG GGGTCTGAAT CATACCCCTT TCGGGTTACA GCCTATCACA 60  
GCATTTTAA TCCTATGCAC TTAACACTTC TGTATAGAAA AAGAACATCA CACTAGAATT 120  
TTGATGACAA TAGATGACAA TATGATGAAT NTTATTATAT GAAGTGTTAA ACTTATTAGA 180  
GCAGATATGG TACTAAAAAT AAAATCCAC CTNCNCTAAA 220

SEQ ID NO:7229

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08468

SEQUENCE DESCRIPTION:

GATCGCGCCA TTCCACTCCA GCCTACACGA CAGAGTGAGA CTCCATCTCG AAACAAAAAA 60  
AAGACTTGAT TTTTATTTTC ACTATCTTTA GCATAAATTG TTCTAAGAGT GAAA 114

SEQ ID NO:7230

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08469

SEQUENCE DESCRIPTION:

GATCTTATAC AGAGAAGTAT TTTATTAAAA ATTCAAAAGG GAAGACTTTT ATGTGCTCAT 60  
TTTGTAATTT TTAATTTTAA ATATCTTTAC ATTGTCTGCC AATTAAAGTG TTTTAACTT 120  
GCATTGGAAT GGNCTCTGAA TGTATTTNTN TGGTGTNACG TTATCCGTAG ATTTCTAGCA 180  
TGANGTTAGC CTCACGATGC TGTGCAAAGG ATTTTNAAT ATGAGAGTCA CTGANAGAGT 240  
TTAANCATCT GTCCATGTTA AATGCTCTAT GGGN 274

SEQ ID NO:7231

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08470

SEQUENCE DESCRIPTION:

GATCCTTTGT TCACGGCTCT CCTTAATGAC TGAGTGAACA GTTCCTATCT GTATATTTGA 60  
CTAAACCTTT TCCTAAGCTA TCTCTCATGG TTCCTATGTT TTTTATCAT AATTTAAAGC 120  
AAAACCATCT GGAAG 135

SEQ ID NO:7232

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08471

## SEQUENCE DESCRIPTION:

5 GATCGAGCGG AAAATTCCAG AACTGTACAA GCCAATATTC AGAGTTGAGA GTCAAAAGAG 60  
AACATTGTGC TGTCTGTCAG CATATGTATA TCAGCTACAA AATATATTCA ACTTTGACTT 120  
CTTTTGACAA AGGACTTTAG GAAAAAGAGG AACAAAGACA TTATTGAGA ATTAAATTAT 180  
ATATTTTAAN TATGACTGTG ACCTTGACTG ATAATAAAGA TGTAAATAAGA NTTGCAAA 238

SEQ ID NO:7233

10 SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08472

## SEQUENCE DESCRIPTION:

15 GATCAGTTCA GCCAAGCAAC TGACAAATCA AAAACCCACT TGTCAGTTCT GTAAAATAAT 60  
TTGGTCAGAA A 71

SEQ ID NO:7234

20 SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08473

## SEQUENCE DESCRIPTION:

25 GATCTAGAGG GCTTCGAGTG AAGCCAATCA TGTTGAACGA AACTGGGTTT AGTGTAGATG 60  
AANTAGAGTG AGGCGTATGC AGTCATAAAA TGAAGGGTGG ACAGGAGATT ACATTGAAG 120  
AAAGGATAAG CACTCAGACT TGGTCTCTTT TAAATTAAAA TATTTCTTTT CTCATGTGCA 180  
AATGTATATC AAAGACTTGA ACAGGTATTC TCTTGAAATT TGAGGATTTT TAGTTTTTAA 240  
30 TGCTGNCCTT GCTTANNATT AANNATGNGT NGCCTATTGG TTCCCAAATT GTNTGGGGNC 300  
CCTAANNGTT NCCCCTNGAG GGGTNCATTT TTGAAGGNGG GTTANGN 347

SEQ ID NO:7235

35 SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08474

## SEQUENCE DESCRIPTION:

40 GATCTTGTGT TTTGCTATCC TTTTACTGT AAAATGTAAA TATTTTAAGG GATATTTTGA 60  
TTCTAAATAT GATAAAATAA TTTCTCACCT AAA 93

SEQ ID NO:7236

45 SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08475

## SEQUENCE DESCRIPTION:

50 GATCCCAATT CAACTTATCC AGAATAATTC TCTCCATTCT CAAAATTTCA NATGAGGAAC 60  
ATNNNNAGAA ACTGTCTCTT GCCAATACCT TTAGTACTGG AATTCTCTCA TCTTCCTCAA 120

55

EP 0 679 716 A1

CAGTCTTGGC AGCTAGGAAA AAACAGCTGA TTGCAATACA ACTCAAGTAT TTTGGATGAG 180  
 CCTTTACGGT AGCTAAAAAC CCATCCAAAA GACTGCTAGC CAGAGCAAAT GTTCTGCGGT 240  
 AAAGGTTGAA TTGGTACTTG AGTTTGGCCA GCCATTGANT TACTTCATCT CTCTGGGATG 300  
 GNGAACATTC TGATTGAAG GCATTTCCG CACATTCACT TTCCACATCT GTGNCCTCCCT 360  
 AGTGATTGCC TTTCCACCA GGAANGCCAA TCTCTGTTT TCCAAAGGCC CTNGGAN 417

SEQ ID NO:7237

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08476

SEQUENCE DESCRIPTION:

GATCAGACCC TCCTGTGGGC AGGGTTCTTA GTGGATGAGT TACTGGGAAG AATCAGAGAT 60  
 AAAAACCAAC CCAAATCAAA 80

SEQ ID NO:7238

SEQUENCE LENGTH:409

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08477

SEQUENCE DESCRIPTION:

GATCTGCCTG CCTCGGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCAT TTGCGCCTGG 60  
 CCAGAAAAAT ACCTTTAAAA AGCTGGGCCT GTTGGTGAC CTAAAGGATA ATACAGATGT 120  
 TCCTCTCAAC TTAGCATGGG GGTGTGTCT CAATAAACC ATTTTAAAGT TGAAANCGTT 180  
 ATGTGGAAAA TGCATTTTAT TATACCTAAC CTACTAGACC TCGTAGTTA GCCTCCCTTA 240  
 CCCTACAGGT GCTCAGAAAC CTTTNGNAGG CCCTACAGTT NGGGCAGTCA TCTAACACAA 300  
 AACCTATTTT ATAGGTAAAA GTNGTTTGAA TATCTCAAAG NTAATTTATT TGAATGGTTN 360  
 CCACTTGAAT NGCGGANTCN ANGTGTTTNN NAACCNGTNT GGTNNANN 409

SEQ ID NO:7239

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08478

SEQUENCE DESCRIPTION:

GATCTCATAG ACTTAGTACA AAAAAAGGTG AAATGTCTTG ATATTTTGT ATATTGATTA 60  
 TTGAAATAAC CTTTATGTT GGGCTAAATA CAAATATGTT ATTAAATNA ATTTAACAA 120  
 AAA 123

SEQ ID NO:7240

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08479

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTGAGGG GGAGAGGGAC GGGTCGGGCC AGCTGGTCAG GAAGGGCCTT GAGGGCCTGC 60  
 AGCCAAGAGT AGCAGTTTT TCCTCCGTCT TGTTGTTCTT GGTCCTGGA CCACAGGGCA 120  
 CACAGGCCTG GACACCATAA GGCTGGTGGG CTTTCAGAAT TGTGTTAGGG NNNNNNGAGT 180  
 GGCAGGTTCC TGAATCTCGG TCAATATAGT AACCAGCAGG ACAAGAGGTT CAGGAGGAGC 240  
 CCACATCAGA GGCTTCTAGG GCAAN 265

SEQ ID NO:7241  
 SEQUENCE LENGTH:265  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08480

SEQUENCE DESCRIPTION:  
 GATCTCTTGA ATTGCCATCT GTCATCTAAG TCTAAGGCTT TATGCTTAAT GANTTGTGGT 60  
 GTACTAGCTG GACTAGCTTC AGGAATGTCA GTGTGTTCTA CCATTAAGGT CAGATTGTCT 120  
 ACTACATCGA GATGGTGGTT GTAGTTACAG CTACTTTTAG AAACATGTCT ATTTTTTAA 180  
 GACATAACAC ATGAATGAAG AAATTCAGAA TTTGGAAAAA AGGTCCGTAA TGCCTGACAA 240  
 AGAAAAATGT TCTCCTGAGG GTCTN 265

SEQ ID NO:7242  
 SEQUENCE LENGTH:138  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08481

SEQUENCE DESCRIPTION:  
 GATCCCAGCA CCTTCACATC TTCAGCAACC CAGNNGNTCA AATTGACCT GGTGTTATTT 60  
 TAGCCCCAAA TTTATGACAT TACACAATAT TAAAATGTAA ATGTTTCTTC ACCCAAATA 120  
 CTTCTAGATA TNCTNGNN 138

SEQ ID NO:7243  
 SEQUENCE LENGTH:273  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08482

SEQUENCE DESCRIPTION:  
 GATCCTTTGA GAGATGGTTT GACTTTCCCC GAGCAAAGAG CCTGCGTTGA AAAGCGGGGG 60  
 TGGAATTGAG TCCTCACAGA TAATGAGGGG ACAANACCTA ATTGANCCGN GTATTGCCGG 120  
 GAAGGAAAAG GCAACGGGCC AAGCCTTTGA CAGGGTGCGA AACTGACTTT NATCATCGTT 180  
 ATAGTCTTTA AATCCTGGGA AACGAGTTGG CAACCCCAA ATAAAGAAGT GTAATGACGT 240  
 CTGATGACTT CACCCAAATA CAGACCATT CAN 273

SEQ ID NO:7244  
 SEQUENCE LENGTH:132  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08483



## SEQUENCE DESCRIPTION:

GATCTATAAA ACAGACAGAG ATAAGTACAA CAGAATATCT CGGGAATGGA CTCAGAAGTA 60  
 TGCCATGTGA TGCTACCTTA AAGTCAGAAT AACCTGCATT ATAGCTGGAA TAAACTTTAA 120  
 ATTACTGTTA AA 132

SEQ ID NO:7245

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08484

## SEQUENCE DESCRIPTION:

GATCCGCCTG CTTACGCTC CCAAAGTGCT GGGATTAGAG GCGTGAGCAT TCATGTCCAG 60  
 CCAGCACTGT GCTGTTTTT ACATGCATGT TCTCATT CAN TGCCATGCGG CAGATTCTAG 120  
 GATTATNATT ATNCTCACTT TACAGATGAG GGAGTGAGAC TTAAAGGGGT TAGGTAATTT 180  
 GCCACATCC CCCAACTAGC AAATGGTAGA GCCAGGATTG GAATTTGTTC AGGCTCTTAA 240  
 CCATTGCACT CTTTCAAAT GTTAAAAATA ATGTTGTGTC TCATTTTAAA AAATTAAATA 300  
 AAANCTCTTT GGACCAAGAA A 321

SEQ ID NO:7246

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08485

## SEQUENCE DESCRIPTION:

GATCTCCCCA TTTGGAGACA GAGCCATTTG GATATTTNCC CCTTNACTT CTCCANNNCC 60  
 TGAAGCGTTC CTTCCCTGGA GGAACCTTTT GGTTCAGGG CTAAACTN 108

SEQ ID NO:7247

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08486

## SEQUENCE DESCRIPTION:

GATCTCAGCT CAAATATTCC TTATGCAGAG ATGCCTTCCC CTGATTCCCT AAAC TAGACT 60  
 CGGACCCCTC TGTCTGCAT CTCTGTGGCA TATCATCTGC CCCTTTTGTA AAAC TTATAA 120  
 ACTTGTGGTT ACTTGTA AA 139

SEQ ID NO:7248

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08487

## SEQUENCE DESCRIPTION:

GATCATGTGA GCTCAGGAGT TCGAGACCAG CCTGGGCAAC ACAGCAAGAC CCTGTCTCTA 60  
 TTTTATTCTA TGTTTTAAAA TTAAAAAATT AAAAAGAAAA AAGAATAACA TTTTATAAGA 120

AAATATTTTA TGAGAGACTT ATAAAAGAGA CATTAAGAAT ATGAAGTAAT ATATTNCGTA 180  
 TTCCTTATCT CAATAATGCT GTAGGGAAAA ANCAATTGAA ATAAAAGCAG TAAATGAGTG 240  
 GAAA 244

SEQ ID NO:7249

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08488

SEQUENCE DESCRIPTION:

GATCTAACTT GCAGTGTATT TTCTAGGCTG GAAAGTGGA AATNAAATAT ATTATAATCT 60  
 TAGGTTACAT AAAGTTTCTA AAGTTTCAAA GAGTCTTGAT ACAAATCAG TTTATATTCT 120  
 GAAAATATTT ATAATAAAGT ATTCTAATT CTAAT 155

SEQ ID NO:7250

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08489

SEQUENCE DESCRIPTION:

GATCGCACTG GAAGATTTTA TAAAAGAATT TTTGTGGGTC GGGGGGACAG TAACTTCCT 60  
 GGGCCACGTG GGTCCCTCAG GAGTTTTTCA GGCAAA 96

SEQ ID NO:7251

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08490

SEQUENCE DESCRIPTION:

GATCTNATAT TGAACCCTAT GCCAAATAGC GTGGCATGAG GCCAGAGAAC AGTGCTTNCC 60  
 TTCCCGNCT CCACCCAAAT TGTCCCTTGC TCTNGATATT ATGCCAGTNC CATATTTN 118

SEQ ID NO:7252

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08491

SEQUENCE DESCRIPTION:

GATCTGGAAA CTATTTGGNT TTTNTTTTCA ACTTTTCATT TGGATGTTTG GCGTTGCACA 60  
 CACACATCCA CCGGTGGAAG AGACGCCCGG TGAAAACACC TGTGCTTTT CTAAGCCAGT 120  
 GAGGTTGAGG TGAGAGGTTT GCCAGAGTTT GTNTACCTCT GGGTATCCCT TTGTNTGGGA 180  
 TAAAAAAAT CAAACCAGAA GGCGGGATGG AATGGATGCA CCGCAAATAA TGCATTCCT 240  
 GAGTTNCTT GTTAAAAAAA ANTTTTTTTA AGTAAGAAAA AAAAAGGTAA TANCATGGCC 300  
 AATTGTGTTAC ATAAAATGNC TTTCTGTGTA TANNTTATTC CTAAANATC CTGTTTATAT 360  
 AANNNTTCAG TAGNTGGAGA AACTTTCCAT N 391

# EP 0 679 716 A1

SEQ ID NO:7253

SEQUENCE LENGTH:385

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08492

SEQUENCE DESCRIPTION:

GATCATGAAT CTCTAATAAA TTAAATCTC TTAAACCAGT AGGTGCTTAA TATTTTTTAA 60  
 TTTGATTAAT GCCCATTTAA ATCTCATGGG TTCTATTAAA AATATATATA TATAGGGCCC 120  
 CAATCCATTG CCATCAAATT GCCCTTGGAC TTTTCCAAGG TATATTATGG GGTTTTATGC 180  
 AAAATTCCAA GCTACCATGT AACTTTTTTN AACCATTTAA CAAGGAGGGG GAACTGTTTC 240  
 CTACCTTCTT TACATGTTGT GCATTGTTGT GGTCCAGAAA TGCCAAACCT TTTTAAAGAT 300  
 GGTGCAACTT TGAGTCCTTG GCTTGACTAT ACAGGNCCTG AACTTCATGG CATATCAACT 360  
 TTGNCATATC TGCAGGTGNG CTGTN 385

SEQ ID NO:7254

SEQUENCE LENGTH:414

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08493

SEQUENCE DESCRIPTION:

GATCACCATT TTTTTCCAGG CTTTCTGCCT CCNAGATGTG GCACCATAGT GCGGTGCCCT 60  
 GTGGCTTCAC CGCCCTACTT CCACCTCCGC CCAGCCTGTA ATGTTTATAT AAGCAGCCTC 120  
 AAGGACCAAG AACCATCTGC GAAAGGACAC ACACAGGAAA TTCATAAAAG AAATCTGANT 180  
 GGNTAAAACC ATGAAAAAAA GTATGCTTCA TTAGTAATTA AAGAAAGGCA AATAGAGCTG 240  
 GAAGCNTTTT NCCNTTNGCA AACCATAACA GAAAANNNTA NGACCCAATA TTGGCAAAGA 300  
 GACTACTGAA AANCCATTCC CATACATTGC GTGTGGGNGT ATACATCGGT GCAGGCTTCC 360  
 TGGATGACAG TTGGGTGATA TGTGTCATGT GGCCTAANAG CCTCCATGTC ANTN 414

SEQ ID NO:7255

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08494

SEQUENCE DESCRIPTION:

GATCCTGGTT TTGTGATTGA CAATATTTCA TGCTCTGTAG TGAGAGGAGA TTTCCGAAAC 60  
 TCTGTTGCTA GTTCATTCTG CAGCAAATAA TTATNATGTC TGATGTTGAC TCATTGCAGT 120  
 TTAACATTT CTNCTTGTTT GCATCTTAGT AGAAATGGAA AATAACCACT CCTGGTCGTC 180  
 TTTTCATAAA TTTNCATATT TTTGAAA 207

SEQ ID NO:7256

SEQUENCE LENGTH:412

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08495

## SEQUENCE DESCRIPTION:

5 GATCAAGAGT ACACTTCCTG GCAGTGATTA AGGAGTGTGT ATCTAACAGA AAAAATATAT 60  
ATACCCTGTG AACCCGAATA TGGAATTCAG ATTGTTTCTG CCCTCAGTAT CATACTTAAA 120  
AAACAAGCAT ACAAACAAAC ATAAGGGAAC AACAGCAAC CATAACAAAA ACAAACCTTT 180  
AAAGGTGGGT TTTTGCTGTG ATAAATGAAT ACGGTACTCT GAAGGAGAAA AAAGTTTCTC 240  
AAATGAGCTT AAAGTCAAG TGATTTAAAA NNTAGAGAAT ATAATTCTTA ANGCTATTGA 300  
AAGTTTCAAC CAGAAANCCT CANGTGAAT TTGTATGTAA ATGGCATCTT GNNTGTAAGT 360  
10 TCTGTGNTTC TTTAGGCAAC CAATTAGCTG GAACCTTGGT TTTGTGTGGT TN 412

SEQ ID NO:7257

SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08496

## SEQUENCE DESCRIPTION:

20 GATCTGAAA TCAAGCTACA TGTATTGTG TATAAGACCC TGTGTTTCAGG ACTGGGTGAC 60  
TTTTCTAAGA AATATGGGGT TTAGAATGGG GTTGACTGTA TTTNTAAACC TAATTCTGGA 120  
GAGAAGATTG TATTNTAAC AGTTTTTTGG GTTTGGCTTC CTCTCACAT TTCTTTAGCT 180  
TTGAATTTT ACTAAATAAA TTTCTCTCTG ATTAATTTT TTTTCCCCA TCTGGGAATT 240  
TGAAATCTCG GTGCTTACTG TNACACCAAT TTGTCCAANG GGTGAAATC ACTTTAATGC 300  
CAGACCATGG TAATTTGCAG CCATTTTCAGG CAGGTGGTGG NCCTTTTNA TACCATCGTT 360  
25 ACGGGGTCCC NTTAAATATT CTGGGGGGTG ATGTAAATNT AACGGN 406

SEQ ID NO:7258

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS08497

## SEQUENCE DESCRIPTION:

35 GATCTCCATT TCCGCCAGCT GCCTGTAGCC ACGTGGCATC CTGCCTGTGG TCTGGGTGAG 60  
ATTTACTGTG ACCAGATGTA GAATAAATGT GTCTCATCCT GCATTTTTTT TCTAAA 116

SEQ ID NO:7259

SEQUENCE LENGTH:435

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS08498

## SEQUENCE DESCRIPTION:

45 GATCACTTTT TAGTTAGTTT GAAACCTGCT TTTAGTTTAT ATGTAGTATT TCTACATATT 60  
GTTACTTAAA TTGAACTAAC AATTTACTTT TNAATTTTNC TTCTTCCTTT TAAAAAAGA 120  
GTATATAATC TGACAATGTT AGTACATCTT TTAGAAGGTC ACTATAAAGT TGCTTTCCCT 180  
ATTTATTTGG AAAGGATTAT TTCCTTATNA TTTTAAAAA TCTTTTAATT NNTGTCTTNT 240  
CAAGTAATTT TATCATTGTA CCAAGCCTAA GGATGAGTGG CAATTTAAAA GNCACAAGGT 300  
GTGCATCTTC TATCTGCAA TACTCCAAAC AGAANTTATT CCAGTTTGTG GATACTTTGA 360  
50 GTGGCCCAGG GAAAATGTGT ATGGTTTtag TGTNCTGAAT TGNCATTCCA AAGGGTGCGG 420

AAGGTTNCTG TTAAA

435

SEQ ID NO:7260

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08499

SEQUENCE DESCRIPTION:

GATCAAAAAA GGAATGGATA TACAAAGTGT TTTGTGAAAT AAAAGCTCCC TAAAATGGTA 60  
AA 62

SEQ ID NO:7261

SEQUENCE LENGTH:389

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08500

SEQUENCE DESCRIPTION:

GATCGCACCA CTGCACTCCA GCCTGGGCGA CAGAACGAGA CCCTGTCTCC AAAGGAAAAA 60  
CAAAAAAGAA GAATAAAATA ATTTGGATGA AAATCATGTT TATTTAAATA GTAATGTCAT 120  
GAGACTATTA AAGATGTGCC AGAGTTTCAA TGAAAATCAT TAAAGTAGGA CAGCTAAGAA 180  
ATTAATATTA ATATCAAANT TATTGATANT CTAAATTAT TGATTATTCC TTAACGCACT 240  
CCATTCTCCT TTTACATTTT ATCATGTTTC TTTTGAATAT ATGANTTGGC AAAGGCCTTG 300  
ATGAAACTGA GTACTAAGAT TTGGTCCAGN GTATGTCAGG ANGNCACCTC AGATTGCCAT 360  
TTTAAATAAN GTTGTNCATG ACCAATAAA 389

SEQ ID NO:7262

SEQUENCE LENGTH:302

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08501

SEQUENCE DESCRIPTION:

GATCCCGTGC TACATCTCCT CCCCGGACGA GTGCCTCTGG ATGGACTGGG TCACAGAGAA 60  
GAACATCAAC GGGCACCAGG CCAAGTTCTT CGCCTGNATC AAGAGAAGTG ACGGCTCCTG 120  
TGCGTGGTAC CGCGGCGCGN CGCCNCCCAA GCAGGAGTTT CTCGACATCG AGGACCCATA 180  
AGCAGGCCTC CAACGCCCTT GTGGCCAACT GCAAAAAAAG CCTCCAAGGG TTTCGACTGG 240  
TCCAGCTCTG ACATCCCTTC CTGGAAACAG CATGAATAAA ACACTCATCC CATGGGTCCA 300  
AA 302

SEQ ID NO:7263

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08502

SEQUENCE DESCRIPTION:

GATCGGAAGG TGGTGAATCT TTCCAGAGCA GCTGAAAATN TCAGCATGGA GACAGTAAGA 60

# EP 0 679 716 A1

AAAGAGACGG GGTGTGGATA AGACTCTGCC ACCGTGTCAC ACTAGCATAG GAGGCTGCAC 120  
 GTTCATTTGT TGTGTTTTT TTTTCCTTTG CCAACCTCCG TTCTATTTAT GTGCAAGCAG 180  
 TTTGGATTCA AGTTCTTGTA TCTGTCTGTT CTGGGACCTG GGGATTGTNA GGGTTCCTC 240  
 ACAGCCAGCA CGACCCCGAG AAAGAGGCGT CCCACAATAA ACACGTCACC TGCTAAA 297

SEQ ID NO:7264

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08503

SEQUENCE DESCRIPTION:

GATCAACAGT TCTATTACAG ATTAGAATGT TTCACTTCAC AGTTCTTTGT AAATCATGTC 60  
 AATTTTATN ATAGNTGTCA ATTTGGGAAA ATCTGTATTA AAATTTTAA ATGAAA 116

SEQ ID NO:7265

SEQUENCE LENGTH:442

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08504

SEQUENCE DESCRIPTION:

GATCCCTAAT TGGCCAGGCC TGACCCTCTT GGACCTTTCT TCTTTGCCGA CAACCACTGC 60  
 CCAGCAGCCT CTGGGACCTC GGGGTCCCAG GGAACCCAGT CCAGCCTCCT GGCTGTTGAC 120  
 TTCCATTGC TCTTGGAGCC ACCAATCAAA GAGATTCAAA GAGATTCCTG CAGGCCAGAG 180  
 GCGGAACACA CCTTATGGC TGGGGCTCTC CGTGGTGTTT TGGACCCAGC CCCTGGAGAC 240  
 ANCATTCACT TTTACTGCTT TGTAAGTACT CGTGCTCTCC AACCTGTCTT CCTGAAAAAC 300  
 CAAGGCCNC TCCCCCACC TCTTCCATGG GGTGAGACTT GAGCAGAACA GGGGCTTCNC 360  
 AAGTTGCCAG AAAGACTGTC TGGGTGAGAA GCATGGCAGA GTTTTCCCA GGACAGGTGT 420  
 TGACCAGGGC TTNTTGTTA TN 442

SEQ ID NO:7266

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08505

SEQUENCE DESCRIPTION:

GATCTTCTGA CATTACTGCT GTCTGAGATT TGTATATGTG TAAATACAAG TTCCTTGATA 60  
 CCCTAAACC TTGGATTAAA CAGAATGTGC ATTGTACATC TTAAACAAA ATGTATATTA 120  
 ATTTATTAAA TCTAGTTGTC ACTTTAAA 148

SEQ ID NO:7267

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08506

SEQUENCE DESCRIPTION:

GATCTTAATT CTGTGTCTTA ACAGCAGGAG ATGAAATTCC CACATGGGAG ATGGCCTCCC 60  
 TGTCACAGGA AGGAATANCA TTCTCCCTAT CAATNNNGAG AAATTGGAAC TNGGAGAATT 120  
 CTGTATAGAC CCTTGTTC AA GTAATTNTTC TAGTTTAAAN CNTCCCAAN 169

SEQ ID NO:7268

SEQUENCE LENGTH:89

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08507

SEQUENCE DESCRIPTION:

GATCAAAGAG TCTCATCAA GCAAGTTCTT CCCTCCCTGG TCCCCTTTGG CTTTCTGAAA 60  
 TNATTAATTA AAAGAAAGGC CCTAGGAAA 89

SEQ ID NO:7269

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08508

SEQUENCE DESCRIPTION:

GATCATTGNT TTATTTTGTA GTCCACCTTT CAATCACTTC ATGTATATAA AAAGGGACTT 60  
 TGAATGTAAT AGTCTTCATC TTATTTATTG AAAAGATGTA CTAAAGGAAT GACTATTTTT 120  
 AAAAAAANCT CTAGTATTTA TCAATATGAC TCTAAGGGAA AAATCAAGAA ANTTAGAGGA 180  
 AGGTTCAANT TAGTAGTAAG GAATAGGANC NNNCATATNA NCTNN 225

SEQ ID NO:7270

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08509

SEQUENCE DESCRIPTION:

GATCTGTAGT GATGGAGTTC CTTCTGGTGT CAGCCCCACA GGAGGCTCCC AGGCCTCCCT 60  
 CACTTCCCAT ACCCAGTCTA GGAGCTCCTT CTGGCTCCCA AGCACCAGGA GCTTTCCTCC 120  
 GCCTTTNAGT TTTGGTTCCT CCACTGGAAT GTAGGCTCCT CACGGGCGAT GGCTGTCTTT 180  
 TCTTGACTTT GTATCTTCAC TGCCAAGCAA AAAGTCTGCC AAGTGGGAAT NTTAATAAA 240  
 TATTCATTGA ATAATGAAA 259

SEQ ID NO:7271

SEQUENCE LENGTH:357

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08510

SEQUENCE DESCRIPTION:

GATCCCAGAA GGAATGCTGA CCCCTCGTCG TATGACCTGT GCATAGTCTC CAGAGCTTCA 60  
 AAGGCAACAC AAGCTCGCAA CTCTAAGATT TTNTNAAACC AAAAAACCC TGGTTAGCCA 120  
 TCTCATGCTC AGCCTTATCA CTTCCCTCCC TTTAGAAACT CTCTCCCTGC TGTATATNAA 180

AGGGAGCAGG TGGAGAGTCA TTTNCCTTCG TCCTGCATGT CTCTAACATT AATAGAAGGC 240  
 ATGGCTCCTG CTGCAACCGC TGTGAATGCT GCTGAGAACC TCCCTCTATG GGGATGGCTA 300  
 TTTNATTTTT GAGANGGAAA AAAAAAGTCA TGTATATATN CACATAANGG CATANAN 357

SEQ ID NO:7272

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08511

SEQUENCE DESCRIPTION:

GATCTAAATN AACAGCATTT TTTTCCTTAG CCTCTGTTTG CCACTCTGGG TATCTCTCCT 60  
 ATGGGCAAAG CCATTAGAAA TGCATAAAAC CTCGAGACAT GGTTTTTGGC AAAAACTCCA 120  
 TGACTTTAAA CTAGCTCTTT NACTACTGAC CTTTCACAGA GAAAAAATAT TTCCCTTGAA 180  
 AAAAACTGGG CTTGTNATTT TTNCCCTTGT AGCTTTAAGC AGAGACATAA GTGCCTTGCA 240  
 TTACACATAG TAAACTTTCT TTAATA 265

SEQ ID NO:7273

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08512

SEQUENCE DESCRIPTION:

GATCTTCTCT TTTTGTGGT TCATTTTGT CTGGGTTTG GTTTTCTTCA CAATCTTGAA 60  
 CATTTTACAG TAGAACTCAT CTAAAAATGG ATTTGGGGAT GGGGAAACAT GCACAAAATC 120  
 TTTTCATAAT TAAAAAGAGC CTTACTTTCT TTACATACCA CAAA 164

SEQ ID NO:7274

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08513

SEQUENCE DESCRIPTION:

GATCCGTTCC GTGGTCGCCC TGCACAACCT CATCAACAAC AAGATTGCCA ACCGGGATGC 60  
 AGAGANGAAA GAAGGGCAGG AGAAAGAAGA GAGCAAAAAG GATAGGAAAG AGGACAAGGA 120  
 GAAAGATAAA GATAAGGAAA AGAGTGATGT AAAGAAAAG GAGAAAAAGG AGAAANAGTA 180  
 AAACATGTAT TAANTAGCTT TTTTAATTG TAANTTAANA TCTTACANAC TNGAANCNAN 240  
 NNN 243

SEQ ID NO:7275

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08514

SEQUENCE DESCRIPTION:

GATCACAGGC CTTGAGAGAG NAGAATAAGA CACTCTTGGG GACAGAAAGT TAAAACACCG 60



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TGTGTCCTCA CTTATATGTG GCGCTAAAA AAGTTGATGT CATAGAAGTA TAAAGTAGAA 120  
CAGAGGATAT GGAAGGTGG GAAGGGTAGG GGAAGGGAA GGATAGGGAG AGGTTTGTTA 180  
AAGGATACAA AATTACCACT CGATAGGAGG AGTAAGTNCT AAGTNCTAGT ATTCTATACC 240  
ACTGTAGGAT GACTATAGTT AACAN 265

SEQ ID NO:7276

SEQUENCE LENGTH:261

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08515

SEQUENCE DESCRIPTION:

GATCGCCCGC ATTCCGGAGC CTTCAAGTAA ACGGCGCGCC CCACGAGACC CCGGCTTCCT 60  
TTCCCAAGCC TTCGGGCGTC TGTGTGCGCT CTGTGGATGC CAGGGCCGAC CAGAGGAGCC 120  
TTTTTAAAGN ACATGTTTTT ATACAAAATA AGAACAAGGA TTTTAATTTT NTAAGTATT 180  
TATTTATGTA CTTTNATTTT ACACAGAAAC ACTGCCTTTT NATTTATATG TACTGTTTTA 240  
TCTGGCCCCA GGTAGAAACT N 261

SEQ ID NO:7277

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08516

SEQUENCE DESCRIPTION:

GATCCACATC TAGTGAAATG TCAGTGTCAA AATATTATAG ATTATAGCTA AAATCCAGAT 60  
TAATACTCAT TTGGGGTTTT TAATAGTGGA ACTTCATAGT AATACAAAAA GCAGATTGTC 120  
TTCCTGTCTC CGCTGTCTCC ACAGTAGGTA TTGAAACTGG TAAAANCAGT TTTTGTATAG 180  
TGTGTGTATA TAAGANANNN TAGATACACA CATTCTTTT CCTCAGTCAN CACATTGATT 240  
GACCACTCTG GCAAAGATGN 260

SEQ ID NO:7278

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08517

SEQUENCE DESCRIPTION:

GATCCCACTC CACCCACCT CAACTTATTT AACTTCCTAA TTAAATCAGA CTGTTTGAAA 60

SEQ ID NO:7279

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08518

SEQUENCE DESCRIPTION:

GATCTGGAGA CTTAAAAAGA AAACAAAAAC AAATGGCAAG TTCACTTAA GGGTGGTTTG 60  
CCCTTAAGAA GAAAGCTGTT GGGACAAAGA CACCGAGCCA TTATACCCAG AATAAAATAA 120

TACATTTATG CTGGATTTTA TTCAGACCAA ACTAAA

156

SEQ ID NO:7280

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08519

SEQUENCE DESCRIPTION:

10 GATCATTGTT TAGAATATTT CCGCCACCTT AGAAAGTTTT GTCATGCCTT TTTTTCAGT 60  
CAGTCCCTCC CCTTCACTCA CTGCAAGACC ACCACTGTTG TGACTIONTAT CATCTAAATG 120  
TAGCTTTGGA ATCATGTAGT ATGTACTCTC ATGTCTCTGA AATTCATCCA TGTGTGTGCA 180  
TAATTCAGTA GTTCACTACT TTTTAATTC TGATTAGTAT TTCATTGTAT GGGTGTACTG 240  
15 TAATTTGTTT AACCATTAC CTGCTGTTTA ATCTTTTGAG CTGTATGCAT TTGGCTATTA 300  
TGAATAAAGC TGCTTTGAAC ATTCCTAAA 329

SEQ ID NO:7281

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08520

SEQUENCE DESCRIPTION:

25 GATCAGAGAA GACCCCTGAG ATGAATCAGG GCCCTGCCCT GNCCACCAAC TCTTTTCTAG 60  
CAATCATGTC CTGCCAGGC TGCAGGCTTC ATTAGGCTCC TGCTGTCTC CATGATGTGA 120  
CTAGCACAAG GTGTATATAT GTTTTGTACC TCTGCCGATG GCTGTACATA GTGTATGAAA 180  
GTTATTTAAG CCCCATGTTG TACATTCTG TTCCTAGATT GGATGTGTGT GTTCTAAGAA 240  
30 GTTGTCTATA ATAAAACCTG AATGACCAAA 270

SEQ ID NO:7282

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08521

SEQUENCE DESCRIPTION:

40 GATCCAATTA TTAGAAAAGC ACTCTTAAGA GTGCAATGAA TGTGATTTGA AAACCTTGAAA 60  
GCAGCCTAGA TTTTACTATA TTTGTTATTG TTATCAATGG GGGTTTGTCA ACCTTAAAAA 120  
TTATTTTNA TGTAAGATA CCTAGGAATT TCTAATAACT GTATTGTTT TAATAAACTT 180  
TGACTTTGCT GTAAA 195

SEQ ID NO:7283

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08522

SEQUENCE DESCRIPTION:

50 GATCTACCTC AGTTAAACAG TTGGGTGCTA TACTAAGTC TGTCAAATTA AATTGGAAAA 60

55

# EP 0 679 716 A1

AGTAACCAAA CGGTGAGATA CAACTCCACA TGAAACTTGA AATTGTAATT TCCGTTTATT 120  
 TAATGATATT TTNATTTATT TGTGCCITTT ATGTTGAACC CCAATGCATT GAAAAANTTC 180  
 AGTATGAAAC AGTACATATT TNATTTATAT TACAGGTGGG AGAAAAGTCC AATTGGTCAT 240  
 GGAATTTGAT AGACTTTTCC CCAGCCAACT GCTACAGTGT ATTATAATCC CGACTGCCCC 300  
 CCTGTGAAAA GANAAAAAAA ATTGTCCANG GGCAATTTTN CCATTNCNA ACCANTANNG 360  
 NCCANNCTCC TTAAAAANGN GNGNNN 386

SEQ ID NO:7284  
 SEQUENCE LENGTH:187  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08523

SEQUENCE DESCRIPTION:  
 GATCAGTTAG TAGGCTTTTCG NTGTCTTCTC TTTCAATACA TGTACATCTT TACTGTTTGA 60  
 AAAGTGTTAC AGCTGTCAAA GAATCTTCAT GGACCTGAAG ATAATTTNTT GTGAAGTTGA 120  
 ATGCAAGTNT ACTGTCATTC ATAGTGTTAA TATCAAANTA CCAGGAATNT TNACTTTTNC 180  
 NACCTNN 187

SEQ ID NO:7285  
 SEQUENCE LENGTH:113  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08524

SEQUENCE DESCRIPTION:  
 GATCTCAGAA ATTGTATCTN AGTTGGTATC AACCAAATGG AGTGACTTAG TGTACATGAA 60  
 AGCGTAAAGA GGATGTNTGG CATTNNACT TTTGGCTTGT AAAGTACNGG CTN 113

SEQ ID NO:7286  
 SEQUENCE LENGTH:120  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08525

SEQUENCE DESCRIPTION:  
 GATCAAAGAG TAAGCCACAC ACGGATAATC AGTTACTAGG GATGGAGGTG TGAGGGTTCA 60  
 TTATATTATT CATTTTACTG TTGTATATGT TTGAAAATNT CTATAATAAA AAGCTTTAAA 120

SEQ ID NO:7287  
 SEQUENCE LENGTH:65  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08526

SEQUENCE DESCRIPTION:  
 GATCATGTGT ATGAATTGTT GGTGCTCTAA AGAACAGCAC AAATAAAATN ATTTTCAAAT 60  
 TTAAA 65

# EP 0 679 716 A1

SEQ ID NO:7288

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08527

SEQUENCE DESCRIPTION:

GATCCGNCCT CCTCAGCCTC CCAAAGTGCT GGGATTACAG GCATGANCCA CTGCACCCGG 60

CCCCATTCCT CACTTTAGCC TCAGGCAGAG AAGACNGCGC GATGGGGNNN 110

SEQ ID NO:7289

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08528

SEQUENCE DESCRIPTION:

GATCTGCGAC ACTGTGGACT GAACACACTG AAGCTCTGAT GGGAAAACCT GGTGACTGAT 60

ATAGTTGTTC AGCAATAATT CATAGTCTGT GATGAAGAGT AGTGAATACA ACACACAACC 120

AGGCAGCCTT CTTGACTATA CTTTGACAT GNTTCTTTA GGAATTCAC CACACATTTA 180

AACCAGTTAG TGCCTTCTAG AAGAATGGCT TTCCTTTNTN CTACACAAAN TTTGAATTAT 240

ACAAGNNTCT AAATATAATA CCTTTNAATA AAAAGGNTAA TTNGNCCCT CTGAAA 296

SEQ ID NO:7290

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08529

SEQUENCE DESCRIPTION:

GATCAGGTCC AAGCAAAACG TCCAGAGTGC TACAAAATGT TCGTTTCTCA GTCCAAAAG 60

AAGTGGA AAA GAATCTGAAG TCATGCTTGG ACAATGTTAA TGTGTGTCC GTAGACACTG 120

CCAGAACACT ATTCAACCAA GTGATGGAAA AGGAGTTTGA AGACGGCATC ATTAAGTGG 180

GAAGAATTGT AACCATATTT GCATTTGANG GTATTCTCAT CAAGAACTT CTACGACAGC 240

AAATTGCCCC GGATGTGGAT ACCTATANGG NGATTTCATA TTTTNTTGG GAGTTCATAA 300

TGAATAACAC AGGAGGATGG GNTAAGGCAA AACGGAGGCT GGGTATGTGT GATGGGAAAA 360

CTTCTTCAT TGGTNCTTTC N 381

SEQ ID NO:7291

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08530

SEQUENCE DESCRIPTION:

GATCACCCCC GCCGACGGCC CCGGGCCCCG ACGGCCCGGA AGTTCGCAA A 51

SEQ ID NO:7292

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08531

SEQUENCE DESCRIPTION:

GATCATTCTG TTCTTTCAAG GAGAAATAAG CCTAAAAGAA GAAAAACAAA AAAAATTCTG 60  
TATAAAACTG TAATCCTTTG TATTCATGTT TACAGTGCTA TTACTATAAT NCAAAATTAT 120  
GTATGTGACT TAGAGTTATA TAATCATAAT TTATGTTTAT TTCAAATATC TAAGTTTATT 180  
GCTTGGATTT CTAGTGAGAG CTGTTGAATT TGGTGATGTC AAATGTTTCT AGGGTTTTTT 240  
TAGTTTGTTC TTATTGAAAA NTTAATNAT TTATGCTATA GGTGATATTC TCTTTGAATA 300  
AACCNATAAT AGAAAATAGC AGNCACCATA ANCATCTTTG TAAATNN 347

SEQ ID NO:7293

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08532

SEQUENCE DESCRIPTION:

GATCCAGAAA CTTTCCCAA GAAGCTTGGA CATGGATTGC TGGTAAACAC AAAAAGCTGCA 60  
TGGAGGGCAG AGCAGCCGGT TGAATCCCCC TTGTCAATAT CTAAAGTGG AAAAGCTTGA 120  
AA 122

SEQ ID NO:7294

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08533

SEQUENCE DESCRIPTION:

GATCATCTTT CCTGTTCCAG AGAAGTGGGC TGGATGTCTC CATCTCTGTC TCAACTTTAC 60  
GTGTACTGAG CTGCAACTTC TTAAGTTCCC TAACTNAAAG ANCGACTCTG ACAGAAACTN 120  
TNTTNCNCA ACAGTTTN 138

SEQ ID NO:7295

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08534

SEQUENCE DESCRIPTION:

GATCCTTCCG GNGGAGTGTC GGAGAAGAGA GCTTGCCGAC GATGCCTTCC TGTGCAGAGC 60  
TTGGGCATNT CCTTTACGCC AGGGTGAGGA AGACACCAGG ACAATGACAG CATCGGGTGT 120  
TGTTCTCATC ACAGCGCCTC AGTTAGAGGA TGTTCTCTT GGTGACCTCA TGTAATTAGC 180  
TCATTCAATA AAGCACTTTC TTTATTTTAA A 211

SEQ ID NO:7296

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

# EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08535

SEQUENCE DESCRIPTION:

5 GATCAACGGT ACTTGTTTAA AAGAAGCTTA TGTGGACTTT GTCTTTTCTC GTTGCCACAA 60  
CCTCTTTTAA TGTGCCTATA GTCCACTATA GCATGCATAT CTCAAATTGC AATTCCTTGC 120  
AATTCCTGGA TAAACGCTTT ATTTTGGAGA AA 152

SEQ ID NO:7297

10 SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08536

15 SEQUENCE DESCRIPTION:

GATCTGCTGA CTTATATAAA GCTTTTTGAT TCCTACTAAG CTTTAAGATT TAAAAATGT 60  
TCAATGTTGA AATTTCTGTG GGGCTCTATT TTNCTTTGG CTTTCTGGTG AGAGAGTGAG 120  
GAAGCATTCT TTCCTTCACT AAGTTTGNT TTCTTGCTT CTGGATAGAT TGATTTTAAG 180  
AGACTAAGGG AATTTACAAA CTAAAGATTT TAGTCATCTG GTGAAAAGG AGACTTTAAG 240  
20 ATTGTTTAGG GCTGGGCGGG GTGACTCACA TCTGTAATCC CAGCACTTTG GGAGGCCAAG 300  
GCAGGCAGAC CACTTGANGG AGTTCGGGNC CAGCGTGGCC ACCGTGGTGA ANCCCTGTNT 360  
CTNCTAAAAA TNCAAAATTT N 381

25 SEQ ID NO:7298

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08537

30 SEQUENCE DESCRIPTION:

GATCAACAGC CTCCTCTCTT GGGGACTCTC AAGAGCCTGT TTCATCTAG AAGTAGTAGT 60  
TTGATTCTGG TTTCCCTCCT ACAGTGTGTC CTCCGTCTCT TTGCAGCTCC GTCATTACCA 120  
TAGGGGACTT GGTTTTAGAC TCTGATGAGG AAGAAAATGG CCAGGGGGAA GGAAAGGTGA 180  
35 GTGGGAAGGA GCAGAAAGCT GGGAAAGGGG ATGGGTAGAA CAAGACTGAG AAATCCACAT 240  
GCTTCAGANT TCAGAGGGTT CAGGGAATNG TTTCGGATAG TAGGCTCTCC CTGCTCCCTT 300  
CTCTACAGGA ATCTNTGGAA AACTATCAGA AGACAAAGTT TGACACCTTG ATACCCACTC 360  
TNTGTGAATA CCCTACCCN 379

40 SEQ ID NO:7299

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08538

45 SEQUENCE DESCRIPTION:

GATCATTACA AACAAAAACT GTAATTTTNT TATATTTGAT TCAATGGAAT TTACCTAAAA 60  
AATAAAGACT AAAAAATGTGA AA 82

50 SEQ ID NO:7300

55

EP 0 679 716 A1

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08539

SEQUENCE DESCRIPTION:

GATCCCTTTA TTGACAGCCA GTTTGAGGAC ACTGTCCCAG CATCTCTAAT GGAGCCTGAG 60  
CCGGTGTGAG GACCAGGATG TCTTTTCCCA GCCCCAAGAG ACCTGTTGCT GCTTTCTTGT 120  
AATNATGGGG CTCCCAGAG TCTGCGTAAC AGTCTCCAC TGGCTGGCTC ACCCACAGGT 180  
GCCATGTGCA CACTCCTGGT TTTCAAACAA TTCTCTGGAT TTAAA 225

SEQ ID NO:7301

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08540

SEQUENCE DESCRIPTION:

GATCATGCAT GCCAATCCCT GTTGCCGCAT GGAGCTCCTC AGCCCACTGA CCTCTCCGTG 60  
CCTGGTGCAG GCCAGGCCCC CGTCTTCCGC CTGCCTCTGC TTCCCCGTCA TGCATGGTGG 120  
TGGTGTCTTCT ACGGTGTCTG GTTCTGTGCC CGTCTCTGAG ACAGTCTCTG TGTGGAATNT 180  
GCCTTAAACT GAAGTAAATN TGGTTCTTTT AGTAAA 216

SEQ ID NO:7302

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08541

SEQUENCE DESCRIPTION:

GATCAATTCA TGCAAGATAT AATCATATTT TTTAATTAAG AAAATTTTTT TTGTAGAGAT 60  
GGGGTTATGC TGTGTTGCCT GGCTGGTCTC AAACCTCTGGG TCTCAAAGCG GTCCTCCTGC 120  
TTTGGCCTCC TAAGGTGCTG GGATTATAGG CATGAGCCAC TGTGCCAGGC CTGAGGATAT 180  
TATCATTATA AATATATATG TACCCACAC TGGATGACCC AGATATAAAG CAAATATTAT 240  
TAGATTTAAA GGGAGAAATA GACTCTAATA CAATAGTAGT TGAGGACTTC ACTCTACTCT 300  
CAGCATTGGA CAGATTTTCT AGACATAAAA CCAATAAATA TTGGATTTAA ATTGCACTTT 360  
ACACCAAATG GTCN 374

SEQ ID NO:7303

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08542

SEQUENCE DESCRIPTION:

GATCCCATT CTATGAAATG TCCAGGGCAG GCCCAGCCAC AGAGACAGGG AGTAACGTGG 60  
TGGTTTATTA TAAATTTTTC ATGAAAATAA AATATACAGT ACTCTCGTGN AAA 113

SEQ ID NO:7304

# EP 0 679 716 A1

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08543

SEQUENCE DESCRIPTION:

GATCTGCACA GCCTCTAGAG GCCTCCCAGC AAATGCGGGG AGCCATGCCC CCAGGGTCTA 60  
CACACTCTCG TTCATCAACA TCACAACTGG AATTCGGGAT TTGTGAAGTT TAGAGCTGNA 120  
CAGACTGTGA CAGATTATGA GTCAACACGT ATATTTTCTC TTTCAAAATA ATAATATTTT 180  
GTTTTTGACT TTTTACTAAG TGAATATTAT TTTTAAATC TGCCTATATA TTGGAACCTC 240  
TATTTTATAA TAATAATGAT AATAAATCAG TACCCAGAAG TATAAA 286

SEQ ID NO:7305

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08544

SEQUENCE DESCRIPTION:

GATCTAAATN ATGTACTTGT TAGTGTATTC ATTCATATTG ATTGTAAAGG ATTATTTTTC 60  
ACTCAGTACT GATGTCCTTG GAAATCTTAC CTGGAAACAT GTTTGCAAAA AACAAA 116

SEQ ID NO:7306

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08545

SEQUENCE DESCRIPTION:

GATCCCAAGT CTACCTGGA AATNCCCAGG CACAGCATGC CTGGAGGTGT GAGCCGCCTC 60  
TTAGAAGCTT TATAATCCCG GATAATNCTG CTGTAATTGG CATTGTTTTT CCATTACAAT 120  
CCTTTCATTA CTGAAA 137

SEQ ID NO:7307

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08546

SEQUENCE DESCRIPTION:

GATCCCAGCT TGGTGGGAAA GTGCAGAAGA ATTGCAAAAC TGACATCCCA TNTNACAGCA 60  
ATAGTGACCT TTATTTAAAT TGTGTGTGTTA TAGTTTATGC TTCTTAAATC ATTTTCAAC 120  
NTAAACAGCC AATTCTAAG CAGACAGGAA AACTAAATAA TAAGTTNATT NATATAACAA 180  
AGATGCAGGT TCCTGCTCAT TCCAGTAATG TCTTTGAAAG CANNNCTNAT ATTTNTTTC 240  
TAGATTATCC CTGTGAATAA TTGAGANCTT TTTGGAGTCA AGNATGAATA AAGGTGTGGC 300  
AAGGNTATAA ACANNAN 317

SEQ ID NO:7308

SEQUENCE LENGTH:337



SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08547

SEQUENCE DESCRIPTION:

GATCTGTCAG AAAAGACATA TTTTGGAGAT AAAGGAGTTT CTAAATAATG AATTATTGTT 60  
TAGTACCAGC TTTTGGGAATC CTTACATTTT AAGGAACTTG AATAATTTAA ATATTAGATA 120  
ATGTAACCTC TCATAAAAAC AGTGTCTAGA CAAGGGCCAA TATTGCATTG AGATTGGATG 180  
AACATTTTAT TTTGCATATA ATTGTTGTCT ATAAAACAAA ATACTAATAA TAATGGCTAC 240  
CNGTTAGNCA NTTTAGNNCN TGTCTTACTA TTTACCNNTG TGGNAAAACA TTGCATGNTT 300  
TAATNTTTTT CTAATAAAAT ATTNTNCCAT TANCNNN 337

SEQ ID NO:7309

SEQUENCE LENGTH:389

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08548

SEQUENCE DESCRIPTION:

GATCCACCA ATCCTCGTTC CCCCTAAACA TGCTAACAAA AATCCCTTAT TGTGGGTATT 60  
AAAATAATAA CAGTTACACT GTATGCATAT TTATGTGCTC CTTTGTCTG GTTTNCTTT 120  
TCATCATGTA TAAGCTGAAT TCAGCATTAG TTTCTCACAT CTTCCCCCAG GTATCCCCAA 180  
CAGAATTTTT ATGTCCCAGC TTGTATTAAA TAGAAGTGAA ATATTAAGGA AAATAAGGAA 240  
CTTGTGCAAC TTTTTNATG CATTGTTCTC AACCATTTAA TTTATTGAAA GGAGATGCTG 300  
CAACAGTTCT TGATTAGCA GCAGTTATTC TCTTGTTTAC ATAGTTATGG TTTNTGTTG 360  
TTGGTTTTTG CTCTGGTACT GGGAAACCGN 389

SEQ ID NO:7310

SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08549

SEQUENCE DESCRIPTION:

GATCCAGGTC TTCTGATTCT TATTCCAGTG TCCTTTCTAG CATACCATGT TGCCTCTAAA 60  
GATTGCAGCT CCTTATTTAC TAGAAAATTG TTCCTGCCCA ATCTACATCT CCACCTCACC 120  
CCATCTTTTC TTAAGCACTA TGTGTTGTGT TTTATCAGTA TTATATTCAT TGTCTTTGGA 180  
ATACATGTTT TGTGTTGTGT TTGGAAAAAA AATCTCTTTT ACCAGCTTGC ACTCGGACCA 240  
ACTTGAAAAA AAAAANGCTT AAATGTTTTN GCTATGTNCA GTTTAAAAAT GTGAAGTTTG 300  
TNGCTTTTANC TTTTGTAGG AAAATCTANT ANCACTGGCT TAAGTGCTGA CTTGAAATGC 360  
TATCCAN 367

SEQ ID NO:7311

SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08550

SEQUENCE DESCRIPTION:

GATCCAGCGA ACCACTGCAC TCTAGCTGGG GAGACAGAGC AAGACTCCGT CTCAAA 56

SEQ ID NO:7312

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08551

SEQUENCE DESCRIPTION:

GATCTCTTCC CTTAGGAAAT ATCAACATCT TTATGTACAT GTCAGAGTCA TGGTGTGATG 60  
ACGTACTTTG AAGCATGGAG TCAGTTTTCA AA 92

SEQ ID NO:7313

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08552

SEQUENCE DESCRIPTION:

GATCCACTTA TGAAGTGAAC ATTCTCCATG AACAGGTGGT TGGATTGGTA TCTGTCATTG 60  
TAGGGATAGA TAATAAGCTC TTCTTATTCA TGTGTAAGGG AGGTCCATAG AATTTAGGTG 120  
GTCTGTCAAC TATTCTACTT ATGAGAGAAT TGGTCTGTAC ATTGACTGAT TCACTTTTTC 180  
ATAAAGTGAG CATTATTGGA GCATTTTNC ATGTGCCAGA GCCTGTACTG GAGGCCCCCA 240  
TTGTGCACAC ATGGAGAGAA CATGAGTCTC TCTTAATTTT TATCTGGTTG CTAAAGAATT 300  
ATTTACCAAT AAAATTATAT GATGTGGAAA AAAAAAAAAA AATTGCGGGC TTGNANGNTN 360  
GGGGTCAN 368

SEQ ID NO:7314

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08553

SEQUENCE DESCRIPTION:

GATCACACCA CTGTACTCCA GCCTGGATGA CAGAGTGGAG ACTCTGTTTC AAAAAACAG 60  
AAAAGAAAAT ATAGTTTGAT TCTTCATTTT TTAAATTTG CAAATCTCAG GATAAAGTTT 120  
GCTAAGTAAA TTAGTAATGT ACTATAGATA TAACTGTACA AAANTTGTTT AACCTAAAC 180  
AATCTGTAAT TGCTTATTGT TTTATTGTAT ACTCTTTGTC TTTTAAAGAC CCCTAATAGC 240  
CTTTTGTAAC TTGATGGCTT AAAATTCCTN ATTAATNCTG CCATTTCAN TTCCAAA 297

SEQ ID NO:7315

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08554

SEQUENCE DESCRIPTION:

GATCTTTGAA TGAGCTTTTT AAGGAAGAAA TATTATATAT TGTTTGTTAA AGTTTATTGA 60  
AATAAAGAAT -CATTTAAATC TTCAAA 86

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SEQ ID NO:7316

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08555

SEQUENCE DESCRIPTION:

GATCCAAATT GTGAAGCCGT TGGTCAGGTG CCTGGCTACA CACAAATGG TGGAGGCTTA 60  
GCCTAAACAG TTTCTTCATT TCACATTAAA ATCCTAATTN NTGGCTCCTC TCAAAATGAG 120  
TTCTAGAAGC ACNGGNTGTA GATTCCCATG TGGACACAGC CTTCAGGAGG TGAGCAGCAG 180  
CTCCCTGCAG CCAGCTGGAG CCTGCCAGTT TTCCCTAGTG CCCAGCACTC CTGAGCTTCT 240  
GCCCTCCGAG GGATTCCCGA AGTTTTTCT AATGGGNTTA GTGGNGNCNC CTTTGGGGTT 300  
GCTTNGGTTT CNTTNGTTA NGNGCCCTTG NTTTTAAATT AAANCNGGGC CATTNN 356

SEQ ID NO:7317

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08556

SEQUENCE DESCRIPTION:

GATCTGTGGG ACTGTCTGGG CCTGTTACTC ATCCTGCTAT CAATTTCTTA TTAATTAATC 60  
TTGATGATTG TNATTAATTA ATCACATTG CAGGAAATTC AGATGAGGCA AGAAAATTTN 120  
ATTGGCCTGG GNNNGACTGA AAGCATTCCA AATTAGGCTT AGACTGTGCA AAGGGCTTAG 180  
CTAAGTTATC GAGCTTAAAA CCCGTCAATT AANCAAACAT TATTGANCA GTTACTGCAT 240  
GCCACGCACT GTGTTGGGCT TAGTAATAAA ANNNAGNAAA GGTAAGNGCT TGTNCTNGCC 300  
TAAATTAAAG GGTCCCCGGG GGTTTTTTCT NGAGGGGGCN NCTGCCCN 349

SEQ ID NO:7318

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08557

SEQUENCE DESCRIPTION:

GATCACCTGA GGTGAGGAGT TCAAGACCAG CCTGGCCAAC ATGGTGAAAC GCTGTCTCTG 60  
CTAAAANTAC AAAANTTAGC TGGGCATGGT GGTGGGCACC TGTAATCCCA GCTACTCGGG 120  
AGGCTGAGGC AGGAGANTCG CTTGATTCCA GGAGGCAGAG GTTGCAGTGA GCCAAGACTG 180  
CACTGTTGCA CTCCAACCTG GGCAACAAGA GCAAACTCC GTCTCAAAA AAAANGTGTT 240  
TAATTATTCT AAAAAAATT CAGCCAGGTT ATTCCAAATT NTAATTGAAA NCNGGGGCCC 300  
CAGGTTAANC GGGGCCCTTAC CCTTCCCTTN GCNCTTTGGA NTTNNCCAT N 351

SEQ ID NO:7319

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08558

## SEQUENCE DESCRIPTION:

GATCAGCAGT GTTGACCATT TATGCTGCAT AGCTGGTATT ATAGCCTTAT TAGTTGTGTG 60  
 GTTGACCCCTT GGGGTATACA AATGTCAGTC TGAGTGGTGN CTTACTCCTT TGTTTATAAG 120  
 TGAATGATTG TGCATGTTTT GTATGTCATA GTATGTCGTC ACATAAAAGG GAGGGAGCGA 180  
 AAAACCATTA CATTAGATA ATATTGGACC AACTACTTA CTTGCTCTAA ACAGTTACTT 240  
 GTACCCCTTA ACCTGTCTTC AAAAGTTGCA TATAGTTACA GTAGTGATA AATTAAATAT 300  
 TGTGGAAC CANNAANN NNNNANNNNN NNN 333

SEQ ID NO:7320

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08559

## SEQUENCE DESCRIPTION:

GATCAGCTGA AGGTTTCATGG GTTTTAAGTG CTTGTGGCTC ACTGAAGCTT AAGTGAGGAT 60  
 TTCCTTGCAA TGAGTAGAAT TTCCCTTCTC TCCCTTGTC CAGGTNTAAA ACCTCACAGT 120  
 TGATAATGTA CCATTGGGGN CCGTTTAAAC TGGGCCTAGG NACCCCTCA NGAATAACCT 180  
 GNAAGGGCCA AA 192

SEQ ID NO:7321

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08560

## SEQUENCE DESCRIPTION:

GATCGTGCCA TTCCACTCCA GCTTGGACAA CAAGAGCAAA ACTCCGTTTA TTAAA 55

SEQ ID NO:7322

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08561

## SEQUENCE DESCRIPTION:

GATCAGACCC CCACAATATG TCTCAACCTC TGTGAAGGG CTAGTGATGT TTAAAAAAC 60  
 CTGTTATTTC CAATCAAA 78

SEQ ID NO:7323

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08563

## SEQUENCE DESCRIPTION:

GATCTGGTAT TTCCTGGACT AAATCCCCT TGGGGAAGAC GAAGGGATAN TGCAGTTCCA 60  
 AAAGAGAAGG ACTCTCCAG AGTCATCTAC CTGAGTCCA AAGCTCCCTG TCCTGAAAGC 120  
 CACAGACAAT ATGGTCCCAA ATAAGTACT GACCTTCTG TGCCTCAGCC GTTCTTGACA 180

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5 TCAAGAATCT TCTGTTCCAC ATCCACACAG CCAATACAAT TAGTCAAACC ACTGTTATTA 240  
ACAGATGTAG CAACATGAGA AACGCTTATG TTACAGGTTA CATGAGAGCA ATCATGTAAG 300  
TCTATATGAC TTCAGAAATG TTAATAATAG CTAACCTCTA ACAACAAATT AAAAGTGATT 360  
GTTTCAAGGT GGAAG 375

10 SEQ ID NO:7324  
SEQUENCE LENGTH:271  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08564  
SEQUENCE DESCRIPTION:  
15 GATCCACCTG CCTCGGCCTC CCAAAGTGCT GCGATTACAG GCATGAGCCA CCGCGCCTGG 60  
CCGCTTTTCGA TATTTTCTAA ACTTTAATTC AAAAGCACTT TGTGCTGTGT TCTATATAAA 120  
AAACATAATA AAAATTGAAA TGAAAGAATA ATTGTTATTA TAAAAGTACT AGCTTACTTT 180  
TGTATGGATT CAGAATATAC TAAATTAAC TTTTAAAACA CAACTTTTAA AAAATGTATC 240  
AAAATAATAA ACGTGTTCCTG ATATTTTAA A 271

20 SEQ ID NO:7325  
SEQUENCE LENGTH:102  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS08565  
SEQUENCE DESCRIPTION:  
GATCCCCTGA GTTCAAGAGT TTGAGACCAG CCTAGGCAAC CTTGTCTCTA CAGAAAAATA 60  
AATAAATAAA TAAATAAACA AACAAACAAA CCAAAAATTA AA 102

30 SEQ ID NO:7326  
SEQUENCE LENGTH:216  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS08566  
SEQUENCE DESCRIPTION:  
GATCATGAGG TCAGGAGACC GAGCACCATC CTGGCTGACA CGGTGAGACC NCGTCTNTAC 60  
TAAAAATACA AAAGCAAAAA TTAAGTGGGT GTGGTGGCGG GTGCCTGCAG TCCCAGCTAC 120  
TNGGGAGGCT GAGGCAGGAG AATGGCATGA ACCTGGGAGG CGGANTTGCA TTGAGCTGAG 180  
40 ATGGCACCAC TGCACTCCAG CCTGAGCGAN NNNNNN 216

45 SEQ ID NO:7327  
SEQUENCE LENGTH:176  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08567  
SEQUENCE DESCRIPTION:  
50 GATCTGCTCT CTGTTGAGAG TTGGTAATCA TTGGTTTGAA ATGTGATGAA ACCACTCAAG 60  
CCAATGAAGG TGGTGTGTA GGTGGGGAGT ACTTTGCCAT AATATTTTAA AACATTACCT 120

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GGTTAGAGTT CTAAGTGGTA CTTATTTTGG TTTGGTTAGG GGAAAGCCTG AATAAA 176

SEQ ID NO:7328

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08568

SEQUENCE DESCRIPTION:

GATCTCTGGC TGTGTGATT TTTTATATT GTATTTTAA AATNTGTTAA ACAGTGCCCT 60  
GTGAGCACCA AGTACCACTA GATGAATAAA ACGTATTATA TCTAAA 106

SEQ ID NO:7329

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08569

SEQUENCE DESCRIPTION:

GATCCGGCAG GCAGAGAGGA AAAAGGGAAC TTGTACCAAG CACAAACAGG NTCTAGGCAT 60  
AGTGCTGTGT ACTTAGGTTT TTCCTGTGCT TCAGTCTTTC CAATAAATCC AGGGGTTAGG 120  
TTTTAATCTN NCTATTTNAT AGTTACAGAC CATTTTAAAT GGACAAGCAG CCCATTTAAA 180  
GATAAAAGTA CTTAGATGGA CTAGCAGCTT CTCTACCAA TTATTTCAAC ACACAAAGNT 240  
AACATCATTG TGAAATTTGG TTTAGTTAAC ATGCATTCCC TGGCCTGCCT CACACCGGAC 300  
CTNTACCCGG TACCATGCAA ATGCACATCT GCTGCTACAC TTGTGGGATG CTGGTTTAGG 360  
TAATTNTTTT TTATAATNN 379

SEQ ID NO:7330

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08570

SEQUENCE DESCRIPTION:

GATCCCAGCA GAATACCAAA ATCCTATTTT TTTTGACTGA GTATTTGTAG ATGCTTAATG 60  
ACTGAAATNA ATTTGGAGGC ACTGATGAAA GTAATTTTTT NAAAGTTCTC AGGTACTGTT 120  
CAATTATTTA ATGTTAAGTT TAGTATCAAG ATACAGTTGT TTTNAAAATG CCAAAATGCT 180  
GTTTATNATA CAGAATATTT NATTACATTT GCAATATCTT TGTATATAGT GATTTTNTNC 240  
TTGATAATAA ATGGAAAANT TCTAAACCAA A 271

SEQ ID NO:7331

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08571

SEQUENCE DESCRIPTION:

GATCGACCTG CCTCTGCTTC CCAAAGTGCT GGGATTACAG GCGTGAACCTA CCGCGCCTGG 60  
CCCTCAGATA TTTTAAATT TGAAAATTAA GAGTATATAT TAATATCAAG TNGCAGAAAC 120

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AGAATGAAGT GTTATAAAGG CGTTAAGTAG TAGGGNGGCA TAAAACTTAA ATCTTTAAGC 180  
TAGAAATAGC TTGAGGAATT ATCTGATGCA GTACTCTGTT GTAATATAAC AAAAATGGAA 240  
TCACAGTTTT ACAAATCAGG CAGCTGCAGC TCAGNGAGGT TAAATTTCCA CAGACCTGTT 300  
TATGCAGCGC GGTAANTGAG GAAGTAGACC TAAAATTTGG GGCCTCTGCT ACTCTGGGCC 360  
ATTACCTCAG CCTCGCTGGC AN 382

SEQ ID NO:7332

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08572

SEQUENCE DESCRIPTION:

GATCTCACAG GAATCCTTCA ACTGCTTCT ACCAAGCGTT CCATTTGAAC ACGTTAAAGG 60  
AATCAAAGAG CCTCTGGGAT AGGGGGGAAA NCACATGGTA TCTAGCATGG GACAAAGCAG 120  
CAAAATAAAC CAAAAGGACA ATCTCTATTT TATATAGAAA ATAAACATAC TTTTCTGCAT 180  
CCTGTGTACT TTAAGTATAT CTATATTTTT GAAGGGTTCA TACTGTGTTG AATTTTCTT 240  
ATGAAATAGT CACTTCCCCA GTGTATTTTA ATGCAAATGC ATATTCTATA AAATAACCTA 300  
TATTTTAATT TAAA 315

SEQ ID NO:7333

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08573

SEQUENCE DESCRIPTION:

GATCTTTAAT ATCTGATATA TTCCTGGTAC TCGTACTGAT AAGGGATTAT TGGAAAGTCAG 60  
TCACAGAATT TGGAAATAAA TTCTAGTCTN TCCTTAGCTN NNNN 104

SEQ ID NO:7334

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08574

SEQUENCE DESCRIPTION:

GATCTACCTG AGGCTCAGTC CTCATCTGTA AAATGCTGAT AAAAGGACCT ACCACCTAGC 60  
GTTGCTGTGA GGTGTCAGTG AAATAAAATG TAAAATGCTT AGCACAGTGA ACTTTAATAA 120  
ATGGTAGTTG TGTTTGCAA 140

SEQ ID NO:7335

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08575

SEQUENCE DESCRIPTION:

GATCTAAAGT CTAATAAACA AATCCTTAGG TTAAGAAGAA AATAATGCAA TAAATAAAAT 60

GTTATAAATA AATGACATAT TGCNACTTTT AAA

93

SEQ ID NO:7336

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08576

SEQUENCE DESCRIPTION:

GATCATACCC ATGAAACCCA CTGTTTAGAT TTTAAAAAGT TCAATGTTTT TCTGTATTTN 60  
ATCTCTTCAT TTTAAATAA AGTTTTGCAC ATGAAA 96

SEQ ID NO:7337

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08577

SEQUENCE DESCRIPTION:

GATCTAAAAG CAGATGCTGT AGCTGCCTAC TTAAACCCAT TTTTCAACCT GTTTGTTTTT 60  
TAAAGGGCTT CACTAAGGGT NNNNNATGTA CCATTGTAGG GGGCAATTTT AAGTCAGCTA 120  
AGGCAATAAC CTTATGCATG AACATTTCCC AGACTTTCAT GAAGCTGTTG AGGTCCTAGG 180  
CAATTAATGC GGCAGTTGTG ATAAATAAAA ACATCTCACC TAAA 224

SEQ ID NO:7338

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08578

SEQUENCE DESCRIPTION:

GATCNATATT TAGTGACTGC AACATGTTTA TACCACTGAT TCAAATTCCA NNNNTGATGA 60  
AGTTATACAA ATAATGCATA TATTGATAAC TTTTATTGCA AAAATGTAAA TTTAAAACTT 120  
GTATAATGTT CTTGTGCTTT TTTAAATAAA ATATATGTGT ATATTTAAAA AGAAA 175

SEQ ID NO:7339

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08579

SEQUENCE DESCRIPTION:

GATCTGAGGA TGGTTATAAA TACTGTAAGT ATTGTAATGT TATGAATGCA ANNNTATTTG 60  
AAAGCTGTTT ATNATNATAT CATTCCTGAT AATGCTATGT GAGTGTTTTT AATAAAATTN 120  
ATATTTATTT AATGCACTCT AAA 143

SEQ ID NO:7340

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid



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5 TOPOLOGY:linear  
 CLONE:HUMGS08580  
 SEQUENCE DESCRIPTION:  
 GATCACTTGA TTTTAAAGAA ATNAAAAATT GCACTAGGTA GAAATAGTGT ACCAGGCAAT 60  
 AGTCCAGCTT TAGTTTTNTG TCATTTTTNG TCTCTATTTA AAGNNN 106

10 SEQ ID NO:7341  
 SEQUENCE LENGTH:93  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08581  
 SEQUENCE DESCRIPTION:  
 15 GATCTCAAAG CAAATCTGTA TTTAATCTC TCAGGTGTTT ACTAGTATTA CCAGTGACTA 60  
 GTGGAAATAA TAAAAGGAAA TCTTGTTTCAT AAA 93

20 SEQ ID NO:7342  
 SEQUENCE LENGTH:193  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08582  
 SEQUENCE DESCRIPTION:  
 25 GATCTTCGCT CCAGCTTTCT GCATCTGAGC TGGAAAAAGA GCAAAAACGG GTAAAAATTG 60  
 AATCCAAATA TTGTCGNATG TATGCCTAAT TTAGAATGAA ATCTTGGGGT GGCAGACTCT 120  
 GGAGTTCTCT GTGAGGTGTG GCATTCTTTT NTCTAAATCA CTTATTGCCC AATGTATGTG 180  
 TCACTTTGTT AAA 193

30 SEQ ID NO:7343  
 SEQUENCE LENGTH:137  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 35 CLONE:HUMGS08583  
 SEQUENCE DESCRIPTION:  
 GATCTATAAT AAGAGCTCAA TAACTNNGTC AAGGAAAGCT CTAATATATG CAGTGATGGT 60  
 TTATGAAAGG GTGTGGCAAT NTNAAATNTA TATTGTGTGT GATGTTCAAA TAAAGTGGTA 120  
 40 TCTACATNCA TGTGAAA 137

45 SEQ ID NO:7344  
 SEQUENCE LENGTH:389  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08584  
 SEQUENCE DESCRIPTION:  
 50 GATCCCTGGT ATNGTCCGAA TTGTAAAGAA CATCAGCAAG CCACAAAGAA ATTGGATTTA 60  
 TGGTCCCTGC CTCCAGTACT TGTAGTACAT CTNAAGCNAT TTTNTTACAG TCGATACATG 120  
 AGAGACAAGT TGGANACCTT AGTTGATTTT CCTATCAATG ACTTGGATAT GTCGGAATTC 180

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5 TTAATTAATC CAAATGCAGG TCCTTGCCGC TATAATCTGA TTGCTGTTTC CAACCACTAT 240  
GGAGGGATGG GAGGAGGACA CTATACTGCT TTTGCAAAAN ATAACGATGA TGGAAANTGG 300  
TACTATTTTG ATGACAGTNG TGTCTCCACT GCATCTGANG ACCAAATTGT GTCCAAAGCA 360  
GCATNTGTAC TCTTCTACCA GAGACAAGN 389

10 SEQ ID NO:7345  
SEQUENCE LENGTH:367  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08585  
SEQUENCE DESCRIPTION:  
15 GATCTGTTAC CATCAGGTCA ATTCCTAGTA TGCATAAAATT TTTAACCCT TTTAAAAGAG 60  
ACCTATGTTG AAAACCCCTG AAAATTCACT GAAGAAAAAT CATTACTCTT NTTCTCNGTA 120  
AATCATATCA TCTGAAATAT TACAAATTTC AAATTTCTAG GTGCTATATT AATTCAATAT 180  
TACAATAACT CTTACCTAAT TATTCTTACA AGTTTAAAGT TGTGGTAGTT TAGTGATTTT 240  
TTTAAAAGAT GTGTGAAATG TTCTCTGCAA AATAATTCAG GCCACTGTCT CCTTTTATAT 300  
20 ATNATNATNN TNGTNTGTGA TGANGACCAG TGAATTACGA TATTTAAAGT GAGAGACCTT 360  
AATTNTN 367

25 SEQ ID NO:7346  
SEQUENCE LENGTH:23  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08586  
SEQUENCE DESCRIPTION:  
30 GATCCCGTCT ATAATCNAAC AAA 23

35 SEQ ID NO:7347  
SEQUENCE LENGTH:103  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08587  
SEQUENCE DESCRIPTION:  
40 GATCGGCTCC CTGTCGCGCC CGAGGAGGGC TGGACCTTTC GTGTCGNACC CTTGGGNGCG 60  
NNGAGACTGG GTGGGGAGGG TGTGAATAA AAGGGAAAAT AAA 103

45 SEQ ID NO:7348  
SEQUENCE LENGTH:367  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08588  
SEQUENCE DESCRIPTION:  
50 GATCTGGTGG CTGGA AAAAC AAGAGTGACA TTAACAAATC AAAAAAATC AGTTAGGGCT 60  
GTGGTTTTAC ATCCAAGACA TTACACATTT GCATCTGGTT CTCCAGATAA CATAAAGCAG 120  
TGGANATTCC CTGATGGANG TTTCATACAA AATCTTTCCG GTCATAATGC TATTATTAAC 180

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ACATTGACGG TAAATNCTGA TGGAGTGCTT GTATCTGGAG ACAGAAGAAA CTCATCCAGT 240  
CAGCTGGAAA CCAGAAATTA TCAAGNGAAA GNGATTTTAA TGAATGTGGA ATTTTTCCTC 300  
TCTCTTTTTT TTTCTTTTAA ATTAAANAA AAAAGGCTTG GNGTTCATGG GGGNTTCCC 360  
GNCCTTN 367

SEQ ID NO:7349  
SEQUENCE LENGTH:22  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08589  
SEQUENCE DESCRIPTION:  
GATCCCGCCT NTTCTTACA AA

SEQ ID NO:7350  
SEQUENCE LENGTH:378  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08591  
SEQUENCE DESCRIPTION:  
GATCTTTTAA AAATTCATCC CATATCCAGA AAGTACCAGT TATAAAGATT GCTGACCAAG 60  
CAAAGTTTTG CATCAAAGTG TCACCTCATT GCTCTGACCA AAGACTGACT GTTGTGGTTT 120  
TAACTCCTCT CTGTAAAGCA TTTTGCATTT TCCCCAAGCT CCTTTCTGAA AGAAGAACCA 180  
GTGCAGAGCG GCCTTTACTT TCAATTTCTA CTGCTGAATA GACTACTTAG AGAAATGTG 240  
AGTTTCAGTG TGAACAGAAT GGATTAGGAT GACGAGTTTG ATGGGCATTT TCAGTACTGT 300  
ATCTAAGAAA AAAAAATTNG CACAGCTAGG AGCCTCTGAC CATTGTCTGG GTGTTTACG 360  
TGGGTCCTGT TCATCAAA 378

SEQ ID NO:7351  
SEQUENCE LENGTH:379  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08592  
SEQUENCE DESCRIPTION:  
GATCAAAGTC AAAAATAGCA ATGNCTCCCT ATCCCTCACA CATCCAGACA TCATGAATTT 60  
TACATGGTAC TCTTGTTGAG TTCTATAGAG CCTTCTGATG TCTCTAAAGC ACTACCGNTT 120  
CTTTGGAGTT GTCACATCAG ATAAGACATA TCTNTAATTC CANCCATAAN TCCAGTTCTA 180  
CTATGGCTGA GTTCTGGTCA AAGAAAGAAN GTTTAGAAGC NNNNNCACAA AGGGTTGGGA 240  
GCTGATGAAA CTCACAAATG ATGGTAGGAA GAAGCTCTCG ACAATACCCG TTGGCAAGGA 300  
GTCTGCCTCC ATGCTGCAGT GTTCGAGTGG ATTGTAGGTG CAAGATGGGA AAGGNTTGTA 360  
GGGTGCAAGC TGTCCTCAAN 379

SEQ ID NO:7352  
SEQUENCE LENGTH:119  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

# EP 0 679 716 A1

CLONE:HUMGS08593

SEQUENCE DESCRIPTION:

5 GATCTGCTTT AGTGAGAGGA CAATTTCTGA TTGATTGTTT TCTCTTCAGG CCATCTCACC 60  
TCTTCATTCT CTTGTNACAT TTGAAGCAGT TGATATAATG GGTTTATANN NNTAAAAGN 119

SEQ ID NO:7353

SEQUENCE LENGTH:93

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08594

SEQUENCE DESCRIPTION:

15 GATCAGCTAT TTTCAACATA ACTGAAGGCA TATGCTGGCC CATAAACACC CTGTAGGTTC 60  
TTGATATTTA TAATAAAATT GGTGTTTTGT AAA 93

SEQ ID NO:7354

SEQUENCE LENGTH:297

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08595

SEQUENCE DESCRIPTION:

25 GATCTCTGTA GACTTGCCCTC TTCTGGACAT GACATAGAGA AAGGAGTCAT AAATTCTCCA 60  
AGGTGTCTGT TTCTTCTTTA ATGTCATTCC CTGTTTCTCC TCACATTCCC TCCCCATTTC 120  
CTGGGCCCAG TCTCACACTG GTCCTTGCTT ACCCTAAATG CTATTAATTC CATCACTCTG 180  
AGTATGGTGT TTGCTGTCCG CTGAATGCCA AGAGCTTCAA GAGTGTGTGT AAATAAAGCC 240  
ACACCTTTAT TTTTGTATTA TTCTGAACCA TGGCTAATAA ATTGTTTCAC CAAGAAA 297

30 SEQ ID NO:7355

SEQUENCE LENGTH:45

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS08596

SEQUENCE DESCRIPTION:

GATCTCCGAT GTGATGAATA CGAATAAAAG GCCCTTAATG GCAAA 45

40 SEQ ID NO:7356

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08597

45 SEQUENCE DESCRIPTION:

GATCTGTTCA TGCTTTTGTG TTCGTCACCTG CGGCGGGGCC CTTTGATGTC TTCATCTGTA 60  
TGGGGTGGAA AAATCACCGG GAATCCCCCT NNNAGTTCTT TGAAAAAGTT CCATGACTCG 120  
AATATCTGAA ATNAAGAAAA CAAACCGACT CACAAACCTC CAAGTAGCTC CAAATGCAAT 180  
50 TTTTAAATG GAAAACAAAA ATCTGAAAGA AA 212

55

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SEQ ID NO:7357

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08598

SEQUENCE DESCRIPTION:

GATCTAAACT GTATTTTCCA ATTTAAATTA AAAATGTAAT ATAGATTCAG AAAGGTTTCAT 60  
 ATTTTCTAA TGAATTCATT CTATATTATT TTGTTAGGTT GCATAAAGAA GCAAGGAATT 120  
 GTACTTGTAT TAAAAGATGA GGAAAGCTAT TAGGNTTATT GGNCCATGCC TGAAATNGGG 180  
 CCTTTGCCCC TTTAAAGGAA AGGTTGGCCC NTTTTNAAG GGGGCNTTNA TNTGNNTTTN 240  
 TNTTAACCAN 250

SEQ ID NO:7358

SEQUENCE LENGTH:112

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08599

SEQUENCE DESCRIPTION:

GATCTGGCTT NGCCCTAAGC NNCTTAGGNA CAGAAGAGTC CATGGGGGCA TGGCACAGAG 60  
 CTGGTCCTGT ATTCTCCAGG GTCCGGAGCT GGCCAGGGGC GGGGAGGAGG NN 112

SEQ ID NO:7359

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08600

SEQUENCE DESCRIPTION:

GATCTTATTT NACTTCATCC TTCTTGTAAC CATATTGTNA ATCAGGAAAG CTCAATCAGA 60  
 TACAAAAACA GGAAATTCGT TAAAAGTAAC GTTTGTAGAA GATACTAGTT GAGGAGGAGA 120  
 GACTTTTNAG AAAGCCTGTG TGTGTTTGTG AACTCTTGT GACCGTGCCA AGAAAACGTA 180  
 AGCAAATATC AAGCCTCCAA ATCCTAATGC AACANGTCCT GANTCCCTTG CAGGTATGTC 240  
 CTGGATGATG ANTACACAAG CTCAGTAGGC TCCAAATTTC CAGTCCGGTG GTCCCCACCG 300  
 GANGTCCTGA TGTATAGCAA GTTCAGCAGC AAATNTGACA TTTGGGCTTT TGGGGTTTTG 360  
 ATGTGGGAAA TTTACTNCCT GGGGAN 386

SEQ ID NO:7360

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08601

SEQUENCE DESCRIPTION:

GATCCGGGNA TTATACAGGT ACTGTTGGAA GTATCTTGGG GATTTTCCTG ATAAGAACAG 60  
 TAGTGATTGN ATAAAAAGGA CAGGATGTAA AGTGAAATCA GTAAAATATC TTAGTAGACA 120  
 GAGGGTGCTG AAATTTTAAC AAATGTGTAA AAAGTTCTTC CTATGCATTA ATTTCCAGA 180  
 TACCCTTAAA ATGTTTAAGG AATGTAATTC AAAATACTGT TTAANAGAGA CATGTGACCA 240

EP 0 679 716 A1

TCATTCTCCC AGCGAATGTG AATCATTTAG TNGGCTACTC AAAATTAGGN GTAAATGTAT 300  
ATGTACACTA TAAGANTAAN ANTCGNTACC ATTTCTTTAA A 341

5 SEQ ID NO:7361  
SEQUENCE LENGTH:92  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS08602  
SEQUENCE DESCRIPTION:  
GATCCGTCAG NCGACTCTAA AGCTAATTGT TTGTATTGGC ATGGNTTTTG CCAGGCATCC 60  
AAAATTCAGA TTAACAAC AATGCAATCA AA 92

15 SEQ ID NO:7362  
SEQUENCE LENGTH:359  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS08603

SEQUENCE DESCRIPTION:  
GATCTCGTCT GAAACAGTGT TTGGAAGTGG GAACAGTTTT GTCCTGTATG CTGATGTGTC 60  
CAGAATTCA TTTAATGATA GACGGAAAAT GTGTGGTTAC TGAAAAGTGT ATATGATACA 120  
GAATTTTATA AGAGCCATGC TGTGGGGCAA AGCAACTCTT TTTCAACCAC TGCTCATCAG 180  
25 TTTCTGTAGA GACAAAAACT CTGTACATAT TTTGGAATCT GAAGAATCCT ATGTAAATCA 240  
TTTGTACTT AAGTCTGTGA AAAACATATT TCTTTGGAGG AAAATGTATG CATTTATAAG 300  
TGTTCCATGG AATCAGTTTT TATTGTATCG ATATAATTGT CTCTAAGTGT TGAATGTCN 359

30 SEQ ID NO:7363  
SEQUENCE LENGTH:273  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08604

35 SEQUENCE DESCRIPTION:  
GATCTCCTTA CACTGCTATT CCAGAGGAGA AGNCACCAGG TCACTCAACT CTTAGTATCA 60  
TCTACTGGAA ACTGGCTAAG ACAGTATTTA TGTGCTTCTC TCACAATAAC AGGAAGATAN 120  
CTATATCACA CAATGGATAT GGCAGTTGGC TTGACTGCAG TAATCATTTA ACTATGTATA 180  
40 TGTATATCAA AACATCATGT TGCATACCTT AAATATGTAC AATAAAAAATA AAATCTAAAG 240  
GANATAANTT AANATTACCT TCCACCAGGC AAA 273

SEQ ID NO:7364  
SEQUENCE LENGTH:358  
45 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08605

SEQUENCE DESCRIPTION:  
GATCAGGGAT GCAGTACCAC TTGCAGTCAA ATGAATTCCT TCGAAATGTA TTTNNACTTG - 60  
50 GACCCCCAGT GATGCTTGAT GCTGCAACGC TTAACACGAT GAAGATTCT CGTTTCGAAA 120

55

EP 0 679 716 A1

GGCATTATA TAACTCTGCA GCCTTCAAAG CTCGAACCAA AGCTAGAAGC AAATGTCGAG 180  
ATAAGAGAGC AGATGTTGGA GAATTCTTCT AGATTTTCAG AACTTGAAGA CTATTTTCTA 240  
ATTTCTATTT TTTTTTCTAN TTCAATGTAT TTAAACTCTA GACACAGTTT TTATCCTGGA 300  
TTAACTTAGA TAACTTTTGT AGCAGTGGTT ATATTGCTTA TAATTTAATG TACAATTN 358

SEQ ID NO:7365

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08606

SEQUENCE DESCRIPTION:

GATCTACNGT GAATATAAAA TGTTATTAGC CTTATCAAAT AAATAAATGA GCANAGCTCT 60  
TTGTTGCTC TATTGAACTG GGTGATAATN ATTTAGATGT GAATGTTAGG TCAGTTCTAC 120  
TGTAATAACT AATCGTAAAA GTTGTAATN TGTTTAATGG ATGAAATGTA CANTTTTGT 180  
ATTCTNTACA GCTTTGTCTT TTTTAAATAT GAAGTACTTA AATGTACTTA CTATGATAGG 240  
AAATATAATG TGTGCCTTCT AAA 263

SEQ ID NO:7366

SEQUENCE LENGTH:366

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08607

SEQUENCE DESCRIPTION:

GATCTAAGTA AAATGTTTGG AAGTTTATCA GAAACTAAAT GTACTTTTAA AACGTATAGG 60  
GTCAGGGTTG GGGGAAAAAT ACAGGTATAG TAAGNAAGAA AAGTGACCCA TGAAGAAAGC 120  
ATCGTGAGGT TGTATGTTGG TTGACTGTGA TTAAATGCG GGGCTGGTGT AAGTTGTAAG 180  
TGGTGGCTGA TTGCCGTGTA ACTATGTACA TGATTGTTGG GATGGCTGTC CCATATTTTG 240  
TATATTGGAA TAAAAATTC TATAANTTAT NGTAACTAAA AGTAAATATT CTAAATTAAG 300  
TCCCACTNCT TAAGTCACAT GGCTTCTGTC TTGGGAATTT TACCTTTTAA NANGATTATT 360  
TTNAGN 366

SEQ ID NO:7367

SEQUENCE LENGTH:378

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08608

SEQUENCE DESCRIPTION:

GATCTTGGCT GTTCTTTCTA TTCTGCCAGC CATCTTCCAA AAAAACTAA AGCAGAAATT 60  
TGAGTAAAAA TAATCATCTG ATTTTAAGTT TTGCTGTCAT CACCATCTCA GGATTAACAG 120  
CTGCGACTTT AGGTGGGGTA TATTTCTTC TCCTAAGAGA ATAGACAGTT TTTCCAGATT 180  
CATCATCATT GACTGTCAAG AAAGGACCCT TCAGCAAGGC TGTACCNTCA ATGCAGTTGA 240  
TGGCCTGTNT TCACGGNTTT ACAGACTTGG CCTGATGCCC ATGTAANTTC AAGCTTTGGC 300  
TTGTGGNAAC AACCACANGG ANGCAAGGC ATCTGTNGGT GCGGGNGGGC AAAGCAGGCT 360  
TANCTNGGGN GGTGACN 378

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SEQ ID NO:7368

SEQUENCE LENGTH:421

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08609

SEQUENCE DESCRIPTION:

GATCTAGAAA CCCTTTTACC TGGCCCCAAG GCTCTAGCCA GTGGTCTCTG GTGACCCCTG 60  
 CAAGCTCAGA GATGGGGNTG TTGTGTGCCA GGCATGAGCT TCCCCAAGAG GCAGAGGGCA 120  
 TACATCCCAT TTATACATTC CCTAAGCCCA CCCCTGTNTC CTCAGGCACC ACCTGCCCTG 180  
 GTCAGCTCCA GCCAGTCCCT GCTGGAGTGG TGCCAGGAAG TNACCACTGG CTACCGTGGG 240  
 GTCCGAATCA CCAACTTNAC CACATNNTGG CGCAACGGCT TGGCCTTCTG TGCCATCCTG 300  
 CACNGATTNT ACCCAGACAA GATGTGAGCT GCCAGAGGGG TGGGACGAAT GGGGGAGCCA 360  
 TCAGGGAGGG CAGTNTGGAC CCAGCTTTGA CCAGANAATT TTTNGAGTGC TTTGCTNGTT 420  
 N 421

SEQ ID NO:7369

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08610

SEQUENCE DESCRIPTION:

GATCAGCAAT GAGTCGGCAA TTGACTTCTA CAGGAAGTTT GGCTTTGAGA TTATTGAGAC 60  
 AAAGAAGAAC TACTATAAGA GGATAGAGCC CGCAGATGCT CATGTGCTGC AGAAAAACCT 120  
 CAAAGTTCCT NCTGGTAAGA CNNCAGNTGT NAAAANGCCA GCAACCTGNC CAATTTCCAN 180  
 TGANCCTTN 189

SEQ ID NO:7370

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08611

SEQUENCE DESCRIPTION:

GATCTGGTGG AGAAAAGAAG CAAAACCTTG TTTAATTTA CTGTTTTTTT AAAATCTTTT 60  
 TGGATATTGT TTTGCATCCC ATACATTTGC AACTGGCAAT GAAATGTAAG CTTTGGTTCT 120  
 GAAAAAAAAT AAATGTAGCT ATTCAAA 147

SEQ ID NO:7371

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08612

SEQUENCE DESCRIPTION:

GATCCACATG CNTGTGGCAG CCCAAGGCTT TGTGTAGGA GCAATGACTN TTGGTATGGN 60  
 CTATNCCATG TATCGGGAAT NCTGGGCAAA ACCTAAGCCT TAGAAGAN 108



SEQ ID NO:7372

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08613

SEQUENCE DESCRIPTION:

GATCTTTGAG CTGTGGTTTC TCCACCTGTG GAATATAAAT GTNAACAACA TAACCTTCTT 60  
TCTAAGGATA ACTTGAGAAT TAACAGTGCA AGTAAATGGA AAGTATAGTA CCTGTNACCA 120  
GATATTTAAT AGTAGTTATT ACGAAATTGT AACTCACTAC CTGTNTTAGT TGAGGTTTAT 180  
CTTCAGCCAT GCAAATCAAA ATCAGATTAT TTNCACATCA GCAGATAAGG TTTGTNTGAG 240  
ANTCTNATTT TNNATTTGNT ACTCTNATTT NNN 273

SEQ ID NO:7373

SEQUENCE LENGTH:419

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08614

SEQUENCE DESCRIPTION:

GATCACAGAT GTAGTTCCTG AGGTTGAGTC TCCTTCTCAG ATGGATGTTG AATTGGTGAG 60  
TGGGTCTCCT GTGGCACTCT CACCCCAGCC TCGATGTGTG AGGTCTGGTT GTNAGAACCC 120  
TCCCATTGTG AGTAAGGACT GGGACAATGA ATACTGCAGC AATGAGTGTG TGGTGAAGCA 180  
CTGCAGGGAT GTATTCTTGG CCTGGGTAGC CTCTAGAAAT TCAAACACAG TGGTGTGTTG 240  
NAAATAGTCC TTCCTGTTCT CCAAGCCAGT GAAGAGTTAT CTGCTGGGAA AGTGTCGAAG 300  
AGCCTGTTTT TGAACACAA GCTGGGCTTC TGGTAGTGCC TCATCACAAC CCATGATGGC 360  
TGTTTCATGGT TTCACCCCTT TTNTTTCNT CAGCAGAGGC CAGGCTATTG GAGCAGTTN 419

SEQ ID NO:7374

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08615

SEQUENCE DESCRIPTION:

GATCCTAATT TGCACACTAT CACCTAAAGT CCTAGCATAC CTGCATTTC AGGAAATCTA 60  
ATGAGAAAGA AGTCCTGAAA GCCTCTAATT CCTGGAAACA TATGAAACGG CTAGAAAAAA 120  
GTAGACTATT TTGGAGGATT AAAGACAATG GAAACTTTTT ACATTGTTTG TCTCACATAA 180  
TGAATAAAAT TCCACTTTAA AAAATGAAA 209

SEQ ID NO:7375

SEQUENCE LENGTH:422

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08616

SEQUENCE DESCRIPTION:

GATCCGCAGC TCGAAAAAGA ACAAGCCACA GAANCGGGCT CGCTCGTGCC AGGACACAGC 60  
AGTGTCTTTA AAAAAATCAA AACCAGAAGT TTTATCAGCA GCAGGAAGNN TGTGGGACTC 120

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TGTCCAAGTT CACCGTCACC ATCAAGCCAC TGGCTGTGGA AGGAGTTTNT CCAACAGGGT 180  
 CAGTGTACACA GCCACAACCT CAGAAAGCAG CCATCCCGCG TGTCGTCCAA ACAGCAGTGC 240  
 CTGCNTCCCG CTCCACGGAG TGTTCNGAA CACCTCCCTC TGAACATAATC CCGGAGCACC 300  
 CCACCCCCAG CGAGTCCCAC CTGGACCTNT TCAAAGTCAA AACTCTTCTT TNGGGCCAAC 360  
 CAATTNTTCG GGCTTTNGAG GCCTTGAAC TGGGGCACCA AGTTTNTTTC CATGGGAANT 420  
 TN 422

SEQ ID NO:7376  
 SEQUENCE LENGTH:413  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08617

SEQUENCE DESCRIPTION:  
 GATCCCACCA GTTCTGGAC GTGGAGAGTC TGGGGCATCT CCTTCTTATG CCAAGGGGCG 60  
 CTTNNNGTTT TCATGGCTGC CCCTCCAGAC TGCGAGAAAC AAGTAAAAAC CCATTGGGGC 120  
 CTCTTGATGT CTGGNATGGC ACGTGGCCCG ACCTCCACAA GCTCCCTCAT GCTTCCTGTC 180  
 CCCCCTTAC ACGACAACGG GCCAGACCAC GGAAGGACG GTGTTGTNT CTGAGGGAGC 240  
 TGCTGGCCAC AGTGAACACC CACGTTTATT CCTGCCTGCT CCGGCCAGGA CTGAACCCCT 300  
 TCTCCACACC TGAACAGTTG GCTCAAGGGC CACCAGAAGC ATTTNTTTAT TATTATTATT 360  
 TTTTAACCTG GACATGCATT AAAGGGTCTA TTAGCTTTCA GAAAAAAAAA ATN 413

SEQ ID NO:7377  
 SEQUENCE LENGTH:157  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08618

SEQUENCE DESCRIPTION:  
 GATCCACAAA TGAAAGGGAT ATAAAAATAA TGTCATAGGT AAGAAACACA GCAACAATGA 60  
 CTTAACCATA TAAATGTGGA GGCTATCAAC AAAGAATGGG CTTGAAACAT TATAAAANTT 120  
 GACAATGATT TATTAAATAT GTTNTCTCAA TTGTAAA 157

SEQ ID NO:7378  
 SEQUENCE LENGTH:399  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08619

SEQUENCE DESCRIPTION:  
 GATCCTAACA GCTTGCATTA TTTGGTGCAT CTGCTCAATC AAGTCTAATA GACACAAGGA 60  
 TGGCTTTCAT CGGCTCAGGC AGCATCATGA TGAGTATGAA GATGNAATTC GCATGATGTC 120  
 TACCGGCTCC AAGAAGTCCC TCCTAAGCCA TGAGTTCCAG GATGAAACAG AACTGAAGA 180  
 GGAAACATTA TATTCTAGCA AACATTGGNG GNCACATTTT GCATATCTCC CAGCATAAGT 240  
 ACCAAGCAAA ATTACAGTTC CTCTTGGGAG AACACTGCAT TAAGGATGCG AGACTCTCTT 300  
 GCTTCTTCAA AGNGCTTTTG GGAATTTAAA TTGCTAANTA TGTATTCTCA AAANAANNNN 360  
 NGGGANNTTT GGGGGGNNTG GGTTTTNCGG AGNGANGNN 399

SEQ ID NO:7379  
SEQUENCE LENGTH:34  
SEQUENCE TYPE:nucleic acid  
5 TOPOLOGY:linear  
CLONE:HUMGS08620  
SEQUENCE DESCRIPTION:  
GATCGGTCCC TAAACCTCAT TAAAATATTT GAAA 34

10 SEQ ID NO:7380  
SEQUENCE LENGTH:405  
SEQUENCE TYPE:nucleic acid  
15 TOPOLOGY:linear  
CLONE:HUMGS08621  
SEQUENCE DESCRIPTION:  
GATCTNATGG ATATGGCAGT GGACGTGGAT TTGGGGATGG CTATAATGGG NATGGAGGAG 60  
GACCTGGAGG TGGCAATTTT GGAGGTAGCC CCGNTTATGG AGGAGGAAGA GGAGGATATG 120  
20 GTGGTGGAGG ACCTGGATAT GGCAACCAGG GTGGGGNCTA CGGAGGTNGT TATGACAACT 180  
ATGGAGGAGG AAATNATGGA AGTGGAAATT ACAATNATTT TNGAAATTAT ANCCAGCAAC 240  
CTTCTAACTA CGGTCCAATG TNGAGTGGAA ACTTTGGTGG TAGCAGGAAC ATGGGGGNAC 300  
CATATGGTGG AGGAAACTAT GGTCCAGNAG GCAGTNGAGG AAGTNGGGGT TATTGTNGGA 360  
25 NGGNGCCGAT ACTGAGCTTC CTTCTATTT NNCCATGGCA TTTNN 405

30 SEQ ID NO:7381  
SEQUENCE LENGTH:261  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08622  
SEQUENCE DESCRIPTION:  
GATCCTAGCC AGATTACCAG AAATTNCGTT AGTCATCTAA ATCAGAGACA TCAATTTNAT 60  
TATGGAGAAT TTNTGAATCT CCAGCTAGAT GANGAAACCC AATACCAAAC TCCTGTTGAA 120  
35 GAATCTTTNC AAGTAAACAT CTGAAGGCTG TAGACATCTC TCCATCTTTG TACCTGCAAG 180  
TCCCATCTTT AAGGGGGAAA CTACATGANG TCACCGTTAC AGTAACTTGA TGTGTATATT 240  
AATAAAAGTA ATTCAGTCAA A 261

40 SEQ ID NO:7382  
SEQUENCE LENGTH:44  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08623  
45 SEQUENCE DESCRIPTION:  
GATCTATGTA TAGATAAAGA TTAAACATAT CTAGTACAAG GAAA 44

50 SEQ ID NO:7383  
SEQUENCE LENGTH:109  
SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08624

SEQUENCE DESCRIPTION:

5 GATCTGTTTC TTAAAGCTAC AGGGTTTAAA AAATAAAAAAT GAGTGAAAAAT ACTTGATGTT 60  
TCTTGAAAGA TAAATTTAAT AATAATAAAT AAATACATAA ATACATAAA 109

SEQ ID NO:7384

SEQUENCE LENGTH:93

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08625

SEQUENCE DESCRIPTION:

15 GATCATTGTG GCGTCCACAA TGTATATATA AAACAAGTTG TACACATTAC CATGTATAAA 60  
TTTGTGTTTG TCGATTATAT GTCAAGAAAG AAA 93

SEQ ID NO:7385

SEQUENCE LENGTH:54

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08626

SEQUENCE DESCRIPTION:

25 GATCTTAATC TTATTCTCTG CCATCTTCAA ATTAAAAAAA AATTTCTTTG TAAA 54

SEQ ID NO:7386

SEQUENCE LENGTH:140

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08627

SEQUENCE DESCRIPTION:

35 GATCCCTTCA GAAGAAGACA TGATAGGATT GTAAGTTTTT NTCTAACTTT GGATGCAGTG 60  
AGATGACCAG TGTGTTCCAG TTAAAGAAGA AGAGTGTTTT AAAATCATAA ACCAAATAAA 120  
GAATCCTACC TTACATTAAA 140

SEQ ID NO:7387

SEQUENCE LENGTH:206

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08628

SEQUENCE DESCRIPTION:

45 GATCCACCCA CCTCAGCCTC CCAAAGTGCT GGGATTACAA GCGTGANCAC TGTGCCTGGC 60  
CCTTTTTTTT TTAAAGAGA TGGCATCTTG CTATGTCGTC CAGGCTGGTN TTGAACTCCT 120  
GAGTTCAAGC AGTCCTCCTG NTTCAACATA CAGNTACAGG TACCCCCCAC TATACATTTT 180  
NAATANGGNT TCATGGNTCA GNGGGN 206

50 SEQ-ID NO:7388

55

# EP 0 679 716 A1

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08629

SEQUENCE DESCRIPTION:

GATCCCATTTG CTTTCCTGTT TTAAAAATAT TTTATGCTCT TTATTTCCAC TTCTGTGAAT 60  
GTGATATTTT TATTTTNTGA TTATGTTACT GAATAAACAA ACTTGCTACA TAAATNCTT 120  
AGCAATTAAA 130

SEQ ID NO:7389

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08630

SEQUENCE DESCRIPTION:

GATCCAATTG TGGATTTATT TACAAACATC AAATGCCTTC AAGCCAATCC TTTTGCTGT 60  
ATGTTTTGCA GCCTACTGTA GTAGATACGC AACAGATAAT GTGGGAAAAA AAGAGATAAG 120  
AGGAGGAAGC TAATAAGAGA CTGTCAAGAT TGTATACCTT CTTGGTTTCT TTAAAGAATT 180  
TGTTGCCTTT NTACTATNNC AGCAAAGCAG CATTTTGTTA CTGACTGCCT AAAATCACTT 240  
AATCTCAGGT GAACGCATCA CTTGCCAAAC TGTTGGAATG CTATTTGTGT TTTGTTGCAC 300  
TGTTTTTTTC GTTTGTTTGT TTGTTTATTT GGTTGGCTTT TTGGAGAGGG AAATN 355

SEQ ID NO:7390

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08631

SEQUENCE DESCRIPTION:

GATCTAAAAT NAGAGAAGCA TTTAAAAAAT NATTTCTGTC TTGGTTCATC TTATTGTTAG 60  
TGGTTTATGC TAATAAAAAAT TGATTTAACA ATCAAA 96

SEQ ID NO:7391

SEQUENCE LENGTH:411

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08632

SEQUENCE DESCRIPTION:

GATCCAGATA TGTCTGTTAT GAAAGATATC AGTATAGGTA AAGCCACAGG CAGAGGTCAG 60  
TACTGATAAT TAATGTAGTA TAAATACATC ATTTACCATT TTATTTTAAA TAGGAAGCCA 120  
TCAAGCATGC TAGAATTGTG AACTTTTATT ATATNTTTT GTTGTGACA TGAATTAACC 180  
TGGCCAAAAA CAAAAAAGAA NNAAAAAACC ATGCCATTTG TCATGTAAAC CTTTTTTT 240  
TCCCTATGGG CCTTNGGGGN CNGAATCAGT ACTTCAGTTA TTGTAATNGT GNGCTAACCT 300  
CAAATTTNTN TCACCCNGTT GCCCTTTTCA TGNCCTAACC AATTNTCTGG GGGNTTGGTA 360  
TGGTTCNCCC GGTCTGNTC ATGTTTACCG NNCTCTTTT TNGNGGTCC N 411

# EP 0 679 716 A1

SEQ ID NO:7392

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08633

SEQUENCE DESCRIPTION:

GATCTAAGTT CTAAGCCAAA TAACTAACAA ATTCCAGGTA CTATGCCATC ATATAATATT 60  
TATAAATGTG TTATATATAT TATGAGATAT GTATAAGAAT ATAGAATGAA TATGTAATAA 120  
ATTATACTTT TAAATTAATA TTTTCAAATA TATAAATATG TAGTTTCAGA CTGAAACTGT 180  
TCTAAACTAT ATAAATGTAT TATGTATGTT TTATAAAATA CAGTACTCAT AATATGTATT 240  
ATATGAAA 248

SEQ ID NO:7393

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08634

SEQUENCE DESCRIPTION:

GATCCTTCCA CCTCAGCCTC CCCAGTAGCT GGGACTACGG GGTCGCCACT GCACCCAGCC 60  
TGTGTCTTCC AGCTCTAATC AGAAAGCTGC TTGTCGAGGG CATGGGGAAT CAAACTGAAT 120  
GAACTTTTCT CTGCACTGTG GCAAAACTGT TATTTTATG GATTTTACTA AATGGCGTTA 180  
CCTTTTCAAG ATTTATATGT TTGTATAATC ATAAGAAAAT TGAGCCATTA AAGCCTTGTT 240  
ATTCAAA 247

SEQ ID NO:7394

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08635

SEQUENCE DESCRIPTION:

GATCCAGGCT CGTAGNTCAC TCCCTGCCCG TNTCCCAGAG ATGCTTCACC ANCACCTGCC 60  
TCTGAGACCT CGCTCTCTGT TCCAGCAACC CTGGNTTGGG GGGTCANN 108

SEQ ID NO:7395

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08636

SEQUENCE DESCRIPTION:

GATCTTGAGC TCCTGGCCTC CAGAATTGCA GGAGAATAAA TNTGTGTTGT TTTTAATGAA 60  
A 61

SEQ ID NO:7396

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08637

SEQUENCE DESCRIPTION:

5 GATCAGTGTT TGNTTGGGAC TGAAGGGATG ACTAATAAGG AGCAGAGGAA AGCTTTTGGG 60  
 GATGATGGCA CTCTTCTCTG TCTCCATTAC GGCATTGGAT ACAAGTCTCT AGAACTCCCA 120  
 GAACTCGTCA CTGAAAGGGG TGAATAGTAC TGTATGTAAA TTAGGTCCNN ATTTTNAAT 180  
 GGGANAAATA AATATAAAGA CAAATTACAC TGCTGTATTA NNTCANNTGA TAGATGTAAA 240  
 10 AGTCTAATAT ATACGTNTTT TTCNTGATAN NCCCN 275

SEQ ID NO:7397

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08638

SEQUENCE DESCRIPTION:

20 GATCCACGCC CTCCCGCCA GTCTGGAGAG GGCCCTGACC GAGGACTCAA CCCAAACCAG 60  
 TGACACAGCT ACCAATTCTA CTTTACCTTC TGCAGAGGTG GCGTTACAGG CAAAGTGAGG 120  
 AGGGAGCTGG GGGACACTTT CGAGCTCCCA GCTCCAGCTT CGTCTCACCT TGAGTTAGGC 180  
 TGAGCCACAG GCATTTCTCG CTTATTTTAG GATTACCCAC TCATCAGAAA AAAAAAAG 240  
 GCCTTTGTGN CCCNTGTTTT GGGGGGATTA ACCNGTTTGG GGTTTAAA 288

25 SEQ ID NO:7398

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS08639

SEQUENCE DESCRIPTION:

35 GATCTAATTN CTATTTCAAT TATTCAGAAA TAGCATTAG ACATAAAANC CAATGTCTCA 60  
 CTTTGTAATA TAACCTTTGG CTAATTTACA CACATCTAAT ACAGCGTGTT ATATAAGTTT 120  
 TAAGTAATAC AATGAGTCAC TACTATCATT CAGTTTAAAN TATTTTNNGT GTTAACAGGG 180  
 CTGAGAAATAT CATGTGGTTC AGTCTTCTGN NGGNCGTTAT ATNATACCNG CNTAGTGCCT 240  
 TTGACCATGC NGACTATCCT CAAGGCCAGA CATCCTACAN CGGAACTGNN 290

40 SEQ ID NO:7399

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08640

SEQUENCE DESCRIPTION:

45 GATCCNTAAG TACTCTCTC TANAGAATAA AATGCATTAC CTAGGCTTTA ATAGTTAAAA 60  
 GCTGGNATTT ATNGACCCGC ATCTACTTGA TTTCANAATA TGCATTGATT TTAGTATGTT 120  
 GCTGNTCTGT TATCTGTACT CAACTATANC AGAGTAATAT ATTGTGGTNT TCTGGACCAA 180  
 AANTCGTGCT ACACATATGT CTGATGGCCT TNACCTTTTC ANGACAACAG TTGCAATTTT 240  
 50 GAGCACAGTC CNCCTAGTGG TANTCTN 267

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# EP 0 679 716 A1

SEQ ID NO:7400

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08641

SEQUENCE DESCRIPTION:

GATCGGGAGC AGCCCCACTG GACCTAGGTG CCCCATCTGT TGGTCATCCA TCCTGAAGGG 60  
ACAGGAAACC TCCAGGCAG TTATTTTTTT TTCTCTATAT TTCTAGTAAA GTTTTCGATA 120  
TGTTAAA 127

SEQ ID NO:7401

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08642

SEQUENCE DESCRIPTION:

GATCACTAGT GCAGGAGAAC ATTACATTTT CTTCTGAAGG CAAAATGCTT GTAGGTTTTG 60  
CCTCTACTTT GTATTTACTT TTAATAATTGC ACTTGTTTAC CTACCAGTGT TTACGAAATC 120  
CTGTATTTGG GATGCTTTTT CTATAATAAA ATATTATAAT TTGTGAAA 168

SEQ ID NO:7402

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08643

SEQUENCE DESCRIPTION:

GATCATAGTA AAGAGTAGTC AATAGGGTCT TCAGCTATTA ATTGTAGAGG TGATTAAAAC 60  
CAACAAGGAG TTTCATGTGC AAAGGAGATA AGGAATGAAT ATAAAGATTG CTATTTGGGT 120  
GGCTCTTATT AAACGTGTGA TTTTGTACTT ATCACTACAC GTATCCCCCA AATGCTTACA 180  
TGGGAGTTTG AGGTTAGTAT TTTCACCTCC TTGGTGTTAG TACTCTATTC ACATTCTTAT 240  
TGTAACCTTC CTCATTTTAC AGATAAGGAA TCTTTGGGGA TTAACCAACC TCCTTTCTGT 300  
AATGGTAATC ATTAAANTAA GTN 323

SEQ ID NO:7403

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08644

SEQUENCE DESCRIPTION:

GATCACTTAN GCCCAGGAGG CAGAGGTCAC AATGAGCCGA AATTGTGCCA ACTGCACTCC 60  
AGCCTGGGCA ACAGAGGAAG ACTCTTCACA GAAA 94

SEQ ID NO:7404

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid



TOPOLOGY:linear

CLONE:HUMGS08645

SEQUENCE DESCRIPTION:

5 GATCGGGGCT TTGTGTTTAA CCTCATCAGA CATTATTGCA GCCAGCTGTC AGCCAAGCTC 60  
 AGTAACCTTC CAACGCTCAT TTCCATGAGG CTAGAGTTCC TGAGAATCCT CTGTAGCCAT 120  
 GAGCATTACC TCAATCTGAA CCTTTTTTTT ATGAATGCTG ATACTGNTCC NACATCTCCT 180  
 TGTCTTCCA TATCTTCCA GGTAATAAAA GAATTATTTA ACTAAA 226

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SEQ ID NO:7405

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS08646

SEQUENCE DESCRIPTION:

GATCCAGTCA GAGCCAGGGA GAGTGTTTGC CTTAAGGAGG GACTCCCTTG TCCAGGATGG 60  
 GGCTGGCACT AGGGATGGGG TGAATCTTAG GACAGGAGTG GGGGTCAGAA ATGGGAGGGG 120  
 TAAA 124

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SEQ ID NO:7406

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS08647

SEQUENCE DESCRIPTION:

30 GATCGACCAG CAGGTGGTCT ATATCCATCC TTCCAGTGCC CTCTTCAACA GACAGCCAGA 60  
 ATGCCCAAAG AACTTCCTCC CTNTGGTTGC TGTAGGTGTC TCATTGGAGC AGTGCCTCTC 120  
 CAAGTTTGAG GATNTGAACA AAGAACTGGG ACTGGTGACT TGTNANNGNN NAGTTCAGAG 180  
 GGCAGAGGNC CATCATCTCA GCTTNN 206

SEQ ID NO:7407

35

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08648

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SEQUENCE DESCRIPTION:

GATCCATAAG GAGGGCTGTG TGGNGAAGAT TCAGGGACTG ANTAGAGGGA AAATCGTGCT 60  
 ATNCGGTAGC TACAGCAGCC CTGGGAATNC CNTTTTGTCTG AGN 103

SEQ ID NO:7408

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SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08649

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SEQUENCE DESCRIPTION:

GATCCATAAG NAGGGCTGTG TGGAGAAGAT TCGGGNCTGG CTGAGGAAAA ANCGGCTGGT 60

55

GGTAGCTACA GCANCCCTTG GAATACCCTT TTGTCGAGGT TTTGGGNATT GTCTCN 116

SEQ ID NO:7409

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08650

SEQUENCE DESCRIPTION:

GATCTATCAT GTATCTTGGT GATTACAGTT AATAATATAT TGTATATTG ANAATNGAAA 60

SEQ ID NO:7410

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08651

SEQUENCE DESCRIPTION:

GATCGCACCA CCGCACTCCA GCCTGGGCAA CAGAGCAAGA CTGTTTCAAA ATAAATAAAT 60  
AAAATAATAA ATAANNCTTT CCAACTNCAA A 91

SEQ ID NO:7411

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08652

SEQUENCE DESCRIPTION:

GATCTTGTGG CTAACCAGC ATTTCTGTGT TTGAGAGATT TCCTGTTAGG TGCTTCGTCT 60  
GAAAGTGAAC TCTCATAATT CAAATTGTAT AAANTAAAGC TACATTTCTA AGAGCTTGGT 120  
GTAGGGCAAT TGGAATANTG TCCTGTTAGA TAAACAGACA TTTAGCANTC CTGACATTAA 180  
AAGGAAATGT ATTTCTATAC AGGATTATTA GCTGTANTAC ANGATATTTA TTTANCCAAA 240

SEQ ID NO:7412

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08653

SEQUENCE DESCRIPTION:

GATCGCACCA CTGAACTCCA GCCCENATGA CAGAGTGAGA CCCTGTTTCT AAAAACAAAA 60  
CAAACAAACA AACAAACAAC GTATCTTACT GACTAACTG GAATGGAAAT CTTATAATNA 120  
GTGTTGTATT TTTCTGCAAA ATAGTGAATT NGNACTTGGG AGACTTCNNN NCTTTGTTGA 180  
AAAAAATTGC CTTTGTTTTG AAATTATATC ACCTGTGTTC TGANCTAAAA TGNTGGGAGT 240  
TCATNNN 247

SEQ ID NO:7413

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08654

SEQUENCE DESCRIPTION:

GATCCATAAG GAGGGCTGTG TGGAGAAGAT TCAGGNANCT GACTGAGGAA AAATNTGCTG 60  
GTGGTAGNTA CAGCANCCCT TGGAAATACCC TTTTGTGCGAA AAATAAAGGA ATTGTCTTCA 120  
NCCTGCTN 128

SEQ ID NO:7414

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08655

SEQUENCE DESCRIPTION:

GATCCATAAG NAGGGCTGTG TGGAGAAGAT TCAGGGAGCT GACTANAGGA AAAATGTGCT 60  
GGTGGNANAT ACAGCAACCC TTGGAATANC CTTTGTGCGA GAATAAAGGA ATTGTCTN 118

SEQ ID NO:7415

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08656

SEQUENCE DESCRIPTION:

GATCTTTNTN ATATATGCAG TCCCATCCCT TCTGTGCCAC TCAATGCCAT CCAGACATGG 60  
TTTNCCCTC CANGGGCCTT TCTCTCCAGA GGGCACTTCG GCTGCCTCTG CTCCTCTCA 120  
TTCGAGGCCG GNCTCTTNCT NACAGAATAG N 151

SEQ ID NO:7416

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08657

SEQUENCE DESCRIPTION:

GATCCCGTTG CCTCATGGAA CTCATGCATT TCACGCTGCT TGCCCTTTCT GTGCTACACA 60  
GCTGGTTGGG GNGCAAACT GCATCAAATT AATTNCCAA GGTCCAATTG ACTGACGCC 120  
TTGACAGCCA TCTACGACTT TATTAACAGG TTACTGTGAA GATTTNCCA CTAACCTAG 180  
ATTTNCCTT TTTGTAATGC TGTTTATCAG AGGCGGGTGA CANGGGCTGG AAATAAAGNG 240  
AGGGGACATG GTGATGAAAC ATGGCAGGNG TGTACAGATA CCAGTGGTGT GTTGCATGCT 300  
CAANACAGCA GCGTCGTCAA TGGCGTCTGC TTGNTTGNNC CATNATGTCT TTGTCATAAT 360  
TGGNAANNA NNNN 374

SEQ ID NO:7417

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08658

## SEQUENCE DESCRIPTION:

GATCTTTATG TCACTAGTTA TAGTTAAGTT CATTAGACA TAATTATATA AAAACTACGT 60  
GGATGTACCG TCATTGAGG ACTTGCTTAC TAAACTACA AAACCTCAAA 110

SEQ ID NO:7418

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08659

## SEQUENCE DESCRIPTION:

GATCTTTTTA ATTCAGTACA ATCTCTGAAG GTGTTAACAC TAATNTTTTA CAAGAATGTA 60  
GAGGCGACTC GGTGCTATGA AGCGTGTTAA ACAACTCACA CAATTGCTAC AAAACACCAG 120  
GGAGGGGCTT TTTGTGTTTT TAATTTTAA AACATTTTTC CTTTCTTGT GAGCCATAGT 180  
AGGCCTAGAG AGATTACTGG GTTTTATAA TTAAACATT ATTTCGGTGA AA 232

SEQ ID NO:7419

SEQUENCE LENGTH:370

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08660

## SEQUENCE DESCRIPTION:

GATCTTAACC AGTCGAGTGG AGTGTACATT GTCTGAATAC AGGATGCACA ATGTTGTCAA 60  
TCCTGGAAAT GGTCTTCTT TTTTGAAGA TATGTGAATG AAGTGTTGGT GTCCTACCA 120  
AGAGGTGGCA CCTAAGGGTT CTGAGGAAAT AAATGTATAG ACCCTTATGT ACAGACCTGT 180  
GTATAANCAN CTNNGTATA TACATATAAG GATAGCTTTT TTGACCTATA CAGCTGTNCA 240  
TAAAAGTAGC TGATATTAGT TAGGCCTGTG TCACCAGTTT GGNTTTTTTN CACTGGTNCA 300  
TTTGGGATTT NNTTTTNGGT GGT TAAAAT GGCATATGCT AAGGTGTGTG ATTGGGAANA 360  
AANNANNANN 370

SEQ ID NO:7420

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08661

## SEQUENCE DESCRIPTION:

GATCTGTGTT TTAATGAGTT TCACAGTGTG ATTTTGATTA TNAATTGTGC AAGCTTTTCC 60  
TAATAAACGT GGAGAATCAC AAA 83

SEQ ID NO:7421

SEQUENCE LENGTH:394

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08662

## SEQUENCE DESCRIPTION:

GATCCTCTCT TACCCCGTCC CCAGGTTTGA AACACATAGC CTCATTTCAG GGTGTAGCCA 60

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5 GGTTCCTCCG ACTTCTCT GGGATATAAA AAAGGGGGTA AGGGGGCAAA GAGAGCCCTC 120  
 TGGGACTCTC CTCCCATACA CACTACACTG CCCCTTCTCC CCCCATCAAA ACGCTCAGNG 180  
 ACGTTGTGAT GATGCGACTG AGGATTATGC AACGTGGTCC AACCGGAGCG GNCAGCATGA 240  
 CCAGCTGTCC AGGGGCTGNC TNCTGCCTTT TCTTTGTAA AAGCCANGAC CCTTGGGGAG 300  
 TTTTAATNCT GTTTGTACT TGNCTGTGG GGNCTNCACT TGCTTTTCT ATGGGAGACA 360  
 CTTTNAAT TTAACAAGNT GNGGGTTTT TGNN 394

10 SEQ ID NO:7422  
 SEQUENCE LENGTH:134  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08663  
 15 SEQUENCE DESCRIPTION:  
 GATCCCCATG CCTGAGGGCC CCTCGGCTGG CCTGGGCATG TGATGGCTCC TCACTGGGAG 60  
 CCTGTGGGGG AGGCTCAGGT GTCTGGAGGG GGTGTGTGCC TGATAACGTA ATAACACCAG 120  
 TGGAGACTTG CAAA 134

20 SEQ ID NO:7423  
 SEQUENCE LENGTH:69  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 25 CLONE:HUMGS08664  
 SEQUENCE DESCRIPTION:  
 GATCATGNGT TTCCTCATGA GGACAAATAC CTGATTTTGA ATAAAGCAGC ATTCAGTTGA 60  
 AATAACAAA 69

30 SEQ ID NO:7424  
 SEQUENCE LENGTH:52  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 35 CLONE:HUMGS08665  
 SEQUENCE DESCRIPTION:  
 GATCAACATT TTTTAAAAA GAGCATTAAA GAAAGAATTG TGGTACAATA AA 52

40 SEQ ID NO:7425  
 SEQUENCE LENGTH:356  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 45 CLONE:HUMGS08666  
 SEQUENCE DESCRIPTION:  
 GATCACACAT TCAGACTGTT GTGTCTGTGG AGTTTATAGGA GTGGGGGGTG ACCTTCTG 60  
 TCTTTGCACT TCCATCCTCT GCNACTTCCA TCTGGCATCC CACGCGTTGT CCCCTGCACT 120  
 TCTGGAAGGC ACAGGGTGCT GCTGCCTCCT GGTCTTTGCC TTTGCTGGGC CTCTGTGCA 180  
 GGACGCTCAG CCTCAGGGCT CAGAAGGTGC CAGTCCGGTC CCAGGTCCCT TGTCCTTCC 240  
 50 ACAGAGGCCT TCCTAGAAGA TGCATCTAGA GTGTCAGCCT TATCAGTGTT TAAGATTTTC 300

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NTTNTATTTT TAATTTTTTT GAGACAGAAT CTCACTCTCT CGNCCAGGCT GGAGTN 356

SEQ ID NO:7426  
SEQUENCE LENGTH:246  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08667

SEQUENCE DESCRIPTION:  
GATCGTCGCC CCTCTGCCAA CTGCGACCCC TTTTCGGTGA CAGAAGCCCT CATCCGCACG 60  
TGTCTTCTCA ATNAAACCGG CGATGAGCCC TTCNAGTACA AAAATTAAGT GGACTAGACC 120  
TCCAGCTGTT GAGCCCCCTCC TAGTTCTTCA TCCCACTCCA ACTCTTCCCC CTCTCCCAGT 180  
TGTCCCGATT GTAAC TCAA GGGTGAATA TCAAGGTCGT TTTTTCATT CCATGTGCCC 240  
AGTAAA 246

SEQ ID NO:7427  
SEQUENCE LENGTH:286  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08668

SEQUENCE DESCRIPTION:  
GATCCTTGCA GGAACCTAAG GATTACAGCA GCTGCAGATG GCAGGAGCTA CAAGCCAGCA 60  
GCAGCCAATG CTCANTGGGG TACAAATGGC TCAGGCAGGT CAACCAGGGA AAATGCCAAG 120  
TGGAATAAAA ACCAACATCA AGTCGGCTTC CATGCATCCC TACCAGCGGT GAGTGTGGCT 180  
GGCAACCTCG ACTCCCTGGT GCTCTTTGCA GAGTTGGGCA GTGAAATNNN NNNNTGCTCA 240  
AGGCTCACCT AGGATGGGTA CAATAAAAAG AACATGGGCT TTCAA 286

SEQ ID NO:7428  
SEQUENCE LENGTH:177  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08669

SEQUENCE DESCRIPTION:  
GATCACTAAC AGGTGATGGG CTTTGTGCCC ACTCCAGAGA TATTGTGGGA GACAAATTCT 60  
TTTAACAGCC TGTCTCCCG GCATCAGGAG TCATTGAACA ATCATGGATT GTTGTGTTTG 120  
GGATTTTTTT TTTTNGGN TTNNTTTGG GTTTNGNGN GTGTGTGTGT GNCCTGN 177

SEQ ID NO:7429  
SEQUENCE LENGTH:388  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08670

SEQUENCE DESCRIPTION:  
GATCCAGGTG GTCCAGGAGC CCAGGACAGG CCTTNCTGT GGGCCCTGGC CAGACAGGGT 60  
TACCTGGTGA GGTGCAGAGA GTCCCTCTAG TGGCCATTTT GTATGGTAGT TGCTAATGCA 120  
GAACAAGTTC TGTCTGGGC TTAAATTGAC TGAAGACTTT AGGGGGAAG AATAGTAAAT 180

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GCATGTAAAC AAATGGGGAC ACTCTGTTCA GGAGAATAAT CCGACTGGCA TTTGTGGCAG 240  
 TTTTGTAAAT GTAAATGTAT TCATGTGTGT TCTTGTAAT ACGTGTGCT CAGATGTCCT 300  
 TTGAAGTGGG AGGGAATCAA TCCGGGGATA ATTTCAAATG GAATAGAGTA TTTTGATATT 360  
 GTTCATTCAG AGGGTGATGT GTACACAN 388

SEQ ID NO:7430

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08671

SEQUENCE DESCRIPTION:

GATCCCCACT GTCAATGGGG GATTGTCCCA GCCCCTCTTC CCTTCCCCTC ACCTGGAAGC 60  
 TTCTTCAACC AATCCCTTCA CACTCTCTCC CCCATCCCC CAAGATACAC ACTGGACCCT 120  
 CTCTTGCTGA ATGTGGGCAT TAATTTTTTG ACTGCAGCTC TGCTTCTCCA GCCCCGCCGT 180  
 GGGTGGCAAG CTGTGTTTCA ACCTAAATTT TCTGGAAGGG GACAGTGAAG AGAGGAGTGA 240  
 CAGGAGGGAA AGGGGGAGAC AAAACTCCTA CTCTCAACCT CACACCAACA CCTCCCATTA 300  
 TCACTCTCTC TGCCCNATT CCTTCAAGAG GAGACCCTTT GGGGACAAGG CCGTTTCTTT 360  
 GTTCTGAGC ATAAAGAGGA AAATAAATCT TN 392

SEQ ID NO:7431

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08673

SEQUENCE DESCRIPTION:

GATCTTTGGG AAGGGAGACT AGGGCAGGTG GAGACAGCGC AGAACCCCGG TGCTGGGTGG 60  
 GAAGCATGAC CACACGGTGG GTGAGCAGCC CCCATGCACT GATGGTAAAT TCCCCTGTGG 120  
 ACTCAA 127

SEQ ID NO:7432

SEQUENCE LENGTH:353

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08674

SEQUENCE DESCRIPTION:

GATCTGTCTG GCATGTCAGG AGCCAGAGAT ATTTTATAT CAAAAATTGT CCACAAGTCA 60  
 TTTGTGAAG TGAATGAAGA GGGAACAGAG GCGGCAGCTG CCACAGCAGG CATCGCAACT 120  
 TTCTGCATGT TGATGCCCGA AGAAAAATTC ACTGCCGACC ATCCATTCTT TTTNNNNNTT 180  
 CGGCATAATT CCTCAGGTAG CATCCTATTC TTGGGGAGAT TTTCTTCCCC TTAGAAGAAA 240  
 GAGACTGTAG CAATACAAAA ATCAAGCTTA GTGCTTTATT ACCTGAGTTT TTAAATAGAG 300  
 CCAATATGTC TTTATAANCT TTNCCCANTA AAAACCCACT TGTCCTCAAAG AAA 353

SEQ ID NO:7433

SEQUENCE LENGTH:399

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08675

SEQUENCE DESCRIPTION:

5 GATCTAATTG GCTTTTATTA GCAATTCATG AGCCCGGCAG CATCCAGTCT ACAAATAGA 60  
AAGGAGTGCC ACTAAGCTAG ACAGAATGGA TGGGTTTTAT GGCAGAAAAA AGTGGAAGCA 120  
AGCAAGAACA ATGAACAAAT TAATGGATGG ATTGTTTAA GATTACATT CTTTATGGG 180  
AGTAAACAAA ATCTTGTTAG CCTAATGGAA TTTGGCATCA TCTCCTGATT TCTCAGAAGG 240  
10 TCATATCTTG TAAGTGAACC ATTTAGGTTT GGTGACCTGG NACCTTTGGC ATAANGTGAC 300  
TCCATTTTGG GGCCTGCTGC CTTTTCTTT AAAAANGGAG TGACACCNTA ATTTCCATGG 360  
GNNGAGCACA CANNATGCC TGTNTTGA GGACCTNCN 399

SEQ ID NO:7434

15 SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08676

SEQUENCE DESCRIPTION:

20 GATCCTGACC ATATTCCTCA AGGTCTCCTT TTCCTTCCTC CAGTGTAACA AAATTCCTG 60  
CTGGCGTCCT ATGTAAAGAT AATCGGCCCT TTTGGACCT TTTGTTGGN TCAAGAATT 120  
GGGTGGGAGA AAAGAAAGTG GGTATCAAG GGTGATTGA AATTTCTGC AGCATTAAAG 180  
25 CTGGCGCTTA ATAAGAATAA GTAATAATAA AGAAATTCT AACATTCAA 230

SEQ ID NO:7435

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08677

SEQUENCE DESCRIPTION:

30 GATCCTGAAA ATAGCCCGT GAAGGCAGAA ATGTATGTGA CTAGAACGAG GCCACATGAA 60  
TAAGCCACTG CCCACTGGCA GGAGTGAAAA CTGAAGCGCT CCTTACCTGA AGGACCCCAA 120  
35 AACCATATAG AATAGAATAA CCAGGAGTTC AAA 153

SEQ ID NO:7436

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08678

SEQUENCE DESCRIPTION:

40 GATCTCACAA GCNCTTTCCC TCTTGGTGCC TCAGTTTCCT GACCTATGAA ACAGAGAAAA 60  
TAAAAGCACT TATTTATTGT TGTTGGAGGC TGCAAANTGT TAGTAGATAT GAGGCATTG 120  
45 CAGCTGTGCC ATATTAAA 138

SEQ ID NO:7437

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid



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TOPOLOGY:linear

CLONE:HUMGS08679

SEQUENCE DESCRIPTION:

5 GATCATGGCT AAAGATGACC TCTCTGGTGC TGACATCAAG GCAATCTGTA CAGAAGCTGG 60  
TCTGATGGCC TTAAGAGAAC GTAGAATGAA AGTAACAAAT GAAGACTTCA AAAAATCTAA 120  
AGAAAAATNTT CTTTATAAGA AACAGGAAGG CACCCCTGAG GGGCTGTATC TCTAATGANC 180  
CATGGCTGTC ATCAGGAAAA TGGTTGGGAG ATTTCTCAAT CCCTGAAAGG ATGAGGTTGG 240  
10 GGGAGTTGCC CAGAGGAATC CCTGTTCCCA CTGATTTTTA TTAGCAAAAC ATCCTGTGTC 300  
TTTTGGAGTA CGNTGTGTAA GTGCCCATG GGTGGCCTGT TNGGTCCTG TGCAGCAGTT 360  
N 361

SEQ ID NO:7438

15 SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08680

SEQUENCE DESCRIPTION:

20 GATCAAAGTG TAAACACCAT AGGGACCCNT TCTACACAGA GCAGGACTGC ACAGCGTCCT 60  
GTCCACACCC AGCTCAGCAT TTCCACACCA AGCAGCAACA GCAAATNACG ACCACTGCTA 120  
GATGTCTATT CTTGTTGGAG ACATGGGATG ATTATNNNCT GTTCTATTTG TGCTTAGTCC 180  
AATTCCTTGC ACATAGTAGG NACCNNGTTC AATTACTATT GNATGAATTA AGAATTGGTT 240  
25 GCCATAAAAA TAAATNNGGT TCATTTAANG TNN 273

SEQ ID NO:7439

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS08681

SEQUENCE DESCRIPTION:

GATCAGAGGA ATGTTATNTT GTTCAGCCTT CTGTTGGTT CACAGTAGTG ATAGTATTGT 60  
35 AAATACTCAG AGCAATCCTA CAAGAAGAAA ACTACATNAG CCCCCACATG TCCCCCCAA 120  
CATACCCCAT CACAGCAACT GAAAACAAGA GAAATGTTAG TTTTCTGTGG AAA 173

SEQ ID NO:7440

SEQUENCE LENGTH:194

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08682

SEQUENCE DESCRIPTION:

45 GATCTCTTGA ACTCTGGGTT CTCCAGCCC CTTGTCCTTC CTTCCAGCTG AGCCCTGGCC 60  
ACACTGGGGC TGCCTTTCTC TNACTCTGTC TTCCCAAGT AAGGGGGCTC TCTNAGTGCA 120  
GGGTCTGATG CTGAGTCCCA CTTAGCTTGG GGTGAGAACC AAGGGGTTTA ATAAATAACC 180  
CTTGAAAAC TAAA 194

50 SEQ ID NO:7441

55

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08683

SEQUENCE DESCRIPTION:

GATCANATGA AGAAAAGGAG AGGTAGATAC AGTCAGTGTC ACTTCAGGAA AGCTATTTAA 60  
 AAAANCTTGA AATATAATTG AAAGAAGAAA CAACACCAAA NAAGCCTAAN CCTAGCCTCT 120  
 GANCANCACT AN 132

SEQ ID NO:7442

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08684

SEQUENCE DESCRIPTION:

GATCAATCTG AGGAGACTTA ATAATGATAT TNATTCTCCC AATTCATGAA TATAGTATAC 60  
 CCCTGTATTT ATTTGTNTTC TTGAATTTCT TTTATCATTG TTTTGTAGTT TTCACCATGA 120  
 CAGTCTTGCA CATATTTTGT TAAATGTACA GCTGAGAATT TAATTTTTC TGGTGTACAA 180  
 TGCTAATAAA ATGGTGCTTT AAAAGAAA 208

SEQ ID NO:7443

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08685

SEQUENCE DESCRIPTION:

GATCCTCTAA GGTCTACAG TTTACTTCTT GTATTCTCCT TTGTAAGTCA TCTCCAAGAC 60  
 GATGTCCAAA TCCATACCA TTAATAATTA TAGTTTCCTC ACCCACAACA CTTAATATTT 120  
 TAAAAAANGA TACTTTTCAT TGTATTATAA TTAATTGATA CATACATATT TGCTCTGTGA 180  
 GTTCCTTATT CATCATATTA GTGCCTGACA ATAAATGTGT GCTGGATTGA GCTGAATCTT 240  
 TAAA 244

SEQ ID NO:7444

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08686

SEQUENCE DESCRIPTION:

GATCCTGCAA TTCCACTTAT AGGAATTGAC CCACAAGAAA TGAAAGCAGG GACTTGAACC 60  
 CATATTTGTA CACCAATATT CATAGCAGCT TATTCACAAG ACCCAAAAGG CAGAAGCAAC 120  
 CCAAATGTTT ATCAATGANT GATTGATTGG CTAAGCAAAA TGTGATATGT NCCTAACGAA 180  
 GTATCCTTCA GCCTGAAAGA GGAATGANGT ACTCATACAT GTTACAACAC GGACGAACCT 240  
 TGANANCTTT ATGCTAAGTG AAATAAGCCA GACATCANCA GATAANTAGT TTATGNTTCC 300  
 ACCTACATGN GGTACTGNGA GTN 323

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SEQ ID NO:7445

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08687

SEQUENCE DESCRIPTION:

GATCCTCCTG CCTCATCCTC CCAAAATNCT GGGATTACAG GCATAAGCCA CCGTGCCTGG 60  
CCTCTTTAAT AATNTTNAAA ATACCCTAAA GGCTTGTGAA TATACAAGTC TACTGATAAA 120  
TTATGTATTG TCTGGGAATT TGATAGTNAT TGTTTTAGAT AACTGGNTTT TACGCTGTGG 180  
TAGNCNGGCT GTGACACTAG TGTGACACAG GTGTAATTGG TCATCCTATG CCTTCACCAG 240  
AATAACTTGG GAGTGGTGCC AGAANCTAGA GTCTACAATT CTCACTGTTT AGAGAGTGTT 300  
ANTGNCATAC TGTGTATN 318

SEQ ID NO:7446

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08688

SEQUENCE DESCRIPTION:

GATCAAGATA GTAGTATTAT TACACAAGAA ACTTGGTCTG CAGTCTGGAA GCTTGTCTGC 60  
TCTATAGAAA TGAAAATGCA GCATGAAGTT GACATTGTGG AAATGAAAGT AATTGGGTAT 120  
TAGAAATCTG AAAGTACTGT CATCTAANAG CAATTGTGAT TTTNTTGTAA TTGGTTGTCA 180  
CTGTTGTNCG GTGTCTAGNG TTANNGAATA CATGTNANCT TTCATGGTAT TTNGCCTTTC 240  
TTAANTTTTT TTAATAATTA ANCTTTCTAA CCTATGTATT CAACTTCTGT ATTTATATNT 300  
NATCAGTGGT TCATGTN 317

SEQ ID NO:7447

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08689

SEQUENCE DESCRIPTION:

GATCATCAAA GAAAGACAGG GTGACCTGAG GATTATATGT TCAGCCAAGC TCCCCTCCAA 60  
GCATAAAGGC TACAGATAAC CATTTGTACA TATTCAGGAA CTGGAGTAAT GTGATTCCAA 120  
TGAGCCTGTC TTGAAGGAAC TCCTAGGGGA TTAACCTCAG CTAACCTGGG AAGTTATCTG 180  
GAGAAACCAC AACAGAAGGA CTGGTTGTAG TTCGAGGCTG TAGTCAGCTA TGATTGCACC 240  
ACTGCACTCT AGCCTGGATA ATAGAGCAAG ACTTTGTCTC CAAA 284

SEQ ID NO:7448

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08690

SEQUENCE DESCRIPTION:

GATCCCTAGT ATAACACATT CAGTGTTCCT CTTTCAGTCT TACTACTTTN ACCGCGATGA 60

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TGTGGCTTTN AAGAACTTTG CCAAATACTT TCTTCACCAA TCTCATGAGG AGAGGGAACA 120  
 TGCTGAGAAA CTGATGAAGC TGCAGANCCA ACGAGGTGGC CGANTCTNCC TTCAGGATAT 180  
 CAGGAAACCA GACTGTGATG ACTGGGAGAG CGGGCTGANT GCAATGGANG TGTGCATTAC 240  
 ATTTGGAAAA AANTGTGAAT CAGTCACTAC TGGANCTGCA CAANCTNGCC ACTGNCAAAA 300  
 TTGACCCCCN TTTGTNTGAC TTCN 324

SEQ ID NO:7449

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08691

SEQUENCE DESCRIPTION:

GATCACCTGA GGTGAGGGGT TCGAGACCAG CCTGGCCAAC ACGGTGAANC CCATCTCTAC 60  
 TAAAAATGCA AAAATTAGCC GGGCGTGGCG GCACATGCCT GTAATCCCAG CTACATGGGA 120  
 GGCTGAGGTG GGAGAATTGC TTGAACCCAG GAGGCGGAGG CAGAGGCTNC AGTGACCCAA 180  
 GATTGTGCCA CTGCACTCCA CCCTGGGCAA CAGAGCAAGA CCCCATCTCA AAAATAAATA 240  
 ANTATATATA NAAAATAAAA NGCTATTCT NGNNNNTTTC ACTATAAAGT TTTGCTTTAT 300  
 TAAAAAGCTA NTANGCAGCT ATTN 324

SEQ ID NO:7450

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08692

SEQUENCE DESCRIPTION:

GATCTTAAAC TCAGTAAGCC ACTATCTGCA ATTTTGTACA TTATATAGTA TTTTGAAGAT 60  
 ATGGAACCTT ATGAAAAAAA AATAGCAAAT NAGTTCTTTT TCCCCCAGAG GGGAAAGTTA 120  
 TGTNCTGCAA ATAGTGTGTG TCTTATTTTA CTGTTGANCA GCAATNGCNN NTTATTTTTT 180  
 NATTGCTAG AACTTCAACA TGTTGTATAG GAATCCTGTA GTGCCACTAG TTAAATGCCG 240  
 AATTCTCATC TGGATGTTAC CATCAAACAT CAGTACACTT GTCATTTTAC ATGTGTTTAA 300  
 TGTGACAGTT TTTCACTACT GTNTNN 326

SEQ ID NO:7451

SEQUENCE LENGTH:38

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08693

SEQUENCE DESCRIPTION:

GATCTNGTGG GCATAAATAA AGGTGTCATA AAGACAAA 38

SEQ ID NO:7452

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08694

## SEQUENCE DESCRIPTION:

GATCTTAAGA AGTGCTTTGA AGGGTTAAGA ATCAGGGGTC CAAGAGAGAC CCCAGTCCCT 60  
CAATAAAGCC ACAAGAGCCC AAA 83

SEQ ID NO:7453

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08695

## SEQUENCE DESCRIPTION:

GATCTACACT CCAGGCCGGA AAGAGCAAGG GGAGCCCATG ACCCCTCGCC GCACGCCAGC 60  
CCGCTTTGGT CTGTAAGCTG AGGCTGTCCC CAGAGAGGAT GGCAGCAGGT ATTGGGTCCT 120  
CAGCCTTCTG GCGGGAGCCT GAGGCTGCGG ACAAAGCCCT TTAATCTAAG GACTTTAATC 180  
TGTNCATATN ACGGCCCCC AGGGCAGTTC CTGCTGGACC AGACTCTNTG GCAGAGGAGG 240  
TGGAGTTCTT CCATGCAGGA GCACGNCATG GCGGGAGCGG GGCTGCAGAG TATCCGNGGT 300  
GCTGCCGNGG CACGGNGAGG TNGCTNGACC CATCGCATCT AAAANTAGGA N 351

SEQ ID NO:7454

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08696

## SEQUENCE DESCRIPTION:

GATCTAAGGT TTTAAAGAA TTTGGTTTGA AAATATACAG TTGTCTTGAA GGAAA 55

SEQ ID NO:7455

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08697

## SEQUENCE DESCRIPTION:

GATCTGTTCT GTTTCACCAT GTAACACACA ATACATGCAT GCACTGTATT AGTGTTAGAA 60  
A 61

SEQ ID NO:7456

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08698

## SEQUENCE DESCRIPTION:

GATCCCATTT TCCTCTGACG TCCACCTCCT ACCCATAGG AGTTAGAAGT TAGGGTTTAG 60  
GCATCATTTT GAGAATGCTG AACTTTTTTC AGGGCTGTGA TTGAGTGAGG GCATGGGTAA 120  
AAATATTTCT TTTAAAGAAG GATGAACAAT TATATTTATA TTTCAGGTTA TATCCAATAG 180  
TAGAGTTGGC TTTTNTTTTT TTTTGNCCA NGGGGGGGGG TTTTTCCTCC NTGCCCCCCT 240  
GGGGTTTTTN NANTCCCNGT NNNAAAANAA ANN 273

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SEQ ID NO:7457

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08699

SEQUENCE DESCRIPTION:

GATCTTAACC AGTCGAGTGG AGTGTACATT GTCTGAATAC AGGNTGCACA ATGTTGTCAA 60  
 TCCTGGAAAT GGTCTTTCTT TTTTGTAAGA TATGTGAATG AAGTGTGGT GTCCTACCA 120  
 AGAGGTGGCA CCTAAGGGTT CTGAGGAAAT AAATGTATAG ACCCTTATGT ACAGACCTGT 180  
 GTATAAACAA CTNTGTATA TACATATAGG ATAGCTTTT TGTACTATAC AGCTGGTACC 240  
 ATAANAGTAG CTGGATANTT TGGTTAGGNC NGGTTGTCCA CCAGTTTGG NNTTTTTTTT 300  
 CACTTTGNTN CATTTGGGG GATTTTCCTT GTGGGTTGNN TTAAAANTTG CATATGCTTA 360  
 NGN 363

SEQ ID NO:7458

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08700

SEQUENCE DESCRIPTION:

GATCCGTATT TCCAATAAAA TCCCCTACCT GAATATTCAA GTTAAACATG TCCAGAATAC 60  
 TTACTGATT TATTGTAAAT AGCCACTATT CTGTTGTCTG GAATTAAAC CTGTATAACT 120  
 AATTGTCATC CCTTTATCTT CTTAGTCAAT AAAACCTACA ATCCTCTTTC AAA 173

SEQ ID NO:7459

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08701

SEQUENCE DESCRIPTION:

GATCACCCCC CAACTTGCCC TTCAAGTTCT ACTTCAGTTT GATAAGGCTA TAAATGCAGC 60  
 ACTGGCTCAG AGGGTCAGGA ACAGAGTCAA TTTCAGGGGC TCTCTAAATA CGTACAGATT 120  
 CTGCGATAAT GTGTGGACTT TTGTACTGAA TGATGTTGAA TTCAGAGAGG TGACAGAACT 180  
 TATTAAAGTG GATAAAGTGA AAATTGTAGC CTGTGATGGT AAAAATACTG GCTCCAATAC 240  
 TACAGANTGG ATAGAAAANN TATGACTNNT TTACACCATC TTCCTGTTAT TCATTGCTTT 300  
 TTGAAGAGNA GCATAGANGA GACTTTNTTN TTTTATNCTN GGAATTTTN 349

SEQ ID NO:7460

SEQUENCE LENGTH:395

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08702

SEQUENCE DESCRIPTION:

GATCTGGAGT AAGGAATATT GTCATCACCT GGATTTTGAG AAAGAAAAAT AACTTCTCTG - 60

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CAAGATTTCA TAATTGAGAG AATTCCTGAG TTGATAGCTC TAAAGGCAGA TATGCTGTAT 120  
 TTGCCTACTT TAACCCATTT TTCAACCTGT TTGTTTTTTA ANNGGNTTCA CTAAGGGTTG 180  
 ATATGTACCA TTGTATGGGG CAATTTTAAG TCAGCTAAGG CAATAACCTT ATGCATGAGC 240  
 ATTTCCCAGA CTTTCATGAA GCTGTTGAGG TCCTAGGCAA TTAATGCAGC AGTTGCGATA 300  
 AATAAANGNC NTCTCACCTA AGNNTCCNTT TTCTTCNATA ACCATGGTTC CTGGNCATGN 360  
 TTGGGAGGCT NCTCGGCTTT AGGGNAANGG GGTTN 395

SEQ ID NO:7461

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08703

SEQUENCE DESCRIPTION:

GATCGCCTCC CAACAGCAGA TTTCGACATT ACCTGAGAGT CTTGATTTTA GGCTTGTTTT 60  
 TTGTAAACCC ATGTGTTTGT AGAGATTTTA GCGCTCTTCG GATATCTTCT CACCTATGTT 120  
 CCCTGGCTAA GAAGTCAGAG GTAGCCAATG TTTCCTTAAA TTCATTTTAA AACTTACCAT 180  
 TGGTGATAT GTTCCAGATG GCAGATGCTG TCAATAATCT CACCATTGAT GACCTTTGTG 240  
 TATGTAGTTC TTGCATCCTA TACTGGATAA GCCTGTTTTA ACCTGCTATG ATGGGTGCTT 300  
 TCCATTGCTT CNTAATCTTC ATGGAGGGTT GCCATGCTTT TTGCCNN 347

SEQ ID NO:7462

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08704

SEQUENCE DESCRIPTION:

GATCGGNATG TAATAACAGC ATTAACCTAC AGACCTTGGA GCCTAAGCCA TACAGGAGAT 60  
 GGGAAACCAC GCTATGATAC TTNCTGGAAA CATTTTATAT TTNTAATGAT GGACATTTTN 120  
 CTCGATTGGA GCATGCATAA TANCCTGTGG TACCTGTGTG GAATTTTCANC TTTCCTCATG 180  
 CAAAAGGATT TTNTATCCCC GGCCTACTTG ANGAAGTGGT CAGCTAANGG NNTCCAGGTT 240  
 GTTGGTTGGA CTGTAATACC NTTTGATGAN AAGN 274

SEQ ID NO:7463

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08705

SEQUENCE DESCRIPTION:

GATCAGAAAC TTGCATATGC GTGAAAAAAG GAAGAGCAGC AGAAAATAAA TAAATGACAG 60  
 GAAAGCAAA 69

SEQ ID NO:7464

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08706

SEQUENCE DESCRIPTION:

5 GATCTATAGC AATGTGATT TATTTTAAA AAGAAAAGCA GTGTGTTTC TTTTGTGTT 60  
 GTTTTCTTTT GCTTAAGCAC TTCATCAATT GCTTTATTCT GTATCTGCGA AGTNATCTGC 120  
 AATCTCTNTT GNNCTTTNTA AAATTTGGAT NTGTTATAAA AATTGNCCAN ATTGGAAGGT 180  
 GTTTCAGTTA AAAAAANAN 199

SEQ ID NO:7465

SEQUENCE LENGTH:320

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08707

SEQUENCE DESCRIPTION:

15 GATCACAAAC TTGGAGGGCT GTATGGTTTT TCATTTAAGA AAGTAATTGT CGTGCAATAA 60  
 AGTTATTAAG CTTGTTTAA GAATATTTTT ATTTTGTACA TCAAGTGGAG TTGGAAATAG 120  
 TTGGTTTCAT AATGATATAT TTCAAAAGTA TCTTGAAGTC ATCTGGTTCA TTCACTACC 180  
 20 CAGGGCACAC ATTCCTCCTG TAACATCCCA AGTGGTTATT AAGCAAAACA GATTTATTTT 240  
 ATTTAGAAAA NNTTAGTATG ACTGATTTGC TATTGATTTT GTACTTCTAT AAATNAATGT 300  
 GGATACATGC TATATTCAAA 320

SEQ ID NO:7466

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08708

SEQUENCE DESCRIPTION:

30 GATCACTTAC AGGTGCCCTC TCCCCAACA GCCAGAAAGG GAAAACAGAG CCGAGTTTGG 60  
 CCACTGGGGC CTCCACAGCC CTCTGGAAGA AGGGGCTGAC TGATAGGAAG GCACTCCTCT 120  
 GGTGTTCACT GGCCAGACCC CTGTGGGCTC AGAAGACTAC CTAGACCCCA TGAAGAAAGA 180  
 CTCTAGACAC ATTTTATAA TCAGAAACTT ACAGTTTATT GTGAATAAAC CACTCAACTT 240  
 35 TGAGCAGATG ACATTGCCTC ANTTAACTTT TTCGTTGAAG AAAACAAAG ATATATGGTA 300  
 AATTCATGAA A 311

SEQ ID NO:7467

SEQUENCE LENGTH:434

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08709

SEQUENCE DESCRIPTION:

45 GATCATCAAC AAAGACTTGT TAGAAAGGTC TAGTCTTAGC ACTTGGCAGT TAATCTAGGG 60  
 AAGATGAATT AAATGGGTAG ATAGTGATGC ATACCTGTAT TCACTGATGT ATGTTTAAGG 120  
 GATTTGGGGG GGATACCTCA GTTCATGTGG AAGGGACAGT CTCGGTGTGT CCCATGAATA 180  
 ACCTTGAAC TGCAACAAAT GGTTTGTGCT CAGAAAAAGT CTTTCATGGT GACAGGAAGA 240  
 50 CAGTTTCCTT GGAGCTGGCC ATGAAGGCCT TAGAAGCCAT TTCTGGTGTG TGGTGGGTAG 300  
 CAGGCATAGA GATGATGTNC CGAGGTCCCA GTGAACACCA GTAGCCAAAN GAATTGTACT 360



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ACCTTNTATC CATTANTTNG GGGGAAGGTCC TTCCCTNGGG NAACCAATGN CCTTTTTTGN 420  
TGGGCCAAAA TTTN 434

5 SEQ ID NO:7468  
SEQUENCE LENGTH:414  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS08710  
SEQUENCE DESCRIPTION:  
GATCGAGCTG TGGACTTATA CCTGTGTGCN TGGTTTACAG GTCCAGTGGT TCTTCAGCCC 60  
ATGACAGATG AGAAGGGGCT ATATTGAAGG GCAAAGAGGA ACTGTTGTTT GAATTTTCCT 120  
GAGAGCCTGG CTTAGTGCTG GGCCTTCTCT TAAACCTCAT TACAATNAGG TTAGTACTTT 180  
15 TAGTCCCTGT TTTACAGGGG TTAGAATAGA CTGTTAAGGG GCAACTGAGA AAGAACAGAG 240  
AAGTGACAGC TAGGGGTTGA GAGGGGCCAG AAAAACATGA NTGCAGGCAG ATTTCTGTAA 300  
ATCTGCCACC ACTTATANC CAGATGGTTC CTTTCACAAC CCTGGGTCAA AAAGAGAATA 360  
NTTTGGCCTA TNATGTTANA AGGAANGCAG GNNGGTGGGT TNAANTAAAA NTTN 414

20 SEQ ID NO:7469  
SEQUENCE LENGTH:214  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS08711  
SEQUENCE DESCRIPTION:  
GATCAGTATT TTTAATCAAC ACCTGAGAAC TGTTACACCT TTNATTTTGT CTTNAGGAA 60  
ATCCCTGTCT TTCCATTTT TCATGTAAAT NTTGCACAGT TACTTGTCA TATGTAAATA 120  
30 TTTTACTTTC AGAAATNAAG TTTTAATTG CTATTGTTT ATATAGGATT GAAAGAAAAT 180  
NAACTCCTTT ATTAAAAACA AATTATCTG TAAA 214

SEQ ID NO:7470  
SEQUENCE LENGTH:418  
35 SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08712  
SEQUENCE DESCRIPTION:  
40 GATCCATTTT CTCAGGACTC AGTTAGGTGT GCCCAGACGC ACTGACAAAA TNACGTGACT 60  
TCAGGGAAGC CTGGACACCC GAGGCACCTG GACCAGCTAT GGGTAGTTCT GTGGGTGGAA 120  
CACATTCTGT GTAAGAGCCC CACTGAGGGC TCTGCAGCGG AGTGACAGCA ACCCCAGAGA 180  
TGAGGCACCA GAGAGTGCCA CTGCATGAGA CACCTGTGAC CATTGGAAGT CTGAAATGCG 240  
GGGGGGGAGT TTCATTTTTA AGTGAAGACC AAAAGCCCTT TAAAAATAAT AGTTTTTTAT 300  
45 CATTTTATAG TAATCAGCGG NNTCTCTTTT ACTAATATAC TCATTCTNT TGCATATGAT 360  
TGGNCTTTTG GAGCTACATG CTCCNACAAN NCTGTATCTT AATTGGTTAA CTTGTTAN 418

SEQ ID NO:7471  
50 SEQUENCE LENGTH:422  
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS08713

SEQUENCE DESCRIPTION:

5 GATCTTGGCG TTGTGGTAGA TTGCCTTCCT GTGCTCACCA ATTGTTTACA GGAAGAAAAA 60  
CAATATATCT CACTTGGCTG CTGTGTTGAC TTGTTGCCTC TAGTAAAGTC ACTACTTAAA 120  
AGCAAATTTN AAGAATATGT TATAGTTGGT TTAAGTGGC TTCAAGCAGT CATTAAAAGG 180  
TGGTGGTCAG AACTATCATC CAAAACAGGA ATTATAAATG ATGGAAATAT TCAAATTTTA 240  
10 AAACAACAAT TAAGTGGATT ATGGGTACAG GANAACCATC TTAAGTTGGT TCCAGGATAT 300  
ACTGGTAATN TAGCTANGGG TGTAGNTGCT TNTTTTCTTT CCAGTTCNT TGNGGGATT 360  
CCTCTNCCTG NGGGGCATT TGGTTTTTCA ANACCNTCCC NTGGACCTGT TTTANTTTTC 420  
CN 422

15 SEQ ID NO:7472

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08714

20 SEQUENCE DESCRIPTION:

GATCGCCTTA ACTACTGTAA ACATAGCCTA TTTTGTGCT TAANATACTG AATGGAAAAAC 60  
TCCATTGTGT GTTGCTGGAC TGTTTTGGAA ATATNNNGTT AAATGTGTGT TAATTTGGCT 120  
GTAATGGCAT TTAAAGCAAA CAAACAAACA AAAAAAGCTG TGAAAATGGC CTTGGAGCAT 180  
25 TATCTTTAGT TACTTGAAGA GTTTCTAGTT TTTTAAAAT ACAGTTTATG TTAAAATAAT 240  
TTTANTTAAT TTAGAGANGC CAATCATTGT CTGNGGGGAA ACCGGCCTTN CNTTTTGGGN 300  
TTNCNTTTN GTGGGCCATT GGTGAGGTGA GTGCCTNTN CCCGTTTCNT TNGGTTTCN 359

30 SEQ ID NO:7473

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08715

35 SEQUENCE DESCRIPTION:

GATCTTTAAA GTTATTTTAA GGCACATTG TGACAAACAA CTACTTGATA TTGAAATCTC 60  
CNTCAGCCAT TAGAAGCTAT CAAATAAAGT AGGTGTAAAA ACAA 105

40 SEQ ID NO:7474

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08716

45 SEQUENCE DESCRIPTION:

GATCAAGTAT GCTAATNTTA AGCAAATGTA AAAACTCATA AAACAGGTAA ACAGTGGGGT 60  
GATTCATTT GCCATAATTC ACATAAGACG AATTTAATC TAAA 104

50 SEQ ID NO:7475

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08717

SEQUENCE DESCRIPTION:

GATCCTTGTT TTTAAGTTAC TTTCGATGTG TATACGAACA AAGACCAGGG AGAAACAGAA 60  
CTTTTAAAC TATAGGCTGC TGTNTTGGGG CCAGAAATAA GGTGACAAGT AAAGACTTTT 120  
ATAATACCTA CCTTCAAANT TAGAATCAGC AGCACTGTAC AANTAAAGTG CCTGTGCTTC 180  
ACCTCACACC AAGANTCTTG CCTAACCCTG TCAGAGTGCC TAATATCCTG TGGTGATTAT 240  
GTATAATGAA ACAGTCTTAT TTGTGCTCT TTGGTTTCTT AAAAGGAAAG CTTGTTTTCT 300  
TTCCTTTATC ATTACAGAGG TATGTCTTTG GTTCTTANTN 340

SEQ ID NO:7476

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08718

SEQUENCE DESCRIPTION:

GATCTGTGAA AAAATACAGT ATTGTAAATC CAAGACTCTG ATACTGAATT TAAGTTATTT 60  
CACAGTTGTA GCTACACAGT AAGTAGCTTG GTAGATAGTT ATTGANTGTA TTTATGTAGT 120  
GTATTAAGAA GCTTATATTA CTACAAAAA CTTATTTTAA TATATNTNNN TATNTNNGTN 180  
TTATTTATN 189

SEQ ID NO:7477

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08719

SEQUENCE DESCRIPTION:

GATCTGTGTG ACAAATNAT TTCTTAGCTA TAATCAGCAC ATCACTTAGT TCAAACAAAA 60  
TTCCCCAGCA AATGTTAGAT AGTAGGTATA TCAGTCACCT GGGGAGTTTT CTTCATAATA 120  
TGCATATTCA TCTNGTAATG CATACATAGT TATCATCCTC CTTCTCAACC CATCTCCCTA 180  
ACCCACATG CTTGCCAGTT CTTGAAGGGA TAAAGTGATT GTAATAGTGT TTNACTNCTC 240  
TCTGTTCAAT TTANTGTGAT ATAATTCTAG TTAANNNTA TTTNGGACAG TNGCTTAACC 300  
ATGGTCATAA GAGGATTTGT ACTATAGATT ATCTTCNGGG GN 342

SEQ ID NO:7478

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08720

SEQUENCE DESCRIPTION:

GATCTTTGTC AACCAAAACA TGTATTTTCA ATAAATTGAG ATTCCCAGTT CAAA 54

SEQ ID NO:7479

SEQUENCE LENGTH:79

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08721

SEQUENCE DESCRIPTION:

GATCTGTTTC CCTTCACAT TTTCCCCATT TTGTGAGCAT TTCCTTACTT CCTAACATGA 60  
CAAAATATTT CAAACTAAA 79

SEQ ID NO:7480

SEQUENCE LENGTH:281

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08722

SEQUENCE DESCRIPTION:

GATCCCCCTG GCCTGGAGGC AGCAGCTGTA TAAACTCTAC GAGGCCGACT TTGTTCTCTT 60  
CGGTACCCC AAGCCGAAA ACCTCCTCCG AGACTGAAAG CTTTCGCGTT GCTTTTTCTC 120  
GCGTGCCTGG AACCTGACGC ACGCGCACTC CAGTTTTTTT ATGACCTACG ATTTTGCAAT 180  
CTGGGCTTCT TGTTCACTCC ACTGCCTCTA TCCATTGAGT ACTGTATCGA TATTGTTTTT 240  
TAAGATTAAT ATATTCAGG TATTTAATAC GAAATGTGAA A 281

SEQ ID NO:7481

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08723

SEQUENCE DESCRIPTION:

GATCTGAGTC CAGGCAGTGT TTTTAAGNGA TATGAGTTAG TAGTGAAAAT TGAAAAGGAT 60  
ATTTTACAAC CAAATACAGG TTTNNTGGTG TNNTTTGAAA AATCCAAAGA TTTGGCAACT 120  
CGACCTAGGC TCCGACAAAA CCACAGTTGT TGGGAGCTGA GCCGGAGCCA GAACTCACAA 180  
TTCACCGTGG CCCGGCCACC CATCCCCACC ACTCCCGTGG GCTCCTGACC AAGCACCACG 240  
TGCCATTCAT CATGGCTTGC TTTTAGTGTT TTTGGTGTTT ATCTTAAAGT ACAGCGAAGA 300  
AGAAAGGGAA GTATTTNTTA GACCCN 326

SEQ ID NO:7482

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08724

SEQUENCE DESCRIPTION:

GATCTGGATT TGGTAAAGGT TGACTTAATT GAACTCTCTG AAAAATGCTG TAGTGACTTT 60  
AATTTGCACT CAGAATTAGA GCGCTCATTT TTGTCAGANC CATCATCTCC AGGAAGAACC 120  
AAGACTACTA AAGGATTCAA ACTTGGGAAG CACAAGCATG AGACCTTTAT AACGTCAAGT 180  
GGAAAATCTG ANTACATTGA NCCTGCCAAA AGAGCTCATG TTGTGCCACC ACCAAGAGGA 240  
AGGGGCAGGG GTGGNTTGG ACAGGGTATA CGACCTCATG ATATTTTNGG TCAGNGNAAC 300  
CAGNNCACAN GTNGACCACC ATCTNTGCNT N 331

SEQ ID NO:7483

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08725

SEQUENCE DESCRIPTION:

GATCGGAGTC GCCAGGCAGT ATATCCAGTT AGAACTTCCG GGCTTTTGCA TTAGCTTGTC 60  
TGATGCTCAT GCCCCACTCA GAGAAAAGAC ATCAGCAAAT TAAGAAATTT CTGGGTTTCT 120  
GTGACCCTCA GGTATTTTA AAGCAATTGG AAGAGCATAT GAACACGGGC CAGCTAGCAG 180  
GATTTTCACA TCAAATTAGA AGTCTGATT TGANTAATAT CATCAATAAG AAGGAGTTTG 240  
GGATTTTGGC AAAGACCAA TACTTCAAA TGTGAAGAT GCATGCGATG AATACCAACA 300  
ATATCACTGA GCTAGTGAAC TATTTGGCAA ATGACTTN 338

SEQ ID NO:7484

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08726

SEQUENCE DESCRIPTION:

GATCCGCCCT CCTTAGCCTC CCAATCCTCT CTTAAAAAG TGATAGCTCA GAAATATTTG 60  
TAAAGCAAG GTTTTATTT CATTTTGGCT CTGTCATTT CAGAGGCAA GAAGTTGGCC 120  
TGTAAGTAG AGTGCTAGAG CTCTTACGCC CCTCCCCTT TCCCAACTT CCTACTTCT 180  
AGCCCTTTTA TCAACTCCTA GAATAGTTAA AGAGAGACAC ATCTAGATGG GATGAAAGGT 240  
GCCCTAAGCA GGAGAACCTG ANCAAAAGGC TAGAGGCATG GGCCAGGTAA AATTGGGGC 300  
CTAGAGTGAA GNCTGTGCTG TCGTTAAGNG CTTTCGAN 338

SEQ ID NO:7485

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08727

SEQUENCE DESCRIPTION:

GATCACAGTG ACAAAGAAGA TGAACAGCCT CAAGTGGTGG TTTTAAAAA GGGAGACCTG 60  
TCAGTTGAAG AAGTCATGAA AATTAAAGCA GAAATAAAG CTGCCAAAGC AGATGAAGAA 120  
CCAACTCCAG CCGATGGAAG ANTCATATAT CGAAAACAG TCAAGCATCC CTCAGATGAA 180  
AANTATTCAG GTTTAACAGC AAGCTCAAAA AAGAAGAAGC CAAATGAAGA TGAAGTAAAT 240  
CAGGACTCGG TCAAAAAGAN CTCACAAAAN CAANTTAANA TTAGTAGCCT CCTTCTTTT 300  
GACAACGAGG ATGAAAATGA GTAAGTGTA TTTTNTTN 338

SEQ ID NO:7486

SEQUENCE LENGTH:302

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08728

SEQUENCE DESCRIPTION:

GATCTTAATT CATATCTTGA AGATAAAGTC TACCTTACAG GGTATAACTT TACATTAGCA 60  
 GATATACTAT TGTACTATGG ACTTCATCGC TTTATAGTGA GTATTGTAT AGTTACTGGC 120  
 TTTTTTCTG TAGTGTGAG AATGATTTT AAACTTTGT CTTGAATTA AATCAGATT 180  
 GCATTTTGG CTTATCAAAT AAAATGAAA GGAATTCCT TATACAAGGT GCCTTTTGT 240  
 ACAAACCTGC ACGTTGTGAC ATGTACCCTA AACTTAAAG TATAATANTA ATAANNTTNA 300  
 AA 302

SEQ ID NO:7487  
 SEQUENCE LENGTH:334  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08729

SEQUENCE DESCRIPTION:  
 GATCAAAAGT GAATAATGTA TGAATGAGAG CTGTAAGAAG GATTTTNATT TTGTTATAAT 60  
 TTAGTTACCA TTTTCAGTGT TATTTCAAAG GTTCTTTGAA GAATTTTGGG GCAGGGCATC 120  
 AGATTAGAGT TTAAAATTT GAGTATTTTG GATATCAGTG TTCCTCATGA AGATATACAT 180  
 GGATATNCAA TTTTGATGGC TTCCAGATTT GTAAGATTTT ATGTTGTATA TACCATTCTA 240  
 TTAAGAAACA TGTCCACTGT GCTTTCAAAC ATAGATAAAG CATGATAAAG ATTATNATTT 300  
 AAGATATACT TGTATTTATA CCTCAGATAT TCTN 334

SEQ ID NO:7488  
 SEQUENCE LENGTH:337  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08730

SEQUENCE DESCRIPTION:  
 GATCAGCTGG ATACTCNTGT NACCAGAATT CCAAAGGTTT TGATAGAATC AAAGATGGAT 60  
 ACAAAGTGAA CTCACACATA GCTAAGCTGC AAGAGTTATG GAAAACTCCC CAAAATCAAA 120  
 CAATCCACCT CTCTAANTCA NTGATGGAGG CGTCCTTTT CAAGCATCCA GACCTCACCA 180  
 CAGGCCAGAN GCGTTACCNG TGCAGCATTG CTAAANTCTA TAATGCAAAC TATCTGANGA 240  
 TGTTAATGNA GNGGCAGTAC ATGCACGTNC TTCAGCACAG CTCACAAAAG CCAGGTGTCC 300  
 TCACTCATCA CAGNNGCCG CTTNGCTCCC GTTTATN 337

SEQ ID NO:7489  
 SEQUENCE LENGTH:292  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08731

SEQUENCE DESCRIPTION:  
 GATCATTGAG AACACTGNAC ACAGCAGCTT CAGGCAAAGG GAAAAGAACT AAATGAATTC 60  
 CGGGAAAAGC ACAACATTCTG TCTCATGGGA GAAGATGAGA AGCCAGCAGC CAAGGAAAAC 120  
 TCAGAAGGGG CTGGGGCTAA GGCCAGCTCA GCTGGAGTGT TGGTCTCCTA GGGACCAAGG 180  
 CCTTTGCATT TTTTCTACC CTGACTCCCA CTCTAATTT CTCTTTATTG TTATTATTAT 240  
 TATTTTCTCT GCTATTGTAA TATTTTTTTG TTAATTAAAT GTTTTGGTTA AA 292

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SEQ ID NO:7490

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08732

SEQUENCE DESCRIPTION:

GATCAACTGC AAACAGGCAC GAAGGAACTT TTTTGGGTGA TGAAAAATAA AACTTTGGAT 60  
GTCGAACATA TTTTGAACT AGATTGCAAT NATAGTTGCA TAACTNTATA CATTTATTAA 120  
AATCGTGGA CACTTACAAA 140

SEQ ID NO:7491

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08733

SEQUENCE DESCRIPTION:

GATCCGGTCT CCCCCGCCCC CCGGCTGCAG GGTGGATAAA GAGGAAGATG TGAAGAGGAG 60  
GCAGACAAAA GCAAAGGAC ATCCTGTCAG TAGGAAACGG CCGAATTACA ATTCAGATGT 120  
GCAATGTTTG CATAAGTAAA CTGACACGGG ACTATTATAT GCAGAANTCC ACGTGCAAAA 180  
NTTTTCAGAC ACACCTTTGT ACCTCTNCCT AATCCTGCCC TGGTAAAATG GCGGTTATCA 240  
GTGCAAGTTT GAGGATACAT ACAGCTGGAA ANTGGNCATC ACCAAACTGG ACTCCAGAAA 300  
GTNCTGTCTA GGATTTTATT AGACTGCTTT TTTNCAN 337

SEQ ID NO:7492

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08734

SEQUENCE DESCRIPTION:

GATCTATTTC TCAGTAATNA GTGTGTGCCT CATGCCTGTT TCAATATTGG GTTTTGGAGA 60  
CANTATTGTA CCAGGCCTGT TGATTGCATA CTGTAGAAGA TTTGATGTTT AGACTGGTTC 120  
TCCTTACATA TACTATGTTT CGTCTACAGT TGCCTATGCT ATTGGCATGA TACTTACATT 180  
TNTNGTCCTG GTGCTGATGA AAAAGGGGCA ACCTGCTCTC CTCTATTTAG TACCTTGCAC 240  
ACTTATTACT GCCTCANTTG TTGCCTGGAG ACGTAAGGAA ATGNAAAAGT TCTGGAAAGG 300  
TAACAGCTAT CAGATGATGG ACCATTGGN TTGTCAN 337

SEQ ID NO:7493

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08735

SEQUENCE DESCRIPTION:

GATCGGCCTG CGAAAGGATA CTGTGAAATN ACTAATTAAC TAATAAACCT GTCTCAAGTT 60  
GAGGATTGA AGAAA 75

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SEQ ID NO:7494  
SEQUENCE LENGTH:343  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08736

SEQUENCE DESCRIPTION:

GATCTGGGGT ACTTGGCAGG GCTTCCCTCA GACAATACCT TAGAGAGTCA CAACCATTCC 60  
AGGGTCTGGT CTACCTCACA TCCTCATTCA TTGTTGGATG TGCTTAGCAT AGCCAGAGGT 120  
GTCTTCTCTT TGACAGACTT GCTATCTGAA AAATAAACCA GGACACCAAT TTTTTCAGCAT 180  
ATAATAGAGG ACATCCCTTC CCAGCTATAG GAATGCTTGG TATCCTTCCA AGAACTCCTC 240  
CTTTAGAGGA GCCTCACAGA AGTTGCTGGG TAAACATGGG CTCAAACCAA GGAAAGTCAG 300  
GTAACCTGGG TGGNGGTTAT CCCACCACCA ATGGCAGGGG GTN 343

SEQ ID NO:7495  
SEQUENCE LENGTH:95  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08737

SEQUENCE DESCRIPTION:

GATCAATATT GTAAAGAATT TATTCTGATA AATNAGAAAC TGGATATAAT GTCAAAATAG 60  
CTATTTTCTC AATAAAAATC TCAAATCTCC TGAAA 95

SEQ ID NO:7496  
SEQUENCE LENGTH:143  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08738

SEQUENCE DESCRIPTION:

GATCCTCCCT CCTTGGCCCC CCAGTGTTGG GATTACAGGC ATGAGCCACC GTGCTTGGCC 60  
TGGAATNAAT TTTTATTTGA AGTTATTCTG TATCTCCAGT GTTGGCATAT GCTAGACATT 120  
CAATGAATAT TTGTTGATTT AAA 143

SEQ ID NO:7497  
SEQUENCE LENGTH:342  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08739

SEQUENCE DESCRIPTION:

GATCAACAAA ATGTGGTATA TTCATACAGT GGAATATTAT TCAGCCTCTA AAAGGAAGAT 60  
ACGCTGACAT GTGCTGCAAC ATGGATGANT CTTGAGGACA TGATGCTAAG TGAAGTAAGC 120  
CAGTCACTGG AAGACAAATA CTCTATGCTT CCNTTTATGT GAAGTATCTA GAGCAGTCAA 180  
ATGCATAGAA ACAAGTAGAA TGGTAGTTGC CAAGGACTGG GGGAGGAGGA AATGAGGAGT 240  
TGTTTAATGG GTATAGTGTT TCATTTTTCG NAGATAAAAA GTCCTGTGGN TTGGTTGCAC 300  
AGTTAAGTTA TGTGANTGCT GTATGCCCAA CTCANCTGTT NN 342



SEQ ID NO:7498

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08740

SEQUENCE DESCRIPTION:

GATCCAGTCG GCCTGGAGAT TCTACGCCAC CAACCTCTCG CGCACAGACC TGCACTCCAC 60  
GTGGCAGTAC TACGAGCGAA CGGTCACCGT GCCCATGTAC AGGTACCGCC GCCGGGCACC 120  
TGCCACCAAG CAACTGTTTC ATTTTATT TTCCATTGT TCTTAAACCC CACTTTTGT 180  
TGTTCAATTAT TTTGATTGAT TTTNNNTTCT TTAAATGTA TTTTCACAA AGGAAA 236

SEQ ID NO:7499

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08741

SEQUENCE DESCRIPTION:

GATCCTAACC CTTTAGTATG CTGGAATTCT ACTCTTCACT TACTGCATTG ACTGTTGTTG 60  
ATTAGTTATN ATTGCAAAGC ACTGTCACCG GCCTCAGGGA GTTTATGTGT AATAGAATTA 120  
AAAATAATAG CTGTGTATAA CACTTAGCTC AAGCCACAAA 160

SEQ ID NO:7500

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08742

SEQUENCE DESCRIPTION:

GATCTTATTG TGGAGTTAAA CAAAGCACCC TTAAAGTAGC AAGCGAGCAA AATAAAAGCA 60  
AGGAAAATCA GTTGGAACAT AACTTATGTA TTTTATAGGA TTAAGAGTAA TTAACTGAG 120  
TCAATTCAAT ATGTTTTTAA AGGTGTGATT CTAAATNCT TTATGATTGT TTAGATTTCT 180  
ATATCTTGGT AACATGAATA CACTTAAA 210

SEQ ID NO:7501

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08743

SEQUENCE DESCRIPTION:

GATCAGCATT TGTATTTNAG TCCATTAATG GGAAAAATAG CTGATATTGT NCATAGGAAC 60  
TTGGAAACCA CACAGGACTT AAGTCCCTTG TCTGTNTTGA TGGTCAACAT ATCTCCTTTA 120  
ATATCACGAC ATTTTCAACA ACANCTGGTG AACAAAACAG ANCTNCTTTT TGACACCATA 180  
GATTCTCCTG AGGTCAACGT TGCAAAANGC ATAGCAAAGT TNCTCCGAAA TGTTAGATAT 240  
CGTTATCAAC CACTATTAGA CAGATGTAAT ACCGTATTTT TTCAGTAATG TGNCCACCT 300  
TGATTTTGGN TTCCATCAGT ANAGNGACTT AGTGTATACA NNNACNAAAN N 351

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SEQ ID NO:7502

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08744

SEQUENCE DESCRIPTION:

GATCGCACCA CTNCACTCCA GCCTAGGTGA CAGAGGGGAT GACAGAGGGT GCTCTGCGNN 60  
CAGGGAAGGC GGGGTGGTTG GGGGGTAGAG AATGTTGCNC TNATAACCAC AGCTGTGGTT 120  
ATTTNTGGC AGGTACAGGT NAGGTTCCCT CTCCTTTCCA CCAGATGGCA CTGGAGAAAA 180  
GGGATTNAN TTAAN 195

SEQ ID NO:7503

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08745

SEQUENCE DESCRIPTION:

GATCAGAGCA GAAATAAGTG AAATAGAGAC TAAAAAATAG AAAACATCAA TGAAACAAAG 60  
AATTATTTT TAAAAAGATA AACTAAATTG ACAAACCTTT AGCTAGACAA AGAAAAAAGA 120  
GATAAGACAC AGATAANTAA NTTCAGAGAT TAANAAGAAG CCATTATACC TGATACCACA 180  
GAANTACAGA GANTCATAAG AGACANTTAT GTTGTGCACA TGTACCCTAG ANCTTAAAGT 240  
ATAATANNCN NTANTTN 257

SEQ ID NO:7504

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08746

SEQUENCE DESCRIPTION:

GATCTTACAG AGAAAGACTA TGAAATACTT TTCAAATCTA TTAATGGAAT CCTTTNCCCT 60  
GGAGGAAGTG TTGACCTCAN ACGCTCAGAT TATGCTAAAG TGGCCAAAAT ATTTNATAAC 120  
TTGTCCATAC AGAGTTTTGA TGATGGAGAC TATTNCCTG TGTGGGGCAC ATGCCTTGGA 180  
TTTGAAGAGC TTTCACTGCT GATTAGTGGA GAGTGCTTAT NAATTGCCAC AGATACTGTT 240  
GACGTGGCAA TGCCGCTGAN CTTCACTGGA GGTcanttgc ACAGCAGAAT GTNCCAGANT 300  
TTCCCTACTG AGTTGTTGCT GTCATTAN 328

SEQ ID NO:7505

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08747

SEQUENCE DESCRIPTION:

GATCAATTTG AAGTCCCTGT TTGGGAATAA GGCACCTATC AGCATGAAGA ATTTTTTCTC 60  
ATTCTGTGCC ATTTTAAAAA TAGAATACAT TTGTATATTA AA 102

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SEQ ID NO:7506  
SEQUENCE LENGTH:343  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08748  
SEQUENCE DESCRIPTION:  
GATCACCTTC GNACGACTAC ATCGCCTGCT GCGTCAAACCT GAGGGCTCTT ACAGNCAGTT 60  
TTCGAAGNCG GGGTACTGCT CAGCAAGGTG TTGTGAATTT CCCATATGAT GATTTCATTTC 120  
AATGTGTCAT GAGTGTTTAA ATCAAGAGGA AGCTGCATGA ATGTAATCAA CATTCCAACCT 180  
GGAGCTCTCC TTGCTTGTCT CTCTTTGCCT TCGGTAATAT GTATAAACTT ACATCACGAC 240  
TTTCTCTTAA CAGCTGTTGT AAAGTTTATT ACTTTATGTA CAACTGAAGT TTTGTTTTAG 300  
TTTTGATAAT AAAATTCTTT GGAACTTTAA AAAAAAAAAA NGN 343

SEQ ID NO:7507  
SEQUENCE LENGTH:342  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08749  
SEQUENCE DESCRIPTION:  
GATCCAAGTG CTTNTTTGGT ACCAAGAGAC CCGGNTCTNT GCCAGCATAA ACCACTCACA 60  
CCCCAGGGGG ATGAGCTCTC TNAGCCCAGG ATTCTGGCAA GGGAGGTGAA GAAAGTGGAT 120  
GCGCAGAGTT CGGCTGGGGA AGAGGACGTG CTCCTGAGCA AAAGCCCATC CTCACTCAGC 180  
GCTAACATCA TCAGCAGCCC GAAAGGTTCT CCTTCTTCAT CAAGAAAAAG TGGANCCNGC 240  
TGTCCTTCCA GCAAAAACAG CAGCCCTNAA TAGCAGNCCN CGGTCTTTGG GGAGGNGCAA 300  
AGGNAGGCTC CGGTTGCCCC AGATTGGCAG CANNATTATN AN 342

SEQ ID NO:7508  
SEQUENCE LENGTH:369  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08750  
SEQUENCE DESCRIPTION:  
GATCAAGCAA TTAATCTTCT GTAGAACCAA AATTNACTGT AATAACTTGG AGCAGTACTT 60  
TATACAACAA GGAGGAGGAC CTGATAAAAA AGGACACCAG TNCTCATGTG TTTGTNTTCA 120  
TGGTGACAGA AAGCCTCATG AGAGAAAAGCA AAAGTTGGAA AGATTTAAGA NAGGNGATGT 180  
AAGATTCTNG ATTTGCACAG ATGTAGCTGC TAGAGGNATT GATATCCACG GTGTTCTCTTA 240  
TGTNATANNT GTCACCTCTGN CCGATGAAAA GCAAAACTNC GTACATCGAA TTGGCAGAGT 300  
AGGGTGGAGC TGANGGATGG GTCTGGCAAT TNCCCTNGTG GCACCGAAAN NGGACAGGGT 360  
TTNGTACCN 369

SEQ ID NO:7509  
SEQUENCE LENGTH:335  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08751

## SEQUENCE DESCRIPTION:

GATCTGGCCA GAGGGGTGTT GGAGCCCAGC CCACCCACAT ACCAGTCAAG CTCTTAGGGG 60  
 AGCAGAAGAA AAGCAGGAAG AATTAAATG TTAAATTTT TTTNAAATT GACTTTNCTA 120  
 GTTATTAAAA GTTGCTTGTT TCAGCAGTGN TATTGTATAA NGACCATCTT GTAAGNTACT 180  
 CCTGACATCT TGCTTTAGCA CATGTACAGT ACAGTTNCTN TGATAATGTG TTTGCCCTAA 240  
 CTNCCCTGGC TTCNCCTTCA GCCCATCCNC TCTCCTCTAG NGCAGTTGGG TTGGAGGCTC 300  
 NTTGAGGCAA GCNGCANCAT TGGNGGGGGT GCAGN 335

SEQ ID NO:7510

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08752

## SEQUENCE DESCRIPTION:

GATCCGACAC AGAGAACAGG AGGAACTNAG GCGACAGCAA GAGGGCTTTA AGCCAAACTA 60  
 CATGGAAAAT AGAGAACAGG AAATNAGAAT GGGTGATATG GGTCCCCGTG GAGCAATAAA 120  
 CATGGGAGAT GCGTTTAGCC CAGNCCCTGC TGGTAACCAA GGTCTCCTC CAATGATGGG 180  
 TATGANTATG AACANCAGNG CAACTNTACC TGGTCCACCA ATGGGTACTG GTNCTGCCAT 240  
 GGGACCAGNA AGNGGCCGCA ANTNTNGGGN 270

SEQ ID NO:7511

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08753

## SEQUENCE DESCRIPTION:

GATCCCAGGA GAATCAGAAA CTCCAACATT TTGGAATCTT CAAGGGCACA TACTGAGAAA 60  
 AAAAAATAAAA TTGTTTATGA GCAAA 85

SEQ ID NO:7512

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08754

## SEQUENCE DESCRIPTION:

GATCAAACATA TACGCTGTCT ACAAGAGACA CTTTAGATTT AAAGACACAA ATAGGTTGAA 60  
 AGTAAA 66

SEQ ID NO:7513

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08755

## SEQUENCE DESCRIPTION:

GATCTTTTGT ACTGAGGTTT TTAACACTTT ACTTGGGTTT ACCAAGCCTC AACTGGACAG 60

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5 ACCATAAACA GTCCACAGGC ACCGTTCTTG CCAGGCCCCA ACCCACAGGG AGTCTNTCCG 120  
 CAGAGCCTTC TTGGTGTGTC CCTAACTTGC CAGTGGCCTT TGCTCAGAGC CTCCTCCTGT 180  
 GACATGTGAA CAATGAAGAG GCCTGCGCCT CCTGCCTTGC CGCCTGCAAA GCAAAGAAAC 240  
 TGCCTTTNAT TTTTAACTT TAAAAAGTAG CCAGATTAGT ANCANGACTG GCTGGCTTGA 300  
 TGAGCAAAGC CTTTGCTCTC ACGGNAGGAG GGTAGGGTTT NGGNTGTACA ATGGTAACTT 360  
 GCNNTGGGNA CCTTAAAAAG GGAGGTGNAN 390

10 SEQ ID NO:7514  
 SEQUENCE LENGTH:212  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08756  
 15 SEQUENCE DESCRIPTION:  
 GATCACCTGA GGTGAGAGT TTGAGACCAA CTGACCAAC ATGGAGAAAC CCCGTCACTA 60  
 CTAAAAATAC AAAATTAGCT GGGCGTGGTG GCACATGCCT GTAATCCCAC CTACTTGTGA 120  
 GGCTGAGGCA GGAGAATCAC TCGAACTCAG GAGGCGGAGG TTGNAGTGAG CCACTGCACT 180  
 20 GCCTGGGCAA CAGAGCGAGA CTCCATTTC A 212

25 SEQ ID NO:7515  
 SEQUENCE LENGTH:136  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08757  
 SEQUENCE DESCRIPTION:  
 GATCCACCCG NCTTNGCCC CCCAAAGTGC TGGGATTACA GGTGTGAGCC ACTGTGCCCC 60  
 30 GCCGAGTTAA ATATATTTCT AACATAGTAA AAAAAAAG GTANGTTNCA TTAAATAAAT 120  
 CCNGGAAGTN CAAATN 136

35 SEQ ID NO:7516  
 SEQUENCE LENGTH:160  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08758  
 SEQUENCE DESCRIPTION:  
 40 GATCATGAAG ATGGACAGAA CAGACACTGT GGCAATAAGA TACCAAATTG TAAACAGGAC 60  
 CTAAGGCCAT GCCAAGCAAG GGTAAAGTCA TGTAAGAGCC GCCTTCATGC CCCGCCTCCC 120  
 CTGCCCCCAA CTTATGAATA AACTATGTTC TAACTGCAAA 160

45 SEQ ID NO:7517  
 SEQUENCE LENGTH:355  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08759  
 50 SEQUENCE DESCRIPTION:  
 GATCTGGAAC TTGAAGATGC CATTATACA GCCATCTTAA CCCTAAAGGA AAGCTTTGAA 60

55

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5 GGGCAAATGA CAGAGGATAA CATAGAAGTT GGAATCTGCA ATGAAGCTGG ATTAGGAGG 120  
CTTACTCCAA CTGAAGTTAA GGATTACTTG GCTGCCATAG CATAACAATG AAGTGACTGA 180  
AAAAATCCAGA ATTCAGATA ATCTATCTAC TTAANCAATG TTAAGTATG TTTGTTTTG 240  
CAGACTTTTT GCATACTTAT TTCTACATGG TTAAATCGA CTGTTTTTAA AAATGNCACT 300  
TATANNTCCN AATAANCTGT TAANCCNGGN ANANGGNNTT GTNTTNGTGN GGNTN 355

SEQ ID NO:7518

SEQUENCE LENGTH:77

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08760

SEQUENCE DESCRIPTION:

15 GATCTTCATT TTCCTGTTCT GTATTCTGCT ATGAAGTTCT CTGTTTTTCA AATAAAATTT 60  
ATGTGTTAAA TAACAAA 77

SEQ ID NO:7519

SEQUENCE LENGTH:20

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08761

SEQUENCE DESCRIPTION:

25 GATCATCTTG GAACTGCAAA 20

SEQ ID NO:7520

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08762

SEQUENCE DESCRIPTION:

30 GATCGGAGGC TGCAGTGTGA CAGTGCCAGC CAATGTGCAG AGGTGGATGA GGTCTTGTTA 60  
35 AAACCTGGCT CTTTTAACA CGGCCCTCAA GCTCCTTAAG TNAATTGCCG TAACTAATTT 120  
TAAAGGGTTT AGATTTTAAG AATGGTGCTC TTTCATGCCT ATNATCAGTA AGGGGACTTG 180  
TATTAGAGTC AGAGTCTTTT TATTTAGGCC AGTTGTCAAG TGTCATAAAA AGCATCATGT 240  
AATTAAA 247

40 SEQ ID NO:7521

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08763

SEQUENCE DESCRIPTION:

45 GATCTTAATA TTGACTAGTT TCACATCCAG GTTCTAAGA AATGATAAGA TACTTCACTT 60  
TTCCAGAGTG AAATGTAGGA GGGAGCACAT TCTAAGTACA GCTAAAAATT TAGCTCACTG 120  
50 TAACACAGTT TCACTCTCTG AATAAATAAA GCAAAAAACA CAAA 164

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SEQ ID NO:7522

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08764

SEQUENCE DESCRIPTION:

GATCTGCCTG CGAAGCTCCC CACAACACTG TCCCTGGAGA CCACCCATGT GGCAGACACT 60  
CAAAATCTGT TGTATTTGCT AAATAAATTA ATATGGACAA GTTACCCAAA 110

SEQ ID NO:7523

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08765

SEQUENCE DESCRIPTION:

GATCAAATTG TTCATGCCTT GGGATTTTTT CTTCTATAAT TTGGATATCT TTNTCCATTG 60  
CTCATTCTTT TATTGAAAGTT GCTTTCTTAA AAATTGATTT AACTTTGTCC TTGGTATCTT 120  
TAGTTCAGTC CAGAAATNAT TAATTGTGAT GTGATTAAAT TCATTTTTTG GTCTGGTGAA 180  
A 181

SEQ ID NO:7524

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08766

SEQUENCE DESCRIPTION:

GATCTGAATG GTTTTAATAA GGGGCTTTCC CCCTNCTTCG CTCTGCACTT CTCCTTGCTG 60  
CCATGCGANG AAGGATGTGT TTGCTTCCCC TTCTGCCATG ATTGTAAGTT TCCTGAGGCC 120  
TCCCCAGCCA TGTAAACTT TGAGTTAATT AAACCTCTTT CCTTTATAAA TTAAA 175

SEQ ID NO:7525

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08768

SEQUENCE DESCRIPTION:

GATCTGAAAA ATNCTTTTGT TCCTCATTGT TGCAGTTTCA ATTGTAATCC ATTGCATCTN 60  
ATTTTCTTGG GTGTTGGCAC TGTAATATAT TAAAAAATAA TTCAGTGCTC AGTATTGTAA 120  
CAACTGTCCC TACTGAATAT TCCTTTTCAT AAATACTTGC TACCACAGGG AAATTAAGTT 180  
TTCATATAGA ATAAGTAGTT TCAGTAGTAA CCATTGAAGA NTTAANCNTG TGGTTCANGG 240  
CAGATATTTT TCTGGAAAGT TTTCTCTATT GTANAATTTG TNGTATATGG CTATGCTGAC 300  
TATCNTGGAT NCTGTCATGG GACATGCATT ACCACANNTN CNNGCCCTT TCTGTGGTNN 360  
NN 362

SEQ ID NO:7526

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08769

SEQUENCE DESCRIPTION:

GATCCCATGG ACATTTGGGG AAAGGGCTCC TTGGGCTGCT GGTGAACTTC TGTGGCCACC 60  
ACCTCCTGCT CCTGACCTCC CTGGGAGGGT GCTATCAGTT CTGTCCTGGC CCTTTCAGTT 120  
TTATAAGTTG GTTCCAGCC CCCAGTGTCC TGA CTCTGT NTGCCACATG AGGAGGGAGG 180  
CCCTGCCTGT GTGGGAGGGT GGTTACTGTG GGTGGAATAG TGGAGGCCTT CAACTGATTA 240  
GACAAGGCC GNCACATCT TGGAGGGCAT CTGCCTTACT GATTAAAATG TCAATGTGAA 300  
TCTAAA 306

SEQ ID NO:7527

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08770

SEQUENCE DESCRIPTION:

GATCTTTTAG TTATCAAAC GTTAAATACA TTTAACTTT CAAATTTTAT GAATAAAGGA 60  
GATGAATCCT GTTAAA 76

SEQ ID NO:7528

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08771

SEQUENCE DESCRIPTION:

GATCTGAAGT CTGATTGTGT GTACGTTTCG CCGTGCGTTA GTCCCTGCCA CGATTAAAGA 60  
CTTAGACCGN CAAA 74

SEQ ID NO:7529

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08772

SEQUENCE DESCRIPTION:

GATCGCGCCA CTGCACTCCA GTCTGGTGAT AGAGCAAGAC TCCATCTCAA AAATAAAAAA 60  
TAAAATGTTG GNTGTGGGGA GCCAGGCCTC TCACAACTGA AA 102

SEQ ID NO:7530

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08773

SEQUENCE DESCRIPTION:



EP 0 679 716 A1

GATCGAATCC AGGCCCTGGG GCTTCANTTG CCAGACCCAC CATTAGAGAG TGAAGATGAA 60  
 GATGAGGAGG GAGCTACAGC GTTGAACAAC CACAGCTCTA TTCCCATGGA CCCAGAACAT 120  
 GTAGAGCTGG TGAAGAGGAC AATGGCTGGN GTAAGCCTGC CTGCGCCAGG GGTTCCTGCC 180  
 TGGGCTCGGG AGATATCGGA TGCCAGTGG GAAGATGTGG TACAGAAAGC CCTCCAAGCC 240  
 CGGCAGGCAT CCCCTGCCTG GGAGTGACCA CAGTGAGAGC TGCCTTATAT TCCTACATT 300  
 CAGGCCAGAA CN 312

SEQ ID NO:7531  
 SEQUENCE LENGTH:186  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08774

SEQUENCE DESCRIPTION:  
 GATCTGGACT GAGGACCTG CTACTCCCCA AGCCAGAGCC CATCAGCCAG GCCTGCTGTG 60  
 AGCCACCTGC CTGTGGAGTG CTGAGCTCAA CCAAAGGCTG GCAAGCTCTG GGCCTCATT 120  
 AAGGGATTCT GATGAGCCGA TGGGCCCTGG AGGCAGCCCA TTAAAGCATC TGGCTCGTTT 180  
 TTGAAA 186

SEQ ID NO:7532  
 SEQUENCE LENGTH:390  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08775

SEQUENCE DESCRIPTION:  
 GATCACATTG CCATTCCTCC CCTCCAGAGG TAACAATTAT CCACAATTG ATGTTTATCA 60  
 TTCCTGTGTT GTTGTACTTT CACTGTGTAT AACCTAANNC NTCTACTNTT TAGTACTGTT 120  
 TTATATATTT TNAAGCCTCA TACTTGCTCA TTCTACAGCT TTTTCACTC ATTATTGTAT 180  
 AATTATATCT GANGCNCTCG TTCATTAATT TTAGTCCNGT GTAGCAGAAT TCAATTACGG 240  
 GAACTACCAT AATTATCTG TNCTCCAGTT GAAGGCATGA NGTTGTTGCC AGTTTCTGTA 300  
 TTATAACCAC TGTAGTGGGA CCATTCTTCT GCNTTGGGCT CACTGCGGGT TACCNAAGNC 360  
 GGTNCCNCAG GATAANCCCC ATTTGGGNTN 390

SEQ ID NO:7533  
 SEQUENCE LENGTH:378  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08777

SEQUENCE DESCRIPTION:  
 GATCTAGCAT GTGGATTTTA AAAGATTGCT CCTCATTAAC AAGAATAACA TTAAAGGAG 60  
 ATTGTTTCAA AATATTTTNN CAAATTGAGA TAAGGACAGA AAGATTGAGA AACATTGTAT 120  
 ATTTNNCAAA ANCAAGATGT TTGTAGCTGT TTCAGAGAGA GTACGGTATA TTTTGGTAA 180  
 TTTTNTCCAC TAGCAAATCT NGATTTNGTT TGATAGTGTG TGGAATTTNC TTTTGAGGGA 240  
 TAAGACCATG GGANANTTGT GGTAAAGACT GTTTGTNCCC TTCATGANTN CTTCTGAAGT 300  
 TGCCNTCAGT TTTNCTAATC TCCTGTGAAA TGCCTAGGTT TTGCGCCTGT CCCACTTTTT 360  
 NTTTGTGGGN CTTATNTN 378

EP 0 679 716 A1

SEQ ID NO:7534

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08778

SEQUENCE DESCRIPTION:

GATCATTGTA GTGAAAAAA GGTACCTGTN CAAGCAAGCT CCTGGACACC ACAAGAAGGA 60  
GGAATTATTT TAAAAGCTGT ACTCTTAAAT TGTNAGTATC TTTAAAATCA GTTGTGAACA 120  
ATGAAGGATT TGAAAGAGCA TTGACTTGC CACTTAAAAG TATTCTAAA ATAAA 175

SEQ ID NO:7535

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08779

SEQUENCE DESCRIPTION:

GATCAAGGTG AATTTTTGT ATCACTGCCT GTGGAAATCT ATCCTCATCA GTNATTGCAT 60  
TTTTCCCTGC CTATACCTGT GCTCCTTTT NTNACTGTGT TTCAGTCAC TTCCTTTCTG 120  
TNAAGGTTG CTTAGCTTTT NTTTTNAANA TTTGTTGTN 159

SEQ ID NO:7536

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08780

SEQUENCE DESCRIPTION:

GATCCAAACC CACAGTNTTG TCCTGGAGGC AGCAGGGGTG AAGGTGGAGG GTCCAGGGCC 60  
ATGAGGAGCC CCCTTGCCAT CAGAGCCTGG CCTAACACC CTCTTCTCTA CTTACACACA 120  
CATGCATTTT ATAATAGCTC TGACCCAACC TGGCCACTCT GCAGAGACTG GGACAGACAG 180  
GTGCAGGCAA TGGGCCCTCC CACACCCAGT CACCTACAAG GAATTTTCAA ATCCACTTTT 240  
AAAACAGAAA CCGGTAAATG CGCCGTATTG TATATTTTAT TTAAATAAAA AAAATTCCAG 300  
CAAA 304

SEQ ID NO:7537

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08781

SEQUENCE DESCRIPTION:

GATCCACCTT TCCTGGGCCT CCCAAAGTGC CGGGTATTAC AGTCATAAGC CACCACACCC 60  
GGCCTAACAT GCATTTTTTT AATTCAATAA ATATTTATTG AGCACCTAAA 110

SEQ ID NO:7538

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08782

SEQUENCE DESCRIPTION:

GATCCCTCC CCTCTGCTT TTCTGTATTT TTTAAAAATT ATTTTGTTTT TAATTCACAA 60  
ATATTGTATA TGTTATATGG GGTAGAATGT GATGTTGATA TATGTTTAAA ATGTGGAATG 120  
ATTAAATCAG GCTAATTTAC TTTTTTNCC NAAAAGGAAA 160

SEQ ID NO:7539

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08783

SEQUENCE DESCRIPTION:

GATCCACCCA GTTGCTCAAG TAAAAACCT GAGAGACACC TTACGCCATC TGGGAACCTG 60  
TTAGAAATTC TTAAACCTCA TTCTATACCT GCTAAATCAG AAAATGTAGG GATTAAGTCT 120  
GATTATTTGT GTTTTCGCAA GTCATCCNGG TGATTCTGAT GCATGGAAAG TTTGAGAACC 180  
ACTGGTTTAG GTTATTAATA GTTCTTGCTC CCCTATAAA 219

SEQ ID NO:7540

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08785

SEQUENCE DESCRIPTION:

GATCAGAGAA GACTTTAAAA CTCTTGACTT AATTGAGTAA ACTCTTCATG CCATATACAT 60  
CATTTTCATT ATGTTAAAGG TAAAAATATGC TTTGTNAACT CAGATGTCTG TAGCCAGGAA 120  
GCCAGGGTGT GTAAATCCAA AATCTATGCA GGAAATGCGG AGAATAGAAA ATATGTCAT 180  
TGAAATCCTA AGTAGTTTGT ANTTTCTTTG ACTTGAATCT TACTCATCAG TAAGAGAACT 240  
CTTGGTGTCT GTCAGGTTTT ATGTGGTCTG TAAAGTNAGG GGTCTGTTT TNGTTTCCTT 300  
ATTTTGAGGT AAGAGTACTG CTNGGTGGTC GGGGGGGTTA TATNNTNCCC TTTTN 355

SEQ ID NO:7541

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08786

SEQUENCE DESCRIPTION:

GATCAGGTTT CCCCTCAGAA CCTGTGTTGC CTGCCTGCTG TATCTTCCAT GTCTTTCTTA 60  
TTCAACTTCT AGAAGTAGAG AAGGTTGGGA CTTGAGTGTA GAAGAAACAT CAGAATAATT 120  
TCAAAAAACA GGAAGTTGGA ACTATAATTT TTAAATTATT GTATTGTTTT TACGGATTTT 180  
ACATGTATAG TTAAATATTA ANNTTCATCT CTTGCAGTTC ANTAAAAGCT ATAGTATAGA 240  
TTTTATTTTT AAGAAGTTTA TATAATNCTT TTGTGAGCCA ATATGTAAAA CTNGAATATT 300  
TATTANCCT ANTN 314

EP 0 679 716 A1

SEQ ID NO:7542

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08787

SEQUENCE DESCRIPTION:

GATCACAGAG AAAGTGATTA CAGACATTGC TGGGGTAATA CCAGCTGAGA AAATTGATGG 60  
 AGTATTTNCT GCCTGTNAGA GTGGCTCTTT TGACAAACTA GANGCTGTGG TCAAGGATTT 120  
 AATAGATGAG GGTCAATGCAG CAACTCAGCT CGTCAATCAN CTCCATGATG TGGTTGTAGA 180  
 AAATANCTTA TCTGATAANC AGAAGTCTNT TATCNCAGAA AACCTTGCCG AGGTTGCCAA 240  
 ANGCCTGGCA GATGGTNCTG TTGTCCATTT GCANCTCATC NGCCTTTTNG CCCTGNGN 298

SEQ ID NO:7543

SEQUENCE LENGTH:32

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08788

SEQUENCE DESCRIPTION:

GATCAAAATT AAAGACAGTT AAAAAGGTGA AA 32

SEQ ID NO:7544

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08789

SEQUENCE DESCRIPTION:

GATCATCATT TATTGCATCT CATAACTAAA TTTNNTAAAG TTTGGATTGG GACTTTTNAG 60  
 GTCCTTTTTG GAGGGCAAAG GAAGTGCCAG CTTCTNTGGG GAACTTGTTT TAAATCCAA 120  
 AGACTTGAAC CACATTCCCT GCACATGANC ATGTTTGCTT TTATCCCTTC TCTCATTGTN 180  
 TCCTACCCAT CTTAGTACCA TTGTGGTTAT AANCATCTGC ATTTNTNAGA AGCATTTNAC 240  
 CCATTTNNN 249

SEQ ID NO:7545

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08790

SEQUENCE DESCRIPTION:

GATCATATGG AATGTACTAT TTTGTAATGT CTTTTTTCAT TTTACAATGT ATTATCAACC 60  
 TTTTCCTCT CAAAATACA TTGTGAATGA CTGCATAGTA TTCACCTTAT GANTATTTAA 120  
 TTCATTTCAC AGTCTTCTAT TGTNGGACCA CTNACATTGT ACCAAATGTT TTCCTTTGGT 180  
 TTATTCTTTA ATGTATTAGT ATTTTACTGC TGGTCACTCA TGGAATCCTG CAGCTTTANT 240  
 NAAAAGCAAG GATGAAA 257

SEQ ID NO:7546-

# EP 0 679 716 A1

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08791

SEQUENCE DESCRIPTION:

GATCGTGCCA CTGCACTCCA GCCTGGGCGT TGCAGTGAGA CTCCGTCTCA ACAACAACAA 60  
AAAGGTGGAT ACATGTCAAA AGGGCACAGG AGCCACTTGA AGGATTATAC TTGCTAAATC 120  
TGTGTCAATT ATCAAAATAA ACTGGTAGCA ACGTTAAA 158

SEQ ID NO:7547

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08792

SEQUENCE DESCRIPTION:

GATCAAAGGG ATGAGCAACA GGGACTTCTG CCACAGTGAC AATGGAATTG TGTTGTGCCT 60  
TACTTCAGAG GTGGTCTCTN CTTTCTTGTA ATAAAAGCAA TATTATGCG GAAAGCAAGC 120  
AGCTCAAA 128

SEQ ID NO:7548

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08793

SEQUENCE DESCRIPTION:

GATCACATCA AGCTAAAAAA CTTCTACACA GCGAAGGAAA CAAAGTGAAC AGAATAACAT 60  
GGGAATGTTT TCTGTAATTT AGTAGTAACT GGCAATAGTT TACAAACACA TTTTGTGTAT 120  
ACTGCTGTCA TTGCACTGNT TACCTTCTGT TGTAAGTACT TTGTTCTATT AGTCCACTCA 180  
ATTAAATAT TTGGTTTTGT TTAAA 205

SEQ ID NO:7549

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08794

SEQUENCE DESCRIPTION:

GATCTTATTT TTAATGTAGT GAGGATATTA TTAAACTTT TATTTTAACT GGAAATGTCC 60  
TGAAACACAT ATTTAAAATA TTGGGATACA GTGAAAGAAA AATTCAAATT TTAATAACAT 120  
AAAGATTTCC TAACTTTATG TTATTGANCA CTTACTCACT AGAAGTGAGT TCTTTAGAAA 180  
ANTACAGTGA AGGACTCAGT TCAGTCTTGT TTTTATCAGA GTGATAATCA TCCTGTTTCA 240  
CATCCCAATA CTATTTTGAN ATTCTAAACA ATGGAACCCA AANTNCCAAT AANTATAAGG 300  
TTATGCCTTC AATATATTCC TATACANTTC TGTAACCATG GTTTANNATA CACAAGCTTA 360  
NNATACCATG GN 372

SEQ ID NO:7550

EP 0 679 716 A1

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08795

SEQUENCE DESCRIPTION:

GATCCGGTNG TCTAAATGCA TTCATATTTT TATGATTGTT TTGTAAATAT CTTTGTATAT 60  
TTTTCTGCAA TAAATAAATA TAAAAAATTT AGAGAAA 97

SEQ ID NO:7551

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08796

SEQUENCE DESCRIPTION:

GATCTGGGTT TGGCATTAGA AGTATTTTCAT AATTTTGGTT TTTNATTAG GTTTCCTCAA 60  
CATCTGTAAA GTGATTGATT AAATTAGAGG AGGCGTGTAG AATAAATCCC AATCCCATTTG 120  
CAACTGGCAG AGCATTATAA NTNTTTATAA ATNCAGTTAC AACAAAGGAG AGGNTCTACA 180  
TTCTCAAAA AANAAANTTG GCTTACCTGT TTCANCTTTN GGTGGCATTT NNCTGCCATT 240  
NGTN 244

SEQ ID NO:7552

SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08797

SEQUENCE DESCRIPTION:

GATCTGGGAA TTACCCATCA TCATTAAGCA ATGAAACAGA CCGGCTGGTG CACTGGTGCC 60  
ACGGCGCCCC GGGGGTCATC CACATGCTCA TGCAGGCGTA CAAGGTCTTT AAGGAGGAGA 120  
AGTACTTGAA AGAGGCCATG GAGTGAGCG ATGTGATTTG GCAGCGAGGT TTGCTGCGGA 180  
AGGGCTACGG GATATGCCAT GGGACTGCTG GCAACGGCTA TTCCTTCCTG TCCCTTTACC 240  
GTCTCACGCA GGATAAGAAG TACCTCTACC GAGCTTGCAA GTTTGCAGAG TGGTGTCTAG 300  
ATTACGGAGC ACACGGGTGC CGCATTCTG ACAGACCCTA TTCGCTCTTT GAAGGCATGG 360  
CNAN 364

SEQ ID NO:7553

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08798

SEQUENCE DESCRIPTION:

GATCTGTGTG TCTCTGTTT GAGTTTTTCC TGTTTATTTT GAAAAGTACT GTTGGTCAAG 60  
ATAATTGGTC AATAATCCAT GTTGGTTTTA ACAAAAAGCA TTTTAACATT AAAAATATTA 120  
CAGTATAAA 129

SEQ ID NO:7554

SEQUENCE LENGTH:316  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS08799

SEQUENCE DESCRIPTION:

GATCACATTT TNATTTTTTN TTCTCCACAT CAGGATAGTT TACTGAAGCA CAATCTCTTA 60  
 TACTAGTGGG ACAAAGGGA GAAAAAGGAA GCAAGATAAA TGGGTATGTA GGATGAAGGG 120  
 TTATTTAAAA TGGAATAAA GATAGAAGGA GGACTGTAGG AAGANATGGA ATNNTTTANN 180  
 TNTGAGGAAA GATATCTNTG GTAGACATGT CCTTCCATGA CTAATTTCTA ATTGTNACTC 240  
 ANCACACATT GAGGTATGGN CCCTCCTCAG TGACTTNNAC TAGCTCAGAN ACGTACTCCC 300  
 CCACCANCCC CACCTN 316

SEQ ID NO:7555

SEQUENCE LENGTH:365  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS08800

SEQUENCE DESCRIPTION:

GATCAGTGGA ATTCTTGTT TGATGATAAC CTTATTAATT GAAATNTTTT ACTGATGTGG 60  
 CTTTAAAAGA GGTATATNTT GTATATGTTT AGAACTCTCT GATTTTNATG AATTATATGG 120  
 GAATGAGAAA CAGAAGAAGT GGTATTTNCT GGCGAGTTAA ATAGGCAAGG TACCCAGTGA 180  
 TAACACCAAC CAAACCACTC CTATCTGCAT GATTCTGAAC ATCTGGATGC CTGTGGTTTT 240  
 ACTGTGTATA TNTNATTTT AATATATTAC CTTTGTGGAT NCATTTAAGG TCTACTCAA 300  
 NGTANCACTG TCAAAACCAC TAATATGTAT GTNAAANTTG TNCTGTNTAC TACATTACNG 360  
 TNCAN 365

SEQ ID NO:7556

SEQUENCE LENGTH:349  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS08801

SEQUENCE DESCRIPTION:

GATCTTGAGT AACTGAACTT ATTTCCCTTA AGGTATAAAA ATTTAAATAA CCTGTATATA 60  
 TTTGNTAACA NCTTTATNAG GGAGGTAAGT NACTTACAAT ACATTGCACA TATTAAANGT 120  
 ATAGANTTCG ACGAGTTTGT ATGTATGTTT GCACCTGTGA AACCATCACA ACAAACAGTG 180  
 AGCATATCTN TCACCCCTAA NNGTTTCCTC CTGTCCCTTG GTAATCCCTC TTTTACCTGT 240  
 CCCACTTCTG TTCCTCAAGA NCCAATTACC TGCTTTNNTN ACTGTTAATG TACGTGAGTT 300  
 TACATTTTGT AGAGTTTTAT CCAAAGGGNA TCATGANGTA TGTNCTCTN 349

SEQ ID NO:7557

SEQUENCE LENGTH:369  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear

CLONE:HUMGS08802

SEQUENCE DESCRIPTION:

GATCTNATCA ATCTAGCGGG AGAGACAGGA TAACCTGTCC GAAAGTATAG CGCCACTATN 60  
 ACTCCGCCGG AAAAATTACT TTAAAAATCG CCAAAAATTA CTTGGAGCAA AGGGCAGTCG 120  
 GCGGANTTCG CCAAGGCTGG CGCAGTCGGT TTNACCTGT AGCAGAGAAC CNGGNCTGGA 180  
 GAACAGCCTC ACTTCTTTNA TTGANTACTT ACATAATGCA TTGGAACATG ACATGAGATT 240  
 AAGGTTTAAT AATGATAGAN TGAAGACCAC AATAAAAGAG ACCTCTACTT AGCTCAGCAA 300  
 TTCTTACCTT TCTTACCTAT TTGATGGAGG NTGTCTTTTG ANAGGTGTNC TGCAGGGNCC 360  
 AAANTGTTN 369

SEQ ID NO:7558  
 SEQUENCE LENGTH:290  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08803

SEQUENCE DESCRIPTION:  
 GATCTTGAT GCCAAACTTT AATCTGCTTT TATGTTTTCA GGCTGAAGGT GTGAAAATCC 60  
 TAAGAGGATT TCATATTGAA TATGTGTACA CAATCTTAAC TATCGTGGTG GAAAACATAC 120  
 TACTATAATT NATTATTATA TCTNCCAGAT AATGTTATTC ATTTAGAACA AATAAGGTAT 180  
 ATTTNTNAGA ATCANCTTTG TAAGCACTAT AANNNCTTTN ATAAGTTATA AGGTCTATGA 240  
 TGTGTTTACT TTAANNCTTG CTGTTAANAG CAACACGTAT TANNTATGTN 290

SEQ ID NO:7559  
 SEQUENCE LENGTH:55  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08804

SEQUENCE DESCRIPTION:  
 GATCTGGATA AATTTTCATT TCTACTTAAT TAAAACTTCC TATGTAAAAT CAAA 55

SEQ ID NO:7560  
 SEQUENCE LENGTH:109  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08805

SEQUENCE DESCRIPTION:  
 GATCCCGAAT CCCAGAAATA ATTCATAGNG CACCTATCAT GACTATTTAT TTAATCTCAG 60  
 AAGCTGAATC TGTACGTATT TTTCTCCAGG TCATCAGCTT TGGGNNNNN 109

SEQ ID NO:7561  
 SEQUENCE LENGTH:40  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08807

SEQUENCE DESCRIPTION:  
 GATCCTACTC TCTTATTAAA ATCTTGAGTT TATGTTCAAA 40



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SEQ ID NO:7562

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08808

SEQUENCE DESCRIPTION:

GATCTGCCGA CCTCGGCCTC CCAAAGTGCT AGGATTACAG GTGTGAGCCA CCGCGCCCAG 60  
 CCATAACTTT NCTCTTTTCT CCATTAGCTA AAAGATAATA GTAAAACGTA TATTTGAACA 120  
 CTTAATTTTC TCTATATATC TTTTNAGGAT TATATTTAGT GTATTTCCCA ATTTTCCTAA 180  
 AATGATTATC ACTTCTGTAA AGAAGAAAAC AATACTACTG GTATTGCATT TGGAAATATT 240  
 TTNCTATTAA NNTGTCTCAT TTCCTTTNCA TGTATGCACA TACATGTNNT TNGTATAGCT 300  
 CCTTTNNTCA AAANNTATTC TGNGGTTATT ATTTANNN 338

SEQ ID NO:7563

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08809

SEQUENCE DESCRIPTION:

GATCTTGTGG TCAAGAGCAA TCTGAATCCA AATGCAAAGN AGTTTGTCCC TGGGGTGAAG 60  
 TACGGAAATA TTTAAGTAGA CGGGGCCCTC TTTTGGTGGA TGTAGCACAA TTNCCACACT 120  
 GTGAAGGCAG TATTAGAAGA CTTAATTGTA AAANCNCTCT TGTCACTGTG TTACACTTAT 180  
 GCATTGCCAA AGTTTTTNTN AGTCTTGCAT GCTTAATAAA NGTNCTGAGA CTGTTACTAA 240  
 GTAAAANGCT GTCAANCATT TCCTGANAAT AGANTTGGCC CCATGGCTTG ATGTGAAGAC 300  
 AGCAAGGNAA GANGCACCAG TCAAGTTGTG ANCAAGNN 338

SEQ ID NO:7564

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08810

SEQUENCE DESCRIPTION:

GATCCCTGCC ACAAGTTCCT TGGGCAGTGG CCATGTCACC ATTGAGATGA AGATATACAA 60  
 CAGAAAATAG TGGCTGTGTT TGGAAGCTTC AGCCCTGCAC ATTTGAACTA GTCACCTCTCC 120  
 CAGACTTGCG TGGGTCAGTT CTTTCTGAGT AGAGGACTTG CTGGTAAAGG GGCAGATGCT 180  
 TTTTATTAGT ACTGATAAAA CAACTGAGG GAAACATCCC TCTTAGCTGG GAACTTTTA 240  
 CTCTTCAGGA GCTTGGCATC ATGGACTGTT AATGTATGTG ATTTTCCCCC TATTTTCTCT 300  
 CTCCAAAATG ATAAAAACAA TAAN 324

SEQ ID NO:7565

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08811

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCCCACTA CGAAACGCTC CAGAGGCTTC GGTTCGTCA CGTTCGCAGA CCCAGCAAGT 60  
 GTAGATAAAG TATTAGGTCA GCCCCACCAT GAGTTAGATT CCAAGACGAT TGACCCCAAA 120  
 GTTGCAATTC CTCGTGAGC GCAACCCAAG GTGTTCTAGC TGAGCGTTTA AGAGCATGGA 180  
 CTCTGGAACC AGACTTTGAA TCCTTGCTCT GCCACTGCAG CTGTGTGACC TTGAGCAAGC 240  
 TATCTAAATA TTCTGTGCCT TTGTTTGTG ATCTGTACAA TGGAGATGAT GATGGTATCA 300  
 CCTTCATGGG GTTGTCAN 318

SEQ ID NO:7566  
 SEQUENCE LENGTH:313  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08812

SEQUENCE DESCRIPTION:  
 GATCTGAGAC TCAGGAACCT TGGCCCCCTT GTCACCTACA ACTGTGTGTG AACAGGACTA 60  
 ACAGTTTGA CTGAGAGCAC TGANGCTGCT GTGTGTGTG CATATAACTT AATGCTGTGT 120  
 GTTGTGGCTT GCACTGCTGT GGGGGCGGGG AGGGCAGTGG TGGGGAATGG CTGGCATGAA 180  
 GCTTGCTTGA GCCAATGCTA TGCTTGCTGG GCTTTGGCTG ACTGGCTTTG GGCCACCAAC 240  
 TGTATTGCA TAGTGATGGC TTGGAAGTGT CCATAGAAGG GATTGCAATA AAGGTGTGTC 300  
 TTCCTTCTAA AAA 313

SEQ ID NO:7567  
 SEQUENCE LENGTH:316  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08813

SEQUENCE DESCRIPTION:  
 GATCTTGAGT CAGAGAGGAT TGGAAGTGCT TTCTCCTCCA CCCAGGTGAG GTCAGGGGAG 60  
 CTTAGGTCTT AGGGAGATGG CAAGTTGAGG TATGAAGGA AGCTGGGGCT TTTGGAGCTG 120  
 CCGAACAAC GAGGGACCCA GTGCGCCTC CATCCGCAC TAGTGAATAG CGCCCCCTCT 180  
 TCCCCGAAA ACGAGGTGCG AGAGGAACAA TTCCACGCT GGGGAAGGAC TTGTCTCCTT 240  
 TTCTGTGAAA ATGCTTTGTA AAAAGTTGTT ATTGTTTGCA TAGAGCAGAT TCTTGAGAAA 300  
 AACTGTTTTG GACCAN 316

SEQ ID NO:7568  
 SEQUENCE LENGTH:316  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08814

SEQUENCE DESCRIPTION:  
 GATCCCCGTC TGCTGACCAG CTAAACACCA ATTTCTTCCT GCTTTTCTCC ACTTGGTTTG 60  
 GAAAATCACA CAGTTTTCAG GCTCCATCTG TTTGGAGAAA ATACATTCTG AAGCATCCCC 120  
 AATTACCTT CTAAAACTC ATGTGCAGGT TTGATAAACA CCAGAACAGA AGACAGTGAT 180  
 GCTGTATTAT TTTAGATTTA TTACATAGAT TTGGAATTCA CTTTTTTCAT GACCTAGAAA 240  
 AAAACATTCC AGTGTTCANC TGTNTNTAT TATTANGGGG CTTTTNATTT GTGAACCTCT 300  
 GANGGCATGA GTGTTN 316

SEQ ID NO:7569

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08815

SEQUENCE DESCRIPTION:

GATCTGGTGT ACCAGGCGAA GTGGTCCGAG CAGGCTGAGC GATACGACGA AATGGTGGAG 60  
TCAATNAAGA AAGTAGCAGG GATGGATGTG GAGCTGACAG TTGAAGAAAG AAACCTCCTA 120  
TCTNTTGCAT ATAAGANTGT NATTGGNGCT AGNNGAGCCT CCTGGAGAAT AATCAGCAGC 180  
ATTGANCAGA ANGAAGAAAN CAAGGGAGGA GAAGACAAGC TAAANN 226

SEQ ID NO:7570

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08816

SEQUENCE DESCRIPTION:

GATCAAGAGT TAAATAAAAA GCCCCAGGAC GAAACAAGAN GAGAGCACTT CATGCCCTGT 60  
GGTACAAAAA AGAGCAGCTC TACTTAATGC AATTCTTCAT TCAGCATATA GCGAGACATT 120  
TCTCCTGCCT CATTTGAAAG ACATCCCAGC ACAGCATATC ACGCTGTTTC TTAAGTATTT 180  
GTATNNNNNN GTACCTGAAG TGTAGCGAAA ATNCTACTAT GACTCTNCCT GGAATACACC 240  
CACCTACCTT GANCCAGATT ATGGATTGGN TATGTCTACT TCTGGATGCA AATTTTNCTG 300  
TTGTTN 306

SEQ ID NO:7571

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08817

SEQUENCE DESCRIPTION:

GATCCTGCGA GGGTGTCTATA ATACCTTGCT TTTCCATGCT TCCTGTATAT TTATCCATTT 60  
CAGCACATCT GCAGTAGCAA TAACTNCTNA TTTNTAAATT TNCTTTTGTT GGGGGAGACA 120  
GGCTTATGGC TGTCTGAGCA GCTGCTGTAG TGTAAGCAGT GAGGTTAGCA GTGGTTGTNA 180  
GATTTNCTCA TTCCTGAGCA CCATGCTGTT GTGTCAGCAG TTGTAATGGA CTGTGTGGGC 240  
ATACTTCCAG TAGGTGATGC TTGCAAGTAN GANCCAGCTG CAGTGGTAGC AGTAGGGTTT 300  
GTAN 304

SEQ ID NO:7572

SEQUENCE LENGTH:30

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08818

SEQUENCE DESCRIPTION:

GATCTGTACA AATAAAATNC CAAGTCCAAA 30

SEQ ID NO:7573

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08819

SEQUENCE DESCRIPTION:

GATCATCTCT CCTTGGGTTT TNNTTTAAAA AGGGGAATCT NCTATAAAGG TTCTNTTGCT 60  
TCAAACCAAT GTCAAATAGA CTTNATTTTA AGAGTCATGG AATTACAGTG CAACCTTN 118

SEQ ID NO:7574

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08820

SEQUENCE DESCRIPTION:

GATCTACCTA TACAGTCCTA CATTAGCTTC TAAAATATTT GTCAGGAGGG AAA 53

SEQ ID NO:7575

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08821

SEQUENCE DESCRIPTION:

GATCCCGAGG CTTTGTCTTC CTCTCGTCAG TTCTTTTGGT TGTGTTTTTT GTTTTTNTTT 60  
NAANAACCTCA AAAAAAAAAAN AAAAGACTTG GAGGAAGGGA AA 102

SEQ ID NO:7576

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08822

SEQUENCE DESCRIPTION:

GATCCTACTG ACAGCCATCG TGCAGGTGCT CAGCTGCTTC TNTCTCTATG TCTGGTCCTT 60  
CTGGCTTCTG GCTCCAGGCC GGGCCCTTNA CCTCCTGTGG GTGAATGTNC TGGGCCCTG 120  
GTTCACTGCA GACAGTGGCA CCCAGCACC AGAGCACAAT GAGAAACGGC AGCGCCGACA 180  
GGAGCGGGCG CAGATGAAGC GGTTATAGCC ATTGANATTG TGGCCACAGG CCACTGGGCC 240  
CTGGGTGGCT CTGTNAGGGT GCACAGCCCC TCATGCCTGG AGCAATGAGG GTCTAGTCCA 300  
GGGGCCAAAA GCAGTCTTGA GGGTATTGGG GTATACTTAT ACTCTATAGG GGTGCTTTGA 360  
AN 362

SEQ ID NO:7577

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08823

SEQUENCE DESCRIPTION:

GATCACTCAT ATAACATGTC ATTTTTTTGG TTCTGTTTTG GTTTGGTTTT TGCCAATNAT 60  
TTTGTTATAT TTCCAAAAAA CTAAATAAAA ATNATTTTAA TTTTNNAAA 109

SEQ ID NO:7578

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08824

SEQUENCE DESCRIPTION:

GATCTTCACG GGGCTATTAT TTCAGTGACA AAATCCAAAT GCCCCTCTTA TGTGGGTATT 60  
ACAGGAATCC TTCTACAGGA AACAAAGCAC ATTTTCAAAA TTATCACCAA AGAAGACCGC 120  
CTGAAAGTTA TCCCAAGCT AAAGTGCCTG TTCAGTGTGG AAACCGATGG CTTTATTTC 180  
TACATTTACG GGAGCAAATT CCAGCTTCGG TCAAGTGAAC GGTCTGCGAA GAAGTTCAAA 240  
GCGAAGGGNN CGATTGACCT GTGANTTCTT TGCCGTCTAA GGCAGTTGTT TATGACAGCT 300  
GAAACTGGA CACTCCCTAA NTGTCCACCT TTCAGTGAAG NGATAGTTAA GCCAATTCCN 360  
N 361

SEQ ID NO:7579

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08825

SEQUENCE DESCRIPTION:

GATCCAATTC GTGTCTGTGG ATGCTGCAAG GACTGGCTCA TTGGAGCCAA ACCATGTGGC 60  
GGAAACTCCT GAAATTGGTG GAAAAAGTGG AATATGGCAG ATTGGGTAGG TAGGAGAACA 120  
ATTTTGGAGA TTTTTTTTCT TATGTTAAAG TGTCTGCATT TTATTTGCTG TACCCTGCCT 180  
ACTCTGGTTT TNAGGATTTT TTGACTTCTT CGAAAAGCAC TGAATAATCT CTTNCCGGG 240  
TCTAGATTTT TTGATGAGTA CTGTGTAAAA TTGTCAATAT TCAATGGATT ATTAATAAT 300  
ANNTTAAGAN TTCCACTCAT AAN 323

SEQ ID NO:7580

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08826

SEQUENCE DESCRIPTION:

GATCCTAAGT TAAGACTCTC CAAAGCAAAC ANTTGGTTTA AATCATTTAT CTGATGTAGA 60  
TAAAAGGTAG AGAACTTGT AGTGTCTCC ACATAATGGA AAATGTACAA ATGCCTAGTT 120  
GTGTTGCCCA TCAATTTTGT ATATNTCCAT AATTTTNATT GTTGANAATT GCATTATNTT 180  
TTN 183

SEQ ID NO:7581

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08827

SEQUENCE DESCRIPTION:

GATCCACCTG CCTCGGCCTC CCAAAGTGCT GGGATTACAG GCAGGAGCCA CCGCGCCTGG 60  
GCCTTTTTTT AAGTTTAAAG NNCCNATAAA GNCACTGAAA GGTGATGTGT GTGGATGAGC 120  
TAGGAAGACC TGAAATAGGC TCTCTCTAAA TTAATCAAAT TAATCCTGAA GCCATTCTGC 180  
AATACTGTCT TTAATGTATA CTCATTGTT ATAGAAGCCA GGGTTTTTNC CCCTAATTTG 240  
TATCATTGCT ATATGTGTTA TTGTACCAAA CTACACTGTT TTAATTGCTG TAAATTTTAA 300  
TATGTCTTAG TATCTGGGTG TGGGAATCTT GANAGCATGG AGTTTGTGTN 350

SEQ ID NO:7582

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08828

SEQUENCE DESCRIPTION:

GATCCTTGGG AGAGCTATCA CGGGAATCCA GGC GTTACAG GCCAGCAAGT GAGCCGCTCC 60  
ATCAGGGGCC CGAACTNTC AAGCCCCTTT NTGGAGAGNT GCCTGGCTGG ACCGTAGAGC 120  
GCTGTGCTCT GAGCTTAGAA AGGGAGGTGG CGGATGGAGT GGGAAGTGAG AGACACTGAT 180  
TTTNAATAT CAAAATTTCC CTTCTGAAGT CGTTCAGATG TTTCTTAA AAAGAAGATG 240  
GAATTCTCTG TAGAGCGTCT CANTCCACTT TTAACCATGG NTGAGAGCAG ACTCCATTTA 300  
CCNTGAAATA GCAGCTTCTT TTGAGGGGAG AGTGACATGG AAGCAACN 348

SEQ ID NO:7583

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08829

SEQUENCE DESCRIPTION:

GATCTGCAGG TTTGGGCATA TGCTTTCATC ATTAAATTAT CTGATAAAGT TACAAGTCAC 60  
AAAGGAGAAT GAGAACTTAA TGATTCTATT GGATTTAATA TATTAGCAAG AAANCATACT 120  
ATTNCAATAT GTNTAGCTTA GTAAGGCATT ANCATAAGTN CAANACCTAT GANACAGATG 180  
CNTATTTCTT CAACATACTG TGTCAGGTAT ACTGTTTTAT ANTTNGGTTG TTTTAGCCTT 240  
ATTGCACACC NNCTCCCN 258

SEQ ID NO:7584

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08830

SEQUENCE DESCRIPTION:

GATCCATTTC ATTACAAGTA AAATATTACA AAATATTTAC AGGAAAATAT TAAAAATAAC 60  
TCAAACACAA AAGGCAAGAT GAAATAAACT GTTTTTTTTT CTCCAGAAAT CTCTACTCCA 120  
GTGCCCACAG CACACAAGAG TCAAAACAAA TAAGCAACTA AGNTCCTTAC GAAAAAGGNA 180

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CAGNTTGTTTCTAAACCAGAAGAGGAGGTTGCCCAGAAGA AAAAGATATCCGGAGGAAC 240  
CTGAGGANCCNAACTTTTTGCCCGGGGGTAATTCNGNCTTNNATTAA TTTNTTTAN 300  
NGGGNNNN 308

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SEQ ID NO:7585  
SEQUENCE LENGTH:36  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08831  
SEQUENCE DESCRIPTION:  
GATCTCTTATCATAATAAAG AATCTTTGTC ATCAA 36

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SEQ ID NO:7586  
SEQUENCE LENGTH:227  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08832  
SEQUENCE DESCRIPTION:  
GATCTAAGGA GGCCAGTGAA TTTCAAACAG GATTAAAAAG AAAAAAACA GAGTTAGGTA 60  
TCAAATTAAG AATACTGAAA GCAAAGATAT AANTAGAACT TAAAAGCAG CCAGAAAAAC 120  
AAACATATTA CATATAGGGC AGCAACANTA AGANTAACCG CTAACCTTTG ATTAANNNGTA 180  
ATATAATTCA CAATACANTG TAACANCANT TTTNNGTGCT AACNGGN 227

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SEQ ID NO:7587  
SEQUENCE LENGTH:215  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08833  
SEQUENCE DESCRIPTION:  
GATCTATTGA GAATGGAATT GTTTTCTTAA TTTCATTTTC AAATTGTTTG TTGCTAGCAT 60  
ATAGAAATAC AAGTGATTTT NTATATTGCT CTTGTATCCT GTGACTTGC TGAGCTTATT 120  
TTAGTAGTTT TTTTCACTG AATTCTTTAG GATTTTNTAC ATAAAAAATT CATATCATCT 180  
GTGAATAAAG ACAGTTTTAT TTCTNAATTT TAAA 215

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SEQ ID NO:7588  
SEQUENCE LENGTH:43  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08834  
SEQUENCE DESCRIPTION:  
GATCATATTT TAAATAAAG CATTTTTGT AGAAAGTGCT AAA 43

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SEQ ID NO:7589  
SEQUENCE LENGTH:334  
SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS08835

SEQUENCE DESCRIPTION:

5 GATCAGGATA ACCAGGATGA TAGCAGTGAC GATGGATTCC TCGCTGATGA CAACTGCAGT 60  
 TCAGAAATAG GACAGTGGCA TNTAAAGCCT ACTATCTGTA AACAACTTG TATCCTACTT 120  
 ATGGNCTCAC TCCGAGGCC TTCTCGGTCA AATGTTGTCA AAATTTTAAG AGAGTATTTA 180  
 GANGTGGAAT GGGAAAGTTAA AANAGGAAGC NNNAGANGTT TTTCCAAAGA GAAAAGAAAG 240  
 10 CATAAGGNCA CTTACTCAAC AGANGCACCT TTAGGCGGNG GANCAGNACA TTGTGTCAAT 300  
 AGTNTCTCNG GTTTGCCCTT TCTNTTACTT GTCN 334

SEQ ID NO:7590

SEQUENCE LENGTH:235

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08836

SEQUENCE DESCRIPTION:

20 GATCAAATTT AAAAATCAGT TTTAAAAGTG GTTCCCGACT TCTTTCCTTT GGAAGAATTT 60  
 GGNCTNATGC TCATAAGCAG TTCATGAGTG ACAAGTGTAG CAAAAGCCAG CCATATATTT 120  
 CNAGANTCTA TATCCTCAGG AAATGGTCCT TTTTTTCCT ATAANTCACC AACCAACTAT 180  
 CTAANTGGNC ATTTGGGGGA NTTCCCTCCC AAATTGATT TTNTNATTNG AAAAN 235

25 SEQ ID NO:7591

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08837

30 SEQUENCE DESCRIPTION:

GATCCAGAGC ACAGATGGCA AGTTGTGTGG ATGATACTGA ATATNTTTAT TTCCTAAAG 60  
 ATAAATNTCA CGACACGACA TTTCTCAGTT TTAATTTAGA TGTTTATNAC CATGTGTTAA 120  
 CAGAATCTTA AAACCAAGG NATTTCTTCA GTAAACTAGA CTTTGATTCA AA 172

35 SEQ ID NO:7592

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS08838

SEQUENCE DESCRIPTION:

GATCAAGAGG AAGCATGACT TGCACAAGAT GGCAGAGGCC AACCGTGCCC TGGCCCACTA 60  
 CCGCTGGTGG TAGAGTCTCC AGGAGGAGCC CAGGGCCCTC TGCCGCAAGA AACAGTGTGA 120  
 45 GCTACTGCCA CGCTGAAAAC TACCTGTGGG TTAAGGATGT AGTTCCTTTG TAAGGGTGGG 180  
 CAGGCCTCGT AAGAAAGATG TAGCAGCATA TTCACTATCC GTTAATCCTT CTTTCTTTGA 240  
 GGCTGGAAC TGTCTCTCTT GCCCTATTT CCTGTAAAG AGGGAGCACA TTGACTTGGG 300  
 AATTCCTCC AGGAAACTCA GGGCTGTTTT CTCTN 335

50 SEQ ID NO:7593



SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08839

SEQUENCE DESCRIPTION:

GATCTGGGAC TTCTTTAGTA TCGAGTCTCC TTTGCACTCT TAAAAATTGT TGAGGACCCC 60  
AGAGAGCTTT TGTTTTTATG GGTGTATCT ATCAATATTT ATCACATGAG AAATNATTTA 120  
TTTATTTTAA AATAACTTTT TTATTGAGAA AGATAGCAGT GTTTTTTTTT AATCTTGCAA 180  
ATTGTTTAAT GTTTGATTTA ATGGAAGACA GCCAGATTGT CCTATCAGCA TTCAAACTGC 240  
TGCAGTAAGT TGTTTGGACT AATGTATATG AGGAAAACCT GACCTCACTG AGATTTTAAT 300  
TGGAAAATGG AGGAGTATTT TNCCAGCCTT TNN 333

SEQ ID NO:7594

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08840

SEQUENCE DESCRIPTION:

GATCTCCTCC ATACGGAAC TTCTCATCTA CGTGGCCCTC CTGCGAGTCA CTCCATTTAT 60  
CTTAAAGAAA TTGGACAGCA TATGAAGACA GGACATCACA TATGAATGCA CGATATGAAG 120  
AGCCTGGTTA CAGTTTCGAC TCCTCTCTGC AAGTGAATAG GCCCAGAAAG GTGTAAGAGA 180  
CTCTTTGAAT GGACATAAAA TTCTGCTTGT TAAGAACAAA 220

SEQ ID NO:7595

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08841

SEQUENCE DESCRIPTION:

GATCTGTGCT GGCCACGTGC CCGNGTCTC AGCTCTGAAC CTGCTGTCCC TGCTGAGAAG 60  
CTCTGAGGGC CCCTCCCTGG AGGACCTGTG AGGGTGGCTG GCCCCTGGGC TGCCCCTTCT 120  
NATGGCTTCG TGCTGACTCC ATAAACATTG TCTGTTGAGG ATGTCCAGTC AGGGCTTGAC 180  
AGGCCAGGN TCAGCCCGCC GTGGCTGGGA AGGTTCCCTG CAGTGCCAGT GCTGCAGCAG 240  
GGAGAGCTGG GCAGAAGCAG CGAGGGGGCC CAGCTGGCGA GACTGTAGCC CCGTCCCACT 300  
CCCACACTCA CTCTGTAG AGCCTN 326

SEQ ID NO:7596

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08842

SEQUENCE DESCRIPTION:

GATCAGATGT TGGAACGTGC TATGCTGTAG CGTGTCTGGA AACAAAGTAC ACAAACCTGG 60  
CTACGGTGAT GAGTTAGCTT CTGCTTACTA CCTGTNACAA CCAAGTGGG TGACACTAGT 120  
GAACCTTCTC CAGTCTGCAG GCTGGCATAG AAGGCTCTTA GATTATATTG GGCAGCTTGC 180

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AATCTGCCGA AGCAGTGA CTGCAATTTCCA CACTTGGCTT GAGCACTCAA CCCAGAAGGC 240  
 GAAGATAGCT TTTGGTTGTA GCGGGCTTCC TGTATGGGAT ATCCCTCGGT AAGGGTAAAG 300  
 GAGCAGAGGC AAAGGAGAAA AGCAGTN 327

SEQ ID NO:7597  
 SEQUENCE LENGTH:278  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08843

SEQUENCE DESCRIPTION:  
 GATCTTTCTT CCTCCCCTG CATGAGGCAG AGGCAAGCTG CCTGCCAACC CCCTCCCTCA 60  
 AGGAATGGCC TTGCCCAGGA ATGCCACCA CACATACCCT CTNCTTTTTT NNTAGTCAAA 120  
 CTCTTGTTTA TTCCTTGGNT TGCNTCCCTC CTTCTCCCC TCTCAACCTT TACTTCTGAT 180  
 TTNNAATTCA TGAATTG GATTGANGTT AAATAACAAC AGTGCCGCCA ACACCAAGTN 240  
 TTGCAGGAAA AAAATACAAA GAAATTTANC ANANAANN 278

SEQ ID NO:7598  
 SEQUENCE LENGTH:202  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08844

SEQUENCE DESCRIPTION:  
 GATCTTCATT ACCGTTNCAT GATTGAAAT ANTTAAAACA TTGTACAGTT TTAGTATAGA 60  
 GAAATNTAAT GGNTTTTGT AACCAGTTT TGTCTGCATG TAATTTGGAT TTCTCAAATA 120  
 CATTCAATAG TAATTNATCA GTAACATTAG TTTTATTTNN GTCCATCTCC TTATCTATAA 180  
 AANGGGGATA TNCTTAGGAT NN 202

SEQ ID NO:7599  
 SEQUENCE LENGTH:47  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08845  
 SEQUENCE DESCRIPTION:  
 GATCCATAAT ATAGCATCAC ATCTCAATAA ATTTATTTGG AAGCAAA 47

SEQ ID NO:7600  
 SEQUENCE LENGTH:327  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08846  
 SEQUENCE DESCRIPTION:  
 GATCTGCCCA CTTGGCCTC CCAAAGTGCT GGGATTACAG GCATGAGCCA CTGTGCCTGG 60  
 CCCCTTCTTG TAAAATTTT AAATGGAGAA TTGGGTGCNA GATGTGGTTT CCAGCCTGGT 120  
 GCCTGGGGTG CTGAGCTANN NGAGTGGTGC AGTCCAGGAC ACCTTTGCTT TATCTACTT 180  
 ACACGGTCAC CTGGAGCCGG CTCAAGTGGC TAAAGCATCC TGGGGCCCAG AGCCAGGTGA 240

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TAGGTCCTN TGGCCAACTG GACAGTTGAG GCCTGTGGTT ACCCGAAGCC CAGCTTGGGG 300  
CCCTGGTCCA GCCTNGCCTC CCAGGAN 327

5 SEQ ID NO:7601  
SEQUENCE LENGTH:326  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08848  
10 SEQUENCE DESCRIPTION:  
GATCTAGATG CTGGTATTGA GGTGGGAGAC AAGTACTGCC ACCNGAAACA ACAGTCTTGG 60  
TAAATTTAGC CGACGAGGGT AAACACATCC TAACAGGGAA GGTAAACTGT ACGTCCATCA 120  
GTACCACTAG AGGGCATCNC NGGTTTATAG TTCAATACAG TGAATATATC AGANTAATGG 180  
15 CCTTTAGTTT TCCTGAAAGA TTAANTTAGG CTTGCTAACT TGTTTAATGN GATANTCAAA 240  
CATATGATGT AATTTTAAAG GGTTCACATT TTTANAANTT TAATGGTTGC TACATAAAAN 300  
GGGNTTCAGT TAACTNATTT TGCCTN 326

20 SEQ ID NO:7602  
SEQUENCE LENGTH:310  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08849  
25 SEQUENCE DESCRIPTION:  
GATCTCAGCA GGGAACCATG GAAGCACCCA CCCCCTTGCA TTTTGGCTTA CCTGTAGCGG 60  
AATGCAACAG AGAATTTTAT ATGCTAAGAT TTGTGGTTCC GTGGGAGAAT ATTTCAAACA 120  
GGTGGAAACC ATCAAACTAA AAGAGAACCA GAAATCATTT AAAGGTCACG TGAGGAGCTT 180  
CTGNTTGTG CAACCTAAGC CTCACCAGT CTCCTATGCC CAGGTGCCCA GCACCCCAT 240  
30 CATCTGCATA TTCACCATCC TCAGGTCAGA TTCTATGATA CTGNNAAATA AGGCATTCTG 300  
GAAAANTAAA 310

35 SEQ ID NO:7603  
SEQUENCE LENGTH:287  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08850  
40 SEQUENCE DESCRIPTION:  
GATCCGGTCA GCAGCCCCTG TGGCTAGAGG AACACCAGCA CAAACGACAG CCTCAAGTCT 60  
CCTTCGAGCT TTATATCCAT TTGGGGATGA AGTCTACTTT NACAGCTAGC AAGGCGACAT 120  
GCAACTGTTG TTGAATGATG ACAGCAATTC AGGAAAGACT TAAATATGAA AGCAAATTGA 180  
NCACATCGGG TGTTTGTNAT CAGANNAGNG NTGNGATGTG ATAAGACTTG TTTATTGACT 240  
45 AGCCAATATG TCATTCACCT TCNGGTTTAT NTTGTGNANC CCCANNN 287

50 SEQ ID NO:7604  
SEQUENCE LENGTH:66  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

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# EP 0 679 716 A1

CLONE:HUMGS08851

SEQUENCE DESCRIPTION:

GATCGAGTTT TGGTTCGGGT TAACTGTGTG CCTACTGAAC CTGGCAAATA AACATCACCC 60  
TGCAAA 66

SEQ ID NO:7605

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08852

SEQUENCE DESCRIPTION:

GATCTGGAAT GTGAAGCGTT ATAGAAGATA ACTGGCCTCA TTTCTTCAAA ATATCAAGTG 60  
TTGGGAAAGA AAAAAGGAAG TGAATGGGT AACTCTTCTT GATTAAAAGT TATGTAATAA 120  
CCAAATGCAA TGTGAAATAT TTTACTGGAC TCTATTTTGA AAAACCATCT GTAAAAGACT 180  
GAGGTGGGGG TGGGAGGCCA GCACGGTGGT GAGGCAGTTG AGAAAATTG ANTGTGGATT 240  
AGATTTTGAN TGATATTGGA TAATTATTGG TAATTTTATG AGCTGTGAGA AGGGTGTGTGT 300  
AGTTTATAAA AGACTGTCTT AATTTCATA CTTAAGNTN 339

SEQ ID NO:7606

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08853

SEQUENCE DESCRIPTION:

GATCCTTTGT GAGCAAGTTC TATTTGTTCA TTGCTTGCCA GAGATGAACA CAGAATGTTC 60  
TGTTTCATTT TACAAGAACT ATCCTGAGTT TCTGTGGATG GAAACATTAC ATGTAATGCA 120  
GATATAGTGA AACTGGAAA GATTTATTAA AGANTTATAT TTGTGTATAC TTTATAAATT 180  
AGTCCCTCAT TAGATTTTTT TTTCTTAAG CATAAGACTG ANCTTAAATG TGTTAATTTT 240  
AGTAGAATCA GGCCTGCTC GCAGAAGGAN CACAGATTGT NGAGATTAAC ATAAATNGTT 300  
CTTGTCTTAA TATATATNTN TNCCATTTC TGTCGAN 337

SEQ ID NO:7607

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08854

SEQUENCE DESCRIPTION:

GATCCGTGGA TTGAGGGTGC CTTTCCATTT ATTTGGTCT TCTTTACTTT CTTTCAACCA 60  
AGTTTTGTAG TTTTCAGAGT ATAAATTTA TACTTGTTTT GTTCAGCCTA TTAGTGTTTT 120  
ATTTTGGTG CTATTGTAAA TNAATCTTC TTAATTTCAA TTTTCAGATTA TTCCTTAAA 180  
TATACAGAAA TACAGCTGAT AAA 203

SEQ ID NO:7608

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08855

SEQUENCE DESCRIPTION:

5 GATCAAAACT TTTCATAATA CAAAGACATT ATTATTTGNT TTTTTCCTG TCCCCTCCTG 60  
 AATATACAAC GGAGCATTCC AGATGCTAGA GTGACAGCCT CACTCAGACT CAGGGGATGC 120  
 ATGCTTGCNT GTACAGTACT CGTATGTTTT AAATTTGTTT TAACTCCTAA TATGTAAGTA 180  
 TCAATAAATA TAATCACCTT AAGTAAA 207

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SEQ ID NO:7609

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS08856

SEQUENCE DESCRIPTION:

20 GATCTTCGTG GTGGAAAGCT AAATTTTAAA ACCACCCCAA TGGATGCAGA CAGTGATGTT 60  
 GCATTGGACA TTCTAATTAC AAATGTAGTC TGTGTTTNA GAACAAGATG TCATTTAANC 120  
 TTAAGGAAGA TTGCTTTGGA AGGNGCAAAT GTAATTNATA ANCGTGATGT TGGAAAAGTA 180  
 TTANTGAGGC TTAGAAAACC TAGANTTACA GCTACANTTN GGTCTCAGG AAANNTTATT 240  
 TGCNCTGGN 249

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SEQ ID NO:7610

SEQUENCE LENGTH:319

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08857

SEQUENCE DESCRIPTION:

30 GATCTGTAGT ATTTTAATGT GCATCTACTT TAAATGAGTC ATCTTGGGGT TTTTATAATT 60  
 CCCTTATGTT CTCGCCCTC TACACTTGAA ATAACAAAAT GCCTTAATTT TATGGATTAG 120  
 NTCTCTTATA GGAGACAGGC AGCTATATGN AGCAANCCCA GTAAAGTTAT TTTTCAACTN 180  
 TCANAGTTGT AAAATATTTT ATAACAGTTT ACANCAACAG CTGNAGANCA ACATGCCACA 240  
 35 TTTTNTTTC AGCATTTTCA AATANTTTGT TTTGTGGTGT NAGCACAGGN TAAANNTGGG 300  
 GNGCGTCGAT GTGAGGCGN 319

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SEQ ID NO:7611

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08858

SEQUENCE DESCRIPTION:

45 GATCTACAAA AAATTCCTGG AGCCATATAT ATACCCTCTG GTTCCCCCT TCGTTAGTCG 60  
 TATATGGCCT ANGAAAGCAA TACAAGANTC CAATGATACA AACAANGGCA ANGTAACCTT 120  
 TAAGGGTGCA GACATGAATG GTTTACCAAC AAAAGGNCCA ACAGAAATCT GTGATAANNC 180  
 GNAAGACTAA NGAAATTTTC CNAAAGGN 208

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SEQ ID NO:7612

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SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08859

SEQUENCE DESCRIPTION:

GATCTTCCCA CCTTCAGCCT TCCAAGTAGC TGGGACTACA GATGCACACC TCCAAACCTG 60  
GGTAGTTTTT NAAGTTTTTT TGTAGAGGTG GTCTAGCCAT GTTGCCTAGG CTCCGAACT 120  
CCTGAGCTCA AGCAATCCTG CTTTCAGCCTC CCAAAGTACT GGGATTACAG GCATCTNCTG 180  
TAGTATATAG GTCATGAGGG ATATGGGATG TGGTACTTAT GAGACAGAAA TGCTTACAGG 240  
ATGTTTTTNT GTAACCATCC TGGTCANCTT AGCAGAAATG CTGCGCTGGG TATAATAAAG 300  
CTTTTCTACT NCTAGTCTAA A 321

SEQ ID NO:7613

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08860

SEQUENCE DESCRIPTION:

GATCCTTCCT AGGGGATGGG GGAAGCCCTG GCTGCAGGCA GCCTTCCAGG CAATATGNNG 60  
ATAGGAGGCC CACGGGCCTG GCAGTGAGAG GTGTGGCCCC ACACCGATTT ATGATATTAA 120  
AATCTCAACT CCCAAA 136

SEQ ID NO:7614

SEQUENCE LENGTH:47

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08861

SEQUENCE DESCRIPTION:

GATCCCGTCT CTACAAAAAA TAAAAAATAA TTAGTCGTGG TGCCAAA 47

SEQ ID NO:7615

SEQUENCE LENGTH:36

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08862

SEQUENCE DESCRIPTION:

GATCACTTTT TCAATATTAA ATNTTATTTA CATAAA 36

SEQ ID NO:7616

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08863

SEQUENCE DESCRIPTION:

GATCATCATG AAATNATAAG AGGGCTTAAG AATTTGTCCA TTTGCATTCTG GAAAAGAATG 60

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ACCAGCAAAA GGTTTACTAA TACCTCTCCC TTTGGGGATT TAATGTCTGG TGCTGCCGCC 120  
 TGAGTTTCAA GAATTAAAGC TGCAAGAGGA CTCCAGGAGC AAAAGAAACA CAATATAGAG 180  
 5 GGTGGAGTT GTTAGCAATT TCATTCAAAA TGCCAAGTGG AGAAGTCTGT TTTTAAATAC 240  
 ATTTTGTGT TATTTTAAA 260

SEQ ID NO:7617

SEQUENCE LENGTH:102

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08864

SEQUENCE DESCRIPTION:

15 GATCAACTTT AGTCACCAAC CCAAATGGAG GATTNTTGGC TTGTGGGNCC TTATATGCCT 60  
 ATAGNTGTGG ACATTGTCAT TACACAACTG GANTCTTNC TN 102

SEQ ID NO:7618

SEQUENCE LENGTH:228

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08865

SEQUENCE DESCRIPTION:

25 GATCAAGGGG CCTCTCAGAA CCATGTTCCC CAGCCAGGTG AGGACCATT TAACTGGGAC 60  
 CCAGGNCAAA ACCATGTGGG TGCACAAAGC CAGGCACTGC CAAGTGGAAC ATGAGGTTAT 120  
 TTCAAATCA TGGGAGCCAC CAGCAGGGAG AGGGCAGTAT GGAAAATCCC CTGGAGCCGG 180  
 TCAACTNTTT GCTCATGGCT AGTGAAATAA AGTTGTTTGA GTACTAAA 228

30 SEQ ID NO:7619

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS08866

SEQUENCE DESCRIPTION:

GATCTCTTAC TCCCCAGTT TGAATGGTAA ATTTGAATGG TAAATTCCCA TGAACATATA 60  
 TGGAAATATC TTTATCCTAC TTTNTCCAAT AAAGGCTGTT CTTAGCTTTT AAA 113

40 SEQ ID NO:7620

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS08867

SEQUENCE DESCRIPTION:

50 GATCACCTGN CAAATGTTTG AGGACGGAGC TGTGCAGTCA CATTATTGGG GATTCCACAG 60  
 CTGGTGCTGC AGGCCTTGCG CCTCCAACCA GGACTTTNTT CTTAATGCTC TCGACACTTA 120  
 GCTAAACACG ACTATATCCC GGCCCAGCAG GCCCCAGCGC CGTTAGTCTC CAGCTGACTC 180  
 TGTGGGTTGG TCTTAAAGCA AATTCTGTTT TGTGGACTGC CTGGCAATTT TTNAGCTAAC 240  
 TGTAATGATA AAAAGGGAGT NTTAATCTAT TCTGAATCN 279

SEQ ID NO:7621

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08868

SEQUENCE DESCRIPTION:

GATCAAGTTG TGGTGGATAA CGTGTTCCTCA AATTGCATCT TGTTGCTGAA ACTTCCTGGA 60  
CTTGAGAAGT TACTTCATCA TGTGACAGAG GAAAAAGGTA ATCCAGAAAT AGACAACAAG 120  
AAATATTACA AGTNCAGCAA AGNGAAGACA TTAAAGTGGC TGGNAANNNN GGTTAATCAA 180  
NCTGTGGCAG CATTAANN 198

SEQ ID NO:7622

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08869

SEQUENCE DESCRIPTION:

GATCCAGAAA GTAGCAATAT AGGACTTTAA GGGGTATGTA TTAGTGTAAT TAATATATGT 60  
GCAGTCTAGG CTAATCATNT TAATTAATAA CAAATAAGCA TACTTTTTTN CTTTAAAAAT 120  
ATGCCCTCAA AATGGTGGGG GATAAANTGT AAGATATTCT TTAGCTGNNN TTATTTNNCC 180  
GNCN 184

SEQ ID NO:7623

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08870

SEQUENCE DESCRIPTION:

GATCCTAAGT CTCTACAAA AGCTTTGAAT ACTGTGAAAA TTTTTACAT TCCATTTTCA 60  
TTGTGTTGTT TTTTAACTG CATTTTACCA GATGTTTTGN TGNTATCGCT TATGTTAATA 120  
GTAATTCCTG TACGTGTTCA TTTTATTTT ATGCTTTTTT AGCCATGTAT CAATATTCAC 180  
TTGACTAAAA TCACTCAATT AATCAATGNA AA 212

SEQ ID NO:7624

SEQUENCE LENGTH:373

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08871

SEQUENCE DESCRIPTION:

GATCGCAGAC CGCGCTGCCC ACGACGAGTC CCCGGGGAAC AACGTGGTTG GACATCAGCG 60  
TGCCGCCCAC CACGGACGGA CAGAAGTCTC TTTAAGAAAA TAGTTTAAAC AATTNGNTAA 120  
AAAATTTTCC GTCTTATTTT ATTTCTGTAA CAGTTGATAT CTGGCTGTCC TTTTATAAT 180  
GCAGAGTGAG AACTTTCCCT ACCGTGTTTG ATAAATGTNG TCCAGGTTCT ATTGCCAAGA 240  
ATGTGTTGTC CAAAATGCCG TTTAGTTTTT AAAGATGGAA CTCCACCCTT TTGCTTGGTT 300



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TTANGTATGT ATGGAATGTT TATGGATAGG GACATAGTAG TAGCGGTGGT CAGACCATGG 360  
GAANTGGGTG GNN 373

5 SEQ ID NO:7625  
SEQUENCE LENGTH:74  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS08872  
SEQUENCE DESCRIPTION:  
GATCCTACAA GCATGTCTGC TGTAAGTCTA TGTATGTTTT CTGTAAAATC ACATACCTAT 60  
AAAATAAAAA GAAA 74

15 SEQ ID NO:7626  
SEQUENCE LENGTH:53  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS08873  
SEQUENCE DESCRIPTION:  
GATCGTGAAC ACTGCATTCC AGCCTGGGTG ACAGAGCCNG ACCCTGCCTC AAA 53

25 SEQ ID NO:7627  
SEQUENCE LENGTH:379  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
30 CLONE:HUMGS08874  
SEQUENCE DESCRIPTION:  
GATCTACCCA CCTTGGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCAC CGCGCCTGGC 60  
CCTCTGCAGT TGTTTAATAA GGCACAGAAT ACCTGTAGCA TAGGTCAGCC TTACGATGTC 120  
CATGAATTAC ATATTCAGAC GTTTTAGAGC CTGATACATT TTGGAANCGA AAAACAACTT 180  
CTACACCTAT TCTACAGTCC GCATTTAAAA CAATAAATTC CTCTATTAAA AACGTAAAGC 240  
35 CGGGTTTGCT TCGTGCCAC AGGGGGTATA TCCAGGAAGG TTATTATGAA GCTGTCAAAT 300  
CAAGATGATG GNAATAAGGC AGTTTGAACG GACAGTCTTC CCACAGTCAG GCCATTTTGT 360  
CTGATTTGGT TTAGGATTN 379

40 SEQ ID NO:7628  
SEQUENCE LENGTH:212  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
45 CLONE:HUMGS08875  
SEQUENCE DESCRIPTION:  
GATCGGGCGC TGTGCAGTGT GGTGAGCATG GTGAAGAAAG TCATTCCTC GGTGGGCAGT 60  
ATTCCTCTTT ATCTCTCATT AACTGGAAA TGTATTCTTCT GCTGTATCAT CCGTGCTCAA 120  
CGTTTTAGTC TGTCAGGCTC ACCTTCTCTC TGGAAAGAAT TTGCTTAACT TGACATTCCA 180  
50 TGTGCCGCTA ATAAAATATA TTTTGAAAGA AA 212

55

SEQ ID NO:7629

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08876

SEQUENCE DESCRIPTION:

GATCAGAANT AATTACCATT CCCNGTGTTT TGCTGTAGGA CCTTCAGGTC TATGTTCTAA 60  
GTGGGGNTTA TGAAACTGGT AATAGAAAAT AATGGAGAGC AGTTAAAGAG TTAATATACA 120  
TTATTAATAT GNGTGTCTCT TACAGGCACA CAAAGCCTGT AGACTCAACA AATTTACTCC 180  
TGAAGTTTTC CAAATTTGCA AAATCTGCAA TTTNTGTGCC ACATAAAGCT NTCCAGAAAT 240  
TGAAAANCNG TAAANCACCG GGTCTCANTT TNTTCCTGCA TTTCATGAT ACCTTAANTT 300  
ACATAGNTTA NCTTCTTTAN AGCACTACCT TTTTNGCTGT TGNTATTAAAN 350

SEQ ID NO:7630

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08877

SEQUENCE DESCRIPTION:

GATCTCACA CTGCACTCCA GCCTGGTGAC AGAGCAAGAC TCCATCAAAA ATAAACAAAT 60  
AAAACAAACA AACAAA 76

SEQ ID NO:7631

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08878

SEQUENCE DESCRIPTION:

GATCAAAGTC TGCTTCATTG TCTTGTTCCC CATTTTAATG GCAATGTTAG GTATAATNTT 60  
TGCTTTTATT AAGTATAATN TTTGCTTTTG TTGGTAGAGT TTTACGATTT TACATCAGAA 120  
GTACCTGTTT AACTTAATTG CCACGTTTAA GCATCAATTA AAATATTTTC ATTGAACTCA 180  
TGAAA 185

SEQ ID NO:7632

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08879

SEQUENCE DESCRIPTION:

GATCTTTTAG GAATTAACT TGCAATNAA ATGAAATATG TTGGGACTTT GGCATAATTT 60  
GAATATAGCA TTGTGTGAGT TGTGATTGTN TCTTCCTAAT TGTGCTGTAA TAACCTGTGT 120  
ATGAGAATAA AATGATTTC ACCATCAAA 149

SEQ ID NO:7633

SEQUENCE LENGTH:193

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08880

SEQUENCE DESCRIPTION:

GATCTCACTC CATGATTACT GTGTAAAATA TTTTGGCACT GTTGTGAAGT ATTTTAACT 60  
TTTTTCTGTA CATAACTGTG TTCTCAGAGC TGAATGTTA TATCTTTTGC TGTGCAAAAG 120  
AAACANNNA AATGTTGTTC AGTTGTATAT ACAGAAATGT GTATAAAACA TTTTGTATT 180  
TTTNAAGT AAA 193

SEQ ID NO:7634

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08881

SEQUENCE DESCRIPTION:

GATCAAGAAT TTTGTAGAGT GGACAGTCAT TACATATGTT ATAACCTATC CTTTAAAAAC 60  
TATTTTAAAC TTTATCCTTT CAGCTTTACT TAGTGCGATG TTTTAGAAGC AGTCTTCAA 120  
GAATAAAACA CTAACCATGC ATGTGAAA 148

SEQ ID NO:7635

SEQUENCE LENGTH:376

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08882

SEQUENCE DESCRIPTION:

GATCCATTTT TGTGCTCCTNT AGCCTAGTAT GTCTGAACTT CCATTCTTGT TATATATTTA 60  
AACTTTCCCT CTATATTATA GGNNTTNGTGG CNNCCACGGT CAGGTGTAGA GGAAGCTGCC 120  
CCTTGCAAG CTGTACTGTA ATATTTTCT TTTATAAATA TTTTACAGG ACTGATTGTA 180  
CACAGGGCTT GTAATAAAAT TTTAACAAGT TGCTGTGAAA CAACTATGGG GAATCTCCAT 240  
TGAAGGCTAC TTCATGGGCA CCTGAAAGTG GAGTGTTATA GCTATGACTT TCTATTTCTT 300  
GTTTCCTAAG TAAATTAAAC CTAATTTTCA CCCTTTCATT CTGTTTCAGC CTCCTGTNTA 360  
AGGAAGTACC GTTTGN 376

SEQ ID NO:7636

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08883

SEQUENCE DESCRIPTION:

GATCCCATTC ATTGTCCCCT TTGGGGTATT TCCAATACTT GAATGGCAGA TTGGAGTTTT 60  
TCAGAGTATG TGTTCATCT GCTAGTCTTT CTCTCCTTCA TAGCTTTTCT TTTCTGGAC 120  
TTGCTCCTTT TGAGTTGCTT TTGCGTTTCT CATGCCTAGG CAAGTGTAAT AGAAATTATG 180  
TAGCTCCTTA TGTGGGCAA GGAGCTCTAT ATAGTTTCAC TTTGTATACA AGTTAGGNCC 240  
AGCTGTTGTT ACATGTAATA TNNTGGTTCA GAAGTTGAG 279

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SEQ ID NO:7637

SEQUENCE LENGTH:373

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08884

SEQUENCE DESCRIPTION:

GATCTCTGAT TGCATCTATG TGGATTCTTT TTGGAGGTTA TGTTGCTAAA GAAAAAGACA 60  
TAGTATACCC TGGAATTGCT GTATTTTNC AGAATGCCTT CATCTTTTTT GGAGGGCTGG 120  
TTTTTAAGTT TGGCCGCACT GAAGACTTAT GGCAGTGAAC ACATCTGATT TCCCACAGCA 180  
CAACAGCCCT GCATGGGTTT GTTTGTTTTT TTAGTGCTCA CTCCCAACCT TTTGTAATGC 240  
CATTNCTAA ACTTATTTCT GAGTGTAGTC TCAGCTTAAA GTTGTGTAAT ACTAAAATCA 300  
CGAGAACACC TAAACANCAN CCAAAAATCT ATTGTGGTAT GCACTTGATT AACTTATAAN 360  
ATGTTAGGTG GTN 373

SEQ ID NO:7638

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08885

SEQUENCE DESCRIPTION:

GATCACACCA CTGGCACTCC AGCCTGGGCG ACAGAGTGAG ACTCCGTCTC AAA 53

SEQ ID NO:7639

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08886

SEQUENCE DESCRIPTION:

GATCCGAACCT GGACTCACAT CCTGTATGGT GGATGGACTG TATATTGAGG GTTCCATTCT 60  
TCGCGCAGTT TAGACATCTC TGTTTTGATT CTTTGTGTGT GTTTTTATTT TAAAAGGCAC 120  
AAACTCTAGA TATTAGTTGA ATGTTGAGGC TTAACTTTT TCGGTGTCTT TCTACAACTG 180  
TGTTCTGTGA CTCAATTGTG TCGTGTTAAT ATCAGTACAG ACTGTCTCCT CTACGTGACC 240  
GTATAATGTT TTTCTCTTCT TGTAGTCTCT ATGGCGTGTC TTTATGGTGT AATAAGGTTT 300  
TCACGGGTTC AATCTTTTGT GTTTAGGGNN NNCACGGTTC AGACCAAATG GTATATAATT 360  
TTN 363

SEQ ID NO:7640

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08887

SEQUENCE DESCRIPTION:

GATCTGGTTC TGAGGAGGAC ACACCTGGCA TCGGATGACC TTTATAAATT ATCTATGAAA 60  
ATGCCAAAAG CTCTCAAGCC AAAGAAGAAG AAAAATATTT CCCATGATAC TTTTGGTACA 120  
ACTTATGGAA GGATTCATAT GCAGAAGCAA GACCTAAGCA AACTACAAAC CAGGAAAATG 180

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AAGGGGTTGA AGAAGCGACC TGCAGAAAGG ATAACAGANG ACCACGNNGA AAAAGTCAAA 240  
AAGAATTAAA AAAAATTGAT GGAACCTAAA 270

5 SEQ ID NO:7641  
SEQUENCE LENGTH:336  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS08888  
SEQUENCE DESCRIPTION:  
GATCTCTGAA AAGACGTTAT CACCTTAAAG CTCAAATTCT TTGGGATGGT TTAACTTAA 60  
GTCCATTAAAC AATTCAGGTT TCTAACGAGA CCCATCCTAA AATTCTGTTT CTAGATTTTA 120  
AATGTCAAGT TCCCAAGTTC CCCCTGCTGG TTCTAATATT AACAGAACTG CAGTCTTCTG 180  
15 CTAGCCAATA GCATTACCT GATGGCAGCT AGTTATGCAA GCTTCAGGAG AATTGAACA 240  
ATAACAAGAA TAGGGTAAGC TGGGNTAGAA AGGCCACCTC TTCACTCTCT ATAGANTATA 300  
GTAACCTTTA TGAAACGGGG CCNTNTAGTT TGGGTN 336

20 SEQ ID NO:7642  
SEQUENCE LENGTH:331  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08889  
25 SEQUENCE DESCRIPTION:  
GATCCATTTT AGATACTTGT GGCAGCAAAC AAAGCAGTTC ACCTCTACAA ACTGGGAAAA 60  
ATGAAGACAA GAACTCTATC TACTGAAATN ATTTTCANCC TTTCCCCAAA TAACAATATT 120  
TCAGAGGCTT TGAAAAAATT TGGTATCTCA GCAAATGACA CTTCAATTCT AATTGTTTAC 180  
30 ATTGAAGAGG GAGAAAAACA AATAANTCAA GANTACCTAA TATCTCAAGT AGAAGGTCAT 240  
CAGGTTTCTC TGAAAAANTCT TCCTGAAATA ATGATTATTA CAGANGTCAA ANAGGTATAT 300  
AANCTCTCTT CACAGGNGGN ANGTATCGGA N 331

35 SEQ ID NO:7643  
SEQUENCE LENGTH:327  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08890  
40 SEQUENCE DESCRIPTION:  
GATCCACTGT CCGGCAGAGG AAAAATGCCA GCTGTGGGAC AAGGAGTGCA GGCCGCACAA 60  
CCTCGGCAGG CACCGGGGGG ATGTGGCGAT TCTACACAGA AGATTCACCT GGGCTCAAAG 120  
TTGGCCCTGT TCCAGTATTG GTTATGAGTC TTCTGTTTAT CGCTTCTGTA TTTATGTTGC 180  
ACATTTGGGG CAAGTACACT CGTTCGTAGA TTCAGTTACA TCCATCTGTC ATCTGAAGAA 240  
45 GGAGGAAAAA ACCCAACATT TCTTGGACCA AAAGTATAGT GACTATCTGT TCATGAGAGA 300  
AATTTTCTGT NAGCTTGCTG TTTTGAN 327

50 SEQ ID NO:7644  
SEQUENCE LENGTH:287  
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS08891

SEQUENCE DESCRIPTION:

5 GATCAAGATG AAGTTCAGCT AGAAGTCATA CCACCCTCAG GAATCAGCTA AGTAATTATN 60  
 ACTTGATTCT TTTAGCAAAT CAATGCACGT NATCCTACTT AATCCTTAAA TAAGTTTAGA 120  
 TTTAACTAAC CCAAAGTCCA GGAGGATGTT CTTACAAAAN TAGCTATATC ANGGGCTGGC 180  
 ACCTAGACAT TAANCTGTAA TTNGANAATA AGCAACATGT TGCATAACTN GTTGGAATAA 240  
 10 TTCCTGTNC TGTTTAACAC TTGTCATAAN TTAGCAGNGT AANNNTN 287

SEQ ID NO:7645

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08892

SEQUENCE DESCRIPTION:

20 GATCTACCCA ATTAGAAATG CAACTTGAGA AACCCAAACC TGTAACCA GTGACGTTTT 60  
 CCACAGGCAT CAAAATGGGT CAACATATTT NACTGGCACC TATTCACAAG CTTGAAGAAG 120  
 CTCTGTATGA ATACCAGCCA CTGCAGATAG AGACATATGG ACCACATGTN CCTGAGCTTG 180  
 AGATGCTAGG AAGACTTGGG TATTTAANCC ATGTCAGAGC TGCCTNACCA CAGGACCTTG 240  
 CTGGAGGCTA TACTTCTNCT CTTGCTTGTC ACAGNGCACT ACAGGATGCA TTCNGTGGGC 300  
 TTTTCTGGCA GCCCAGTTAA CCATTTN 327

25 SEQ ID NO:7646

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS08893

SEQUENCE DESCRIPTION:

35 GATCTGGCTG CTCATGAAGA CAAAGTTCTG AGTGTAGACT GGACAGACAC AGGGCTACTT 60  
 CTGAGTGGAG GAGCAGACAA TAAATTGTAT TCCTACAGAT ATTACCTAC CACTTCCCAT 120  
 GTTGGGGCAT GAAAGTNAAC AATAATTTGA CTATAGAGAT TATTTCTGTA AATGAAATTG 180  
 GTAGAGAACC ATGAAATTAC ATAGATGCAG ATGCAGAAAG CAGCCTTTTG AAGTTTATAT 240  
 AATGTTTTCA CCCTTCATAA CAGCTAACGT ATCACTGGGG CTTATTTTGT ATTTTATAAT 300  
 AAGNTAGGGT TGTGTTTTNT NAAATNCGN 329

40 SEQ ID NO:7647

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS08894

SEQUENCE DESCRIPTION:

GATCTTCAAG TGAACATCTC TTGCCATCAC CTAGCTGCCT GCACCTGCCC TTCAGGGAGA 60  
 TGGGGGTCAT TAAAGGAAAT CTGGGACAAC AAA 93

50 SEQ ID NO:7648

55

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08895

SEQUENCE DESCRIPTION:

GATCTGCATG CATTGCTTGC ATTTTNTTGG TATCTGAATG TTGGTTCCTT GTTCCAGGAA 60  
 TTCAACATTA NTTTCCAAAA GTATCATGGG ACTTGTGACA ATACANGTCA TGAATCTATG 120  
 TATAAAATTT ATCGGCCTTT CTCATTACC TGCTCTAGTA TTATTGTATT GTGTGTGCGT 180  
 GCGTGTGTGA TGTGAGGCTG CCACGTAAAA CTTCAGAGGA AAATCTTAAA NGCAGGCCAT 240  
 CCTTTTNGC ATGCTCTATT CTAAGTAGGA ATGTTCAATG TAN 283

SEQ ID NO:7649

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08896

SEQUENCE DESCRIPTION:

GATCACCTGT AGGTCAATAG TTCGAGACCA GCCTGGCCAA CAAGGTGAAN CCCATCTNTA 60  
 CTAATAATAC AAAAAATTAG CCAGGTGTGG TGGTGTGCAC CTGTAGTCCC AGCTATTTGG 120  
 GAGGCTGAGG TGGGAGAATC ACTTGAACCT GGGAGGCGGA GGTTCAGTG AGCTGAAATC 180  
 GCGTACCACA CTCCAGCCTG GGTGACAGAG CGAGACTGTG TTTCAAAGAA AAAAAAACC 240  
 AGGCAGCCTT TTGCTTGGTT GGAATCTGAT TTTCTN 276

SEQ ID NO:7650

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08897

SEQUENCE DESCRIPTION:

GATCTAAATA TTCAGGTTTT AAGCCTGCTG CAAACTTTTA AAATATTATG ATAGNTTCTG 60  
 TACTACATGT GGGAAACAAG CAAGAACTAA ATAATCAAAT GTTGTCAACC AAAAGTAATA 120  
 GTTGGGTATT GGAGATTTTT TAAAAATGTT TTTATGTTAT TNGCTATTTG GAGTTAAATA 180  
 AA 182

SEQ ID NO:7651

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08898

SEQUENCE DESCRIPTION:

GATCTNAGAA AACGTTTAAT ATCAGATTTN TTTATTTTN CCAACACAAC TGAATCAGTT 60  
 TTCTTAAATA AAAGTTTATT GTCTACTGTT AAA 93

SEQ ID NO:7652

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08899

SEQUENCE DESCRIPTION:

GATCTAAAGT TAGTTGCCTT TGCCTGTAAA ACATGTGATT TGCAAATTAT TATTTTNNTT 60  
TTTTTAAACA AATGGAAGTA AATTTGTTTC ACGTAAATCT TAATTTTCAA CCTTTCTGGA 120  
TACCTTAATT GTAACGTGCA GTTTGCACTG GTCGGTATAT GGAAACACAT TGCTCTACCC 180  
TGCTACTTAG TTGNTTTTAA AGTGAATTTN CAGTGATGNG AAATTTGTGA AANNTATATT 240  
GTATTTCTTT TGATGTTTCA AAAGGTTGCC TATGN 275

SEQ ID NO:7653

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08900

SEQUENCE DESCRIPTION:

GATCTTTAGG TGTGAACTG GGAATATGCT CTGCAACACC CAGGATTAGG ATAGAGATGG 60  
ATTCATTTT ATATGGGCTA GCATATTATT ATTAAAGACC ATTCAGGAG TGGGACTGTG 120  
AAAGGAGGTG CTCTGTTATC TGGTCCAAGA GTCCTCTGG GAATTAATCC TGGCTGGTTC 180  
TGATGAGCTG GCAAGGNGCA GNGGATTGCA GTCTTTAAGT AGAAAATTNG AACCCCATCC 240  
ATATAACACG TGNACGTGCA TTAAATAGCT TGAATTGTN 279

SEQ ID NO:7654

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08901

SEQUENCE DESCRIPTION:

GATCAAGACC AGAAAGAAAT TATTGATACC AATGGAGCTG GAGATGCATT TTTTGGAGGT 60  
TTTCTGTCTC AACTGGTCTC TGACAAGCCT CTGNCTGAAT GTNTCCGTGC TGGCCACTAT 120  
GCAGCAAGCA TCATAATTAG ACGGACTGGC TGCACCTTTC CTGAGAAGCC AGACTTCCAC 180  
TGATGGAAGA GCTGAAAACA CAAGCCCAGG AGTGCAGACA CTGCCCTAAT TGCTTCCTGA 240  
GAATTCCCAT ATTAATAAAG ANGN 264

SEQ ID NO:7655

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08902

SEQUENCE DESCRIPTION:

GATCTTTTAG GAAAAAAAT AAATATTTT AACATTAAAG CAGTCACTTT GGTTTATCAA 60  
A 61

SEQ ID NO:7656

SEQUENCE LENGTH:66



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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08903

SEQUENCE DESCRIPTION:

GATCTGTTTG CTTAGCTGTC AACAAAAAGA AAACCTGAAG GAGCATTG AAGTCAATTT 60  
GAGGTN 66

SEQ ID NO:7657

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08904

SEQUENCE DESCRIPTION:

GATCTNACTA AGCTTTCTTA GGAAGGGAAA GCATCTGGCA AGGAGTAAAA TGTCTGTTTC 60  
CAACAATTGT CCCTGTTCCC ACTACTTTTT AAAAATGTCC TTAGTAAAAA GTGTATATGA 120  
GGCAAGATTA TATTGAAAAA NTGAATATAA GAAAAAATA TTATGTTAGA GAGNAACGTA 180  
TTCAGCATTG TTNTCAAAAT CACAACTGT TAGGNGACTC TGACATCAGG TTTGTTCTCC 240  
ATATGCAGCA AN 252

SEQ ID NO:7658

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08905

SEQUENCE DESCRIPTION:

GATCTACATG GATGTTCTGT TCTCTGAAC GTCTGGATGA ACCGGTCAAC GGCACATCATC 60  
ATACCTTAGT TTTTAAATCT GCATTGTGGT CATAATCTGT TATTTAATTA ATTTCTCGTA 120  
TTTTTAATAA AAACTTTGCC TATATATTTT AAA 153

SEQ ID NO:7659

SEQUENCE LENGTH:23

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08906

SEQUENCE DESCRIPTION:

GATCCCAAAA GTAGCAAGAG AAA 23

SEQ ID NO:7660

SEQUENCE LENGTH:280

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08908

SEQUENCE DESCRIPTION:

GATCAATTGC AGAATGATAC AGATAGTACA ATGACTTTTT TGTAAATTTG AATTAAAAAGT 60  
TTCCTCATAA AACTCAGTAC TATCTATTGG TAATGGATGC ATATATGTAT GTACATGTTT 120

EP 0 679 716 A1

TTNAAACGGA TTGGAAGGAT ACAGACCAAA CTCTTGATAG TGGTCACCTG TGAAGAGTGG 180  
AGAAGGGGAAA ATNATGAGTG TGGGAGGTGG GATGGGTATT GGTAAANGGG GACTTCAGCT 240  
TTTTATATAA ACATCCACTT CTCTTTCAAA AAGNCTTCAN 280

SEQ ID NO:7661

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08909

SEQUENCE DESCRIPTION:

GATCATTTTA AAAAAGTAA TCTATATNAT NTTAACTTC AGAAGGCATC ATTTATAAGA 60  
CAGTATGGCA GTTAATTATA AAATNATTTT GATGAATTAT GATACAATCT ACATAATAAA 120  
GAATNCTTTT GATTAAA 137

SEQ ID NO:7662

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08910

SEQUENCE DESCRIPTION:

GATCCTAAAA CTGTCTCTCA CATTATATAG TAGATGTTTG TTTATAATGT TTACAAAACA 60  
TTTTGGTGAA TTTCTCAAT GTTTTATAAA TGTACATTTT TTAAGTCCTT AAGCTGACTC 120  
TTAGCCATCA TGTAGCTTAA GGAGTCTGAA ATCTGCCATT AAAACTGCAC CTTTAAGCCA 180  
GGTGTGGTAG CATGTGCCTA TAGTCCCAGC TACTTGGGAG GTGGAGGTGG GAGGATTATA 240  
AATAGAGACT TTCCTTAAGA CTTTAAAAAT GTATTGNNAA ACTATTTTTT ATTAAATACT 300  
TTGTN 305

SEQ ID NO:7663

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08912

SEQUENCE DESCRIPTION:

GATCCTAACC TTGAAGTATG CTTTGAACCTT ATTAACATGG CCATTATAAG AATAAAATAT 60  
GTAGTTGTGT CTTAATGGAA TTAATAAATG TCATTTCACT AAA 103

SEQ ID NO:7664

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08913

SEQUENCE DESCRIPTION:

GATCAAGGAA TAAAGAATCA TTAAAGAATG GGGTGTGGG GGTTCCTTA ATTATCAGTG 60  
ACACATTAAT TTTTTCTT AGAGCTTCAT ACAATAACA CATTGCAGAA AGTTTTAGAA 120  
AGTTTTGCAG GACCTTAAAT TTTCTGCCCT GACACTTTTC GTCATGTTTC CTGTATTCCN 180

GGTTATTGTA GCGCATGCTT TTCAGGTAGT N

211

SEQ ID NO:7665

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08914

SEQUENCE DESCRIPTION:

GATCTTAAAT TTTGTGATAT GGAGCCCTGT AATNTTTTTC TTATATAAAA ATGGGTATCT 60  
 ATATTCATAA A 71

SEQ ID NO:7666

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08915

SEQUENCE DESCRIPTION:

GATCCCAGCT CATGGCACAG CCGTTTGTAT CCTCGGAAGA ACGGAAGGAA CGATGGGAAC 60  
 AGGGCCAGGC TGATTATATG GGAGCAGATT CCTTTGACAA CATCAAGAGG AAACCTTGACA 120  
 CTTACCTCCA GTAGAAACAC TGCATTTTTC TGTGAACACA TCCAATTAC AAGCCTTGTT 180  
 TCTGATACTT AGTATCTAGA GCTGGGTTGA GAAAAGTCTG TTACAGTTGC TAGAGGTTTT 240  
 CATTAAANCT TATCAGGNGG GCGGCTTTT TAGGATAAGA GGTGAGAACT GGGCAAAAGT 300  
 TGTGAAGCAG CAATTCTGTT ATATGGNCAG TGTCTGCTT TTN 344

SEQ ID NO:7667

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08916

SEQUENCE DESCRIPTION:

GATCACGACT GCTGCACTCC AGCCTGGGTG ACAGNGCGAG ACTCCATCTA AAAAAACAAA 60  
 AAGCAAAAAA ACCCACAAAT ACCTCATGGA GATGAACTGT AATAATTGCT TAAAGTTCCA 120  
 TTTAATTATG TTAACCTCTAA TCTAGCAAAA ACATAGATGT ACTTAAAAAT AAATCATGGA 180  
 TAATGATTTT TTAACCTAAA 200

SEQ ID NO:7668

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08917

SEQUENCE DESCRIPTION:

GATCTCATTT TCAAGTNTGA GTCTGACCAA CCATGGAAAA TATTCGACAT GAATTAATGT 60  
 AGAGAACTAT AAAGCATTTA TGACAGCTCC AAGAAAAGTC ATCTACTCTA TGCAGGAGAT 120  
 ATGTTTAGAG ACCTCTCAGA AAAACTTGCC TGGTTTGAGG GTACACAGTA CCATTTTAAT 180  
 CTTCTGAAAA TATCTGTATT CCTGCTCTGG GGNTGCTGTC ACTGTCAATC TGCTATATTT 240

TTCACATATCC TATTAAAATA TTACTGTCTC CTTTAAA

277

SEQ ID NO:7669

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08919

SEQUENCE DESCRIPTION:

GATCTTCTAC ATTTATATTT TTAATCTTCT GTTAAATACA CTTTCCGATA TTGCCTTGCC 60  
TTTTGAGCTC TTGCTACAGT CGCCTTTGCT ACTGCTTTAA GAGAATTTAC AGGTATTGAT 120  
AAAGAACAAG ACTGTTTTAT TAAAAGNTTT ATTCAACTTG AAA 163

SEQ ID NO:7670

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08920

SEQUENCE DESCRIPTION:

GATCCAAATC TGGTTCAAAC ATTCAAAAC TCAAAGATAA TTCATCTTTC GCTAATGCTT 60  
GTGGTTCTGT NGTTCCCTTG AAAAAAATA AAAACCCGAC CCAGCAGCAA A 111

SEQ ID NO:7671

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08921

SEQUENCE DESCRIPTION:

GATCTGTCAC TGTCCCCGT CACCCTCAGA TGGGACCGTC TAGTTGTAGG AAAACAAGCT 60  
CAGGGCTCCC ACTGATTCTA CATTTTGGTG AGTTGTATAA TTGTTATGTA TTGCAATGTA 120  
ATAATAATAG AAATAAAGTG TACGATAAAT GCAAA 155

SEQ ID NO:7672

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08922

SEQUENCE DESCRIPTION:

GATCTGGAGA GGTGTTTGT GAAAGTGGAG AAGATTCACG AAAAGGTCTA AATGAATTGC 60  
GTGTGCAGGG CGCGGATTTA AAGTCCAATT TCTCATGACC AAAAAATGTG TGGTTTTTTC 120  
CCATGTGTCC CCTACCCCC AATTCTTGT CCCCTCTTAA AGAGCAGTTG TCACCACCTG 180  
AACACCAAGG CATTGTATTT TCATGCCAG TTAACCTATT TACAATATTT AAGTTCAA 239

SEQ ID NO:7673

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS08923

SEQUENCE DESCRIPTION:

5 GATCCTTTCA TTAATCAGAA CAGCAGCTTA TNAACTGCTT CATTTTCCAA AAGTGTTTCC 60  
CAAAAATCAG AAACCTAAAC ACCCAACAAC AGGAATTATT GCCATCACAT TGGCGTTTTA 120  
CATATGTCAC GAAGTTCACC TAGCTGGTTT TAAATACAAC TTTCTGANC TCAAGAGTCC 180  
TTTGCACTAC TATGGGAATG CCACCATGTC TTTGATGANT AAGAACGCGT ATCACAATGT 240  
10 GACTGCAGAG CAGCTCTTTT TGAAGGACAT TATAGAAAAA ANACCTCGTA ATCAACTTGA 300  
CTCANGATTG ACTCTACAGA CTCGGAN 327

SEQ ID NO:7674

SEQUENCE LENGTH:377

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08924

SEQUENCE DESCRIPTION:

20 GATCTCCNT AATTGGGAAT GAANGATTTC ACAGACTAGA GTCTCCGATG CTGGTCATGA 60  
TGTCAAAAC AAGTTCTGAC TCATTTAGGG AACTGGATAC TTGGGTCTCC AGAAGGGCCA 120  
ATGGGAGGGC CATAATTCTG TTTATTTTCA AATTGTCTTG TTTTCACCTT GTTAGAATGA 180  
NCTNTGGAAG CCCAGCCAGG GACAATGCAC CTTACAGAG ATTCTGCACT AATCTGAGTG 240  
AAGGTCTAAG GTTTGGAATC TCCCCCTCAT GGAGAGAAGC TTTGTATGGC TGTCATGCTT 300  
25 AGACAGTGAT TCCTGCAACT TGACCTTCAG GCTGGGAGAG GTNGAGAGCC ATGCCTGTTT 360  
CTCCTTNCTT TGCTATN 377

SEQ ID NO:7675

SEQUENCE LENGTH:350

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08925

SEQUENCE DESCRIPTION:

35 GATCTGCTTC CCGCAAGACT CACAGCTGTT GGCAGGAGAC CTCAGTTTGT TGCCACATGT 60  
TCCCCTCCAG AGGGCCTCTC ACAACATGGC AGTTATTTGT CCCCAGAGCA AGCAACACCG 120  
GAGGGCAAGG AAGAAGCCAT GATGTTTTTT GTAACCTAGC CTCTGAAAGT GTCATACCAA 180  
TTCTGTATTT TGTTGGTCAC ACAGACCANG TCAACTACAA CGTGGGAGAC TCCTACACAA 240  
GGCATGAATT CTAGGAGGTG GGCATTTTTA AGTGTCTATCT GGAAGGAGGC TGTCACAACC 300  
40 TGGAAGTTAA AAGCATTGAT ATTCTGAAAT ACAGCGTGTA TTACCATGGN 350

SEQ ID NO:7676

SEQUENCE LENGTH:335

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08926

SEQUENCE DESCRIPTION:

50 GATCTAGAGG AGGATTGCA GGAAGAGCTC GTGGAAGAGG TGGTGGCCCC AGTCAAAACT 60  
GGAACCAGGG ATATAGTAAC TATTGGAATC AAGGCTATGG CAACTATGGA TATAACAGCC 120

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5 AAGGTTACGG TGGTTATGGA GGATATGACT ACACTGGTTA CAACAACACTAC TATGGATATG 180  
GTGATTATAG CAACCAGCAG AGTGGTTATG GGAAGGTATC CAGGCGAGGT GGTCATCAAA 240  
ATAGCTACAA ACCATACTAA NTTATTCCAT TTGCAACTTA TCCCAACAG GTGGTGAAGC 300  
AGTATTTTCC AATTTGAAGA TTCATTTGAG GGNAN 335

10 SEQ ID NO:7677  
SEQUENCE LENGTH:295  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08927  
SEQUENCE DESCRIPTION:  
15 GATCCAAATT TGAAGCTCCA AGGATAGGAA AAAGCTTACT TGTGCCTGTC CTAGACAAGT 60  
ACTAGAGTTT ATATTGAAAT CAAAACCTTCT AAAAATAAAA ATCAGTAAGA TTAATTTTAC 120  
TCATTTTTCT AACACGAGTC AGTATGCTTG ANGTTTTCAT TGTATTTGAT GTCATGTAAA 180  
TTTACTGTAA AAAATAAGAA AANNTTTTAA AATGCTTTAT TGATTAANTT TAGGGTTGCT 240  
TTTCAGTATA CTCAGTAACT CCGAAGTCAG TGTTAACAGT ACTGAGCTTA CATAN 295

20 SEQ ID NO:7678  
SEQUENCE LENGTH:136  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
25 CLONE:HUMGS08928  
SEQUENCE DESCRIPTION:  
GATCTTTTGT TAACTTTTAA ATGGCCTGAG TCCATAGAAA CTGCATCCTG AGAGGTTGCT 60  
CGGCTAGAAA GCGGAAAACC GCTTCACATG AGTGCTCTAC TTTGTAATGA AAATAAACAC 120  
TATTAATACA GGCAAA 136

30 SEQ ID NO:7679  
SEQUENCE LENGTH:310  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
35 CLONE:HUMGS08929  
SEQUENCE DESCRIPTION:  
GATCTGGGAA CGGAAGATGA ATGAATGGAA GATGAATGGT TTCTCTCCCA GTTTTCTCTG 60  
40 AGGCAAACAT AATTATACCT NCTCCTTTGT TCTGGGAGGT TTTTCTCTTC TCATCTCCCC 120  
TCCATTACAC AAAACAGAGT TGGGTCTATA TTNACCCGG CTGGCTCTTG GAACTGCAGG 180  
GAATCCTGGC TGTTTTTATT TTTAAAAAAT TATGAGATTA NCTACCAAAC TTGAGATGTA 240  
AGTTGTGGGT TAGCTCTCGG ATTCTGCTAG ATAACTGGA ACAAAGCATT AACTTCTTTG 300  
AGAGCTTCCN 310

45 SEQ ID NO:7680  
SEQUENCE LENGTH:177  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
50 CLONE:HUMGS08930

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# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCTGCCAT GTAGGAATGA GACAAATACA GTTTGCTTAT GAAAGGAAAG TGGCATACTT 60  
TTAAATTGGT CTACACAGAA AAGTAAAAGT AACTATTCA TTAAATAAG ATTCATTATC 120  
TAATAAATAT TGAGGGAATA TTTTCCTAA ATAAAAATTT TTCTGACTGC TAACAAA 177

SEQ ID NO:7681

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08931

## SEQUENCE DESCRIPTION:

GATCTAAGCT TTCTTTAATA TAAAAAAAT NATACTTCTC TGAAGTGTTC AATAGAGCAA 60  
TAATTAAATA CATCTTCTGA TAAA 84

SEQ ID NO:7682

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08932

## SEQUENCE DESCRIPTION:

GATCTGTTGG GAAAGATAAG AAAGCTATTC AGGCATCAAT TAGACGTAAT AAGGAAACCA 60  
ACACCGTTTT GGCCAGATTG AATAGCGAAT TGCAGCAACA ATTAAAGGAT GTTCTTGAGG 120  
AGAGAATTC CCTGGAAGTT CAACTGGAAC AACTTCGACC ATTCTNTCAC CTATAAGCCA 180  
ATTGCCGTTA ACTGTGAACA TACTTGTTTT TAAGTGTTTT TGGGTTCAAA GCCAATTTGG 240  
AGACCTAGAC ATTCAGCTCA CTGCTTAACT CANTATTAA TTTN 285

SEQ ID NO:7683

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08933

## SEQUENCE DESCRIPTION:

GATCTCAATT CTGTTTCCTC TCACATGATT ACTTGATAGC TAAGCATCTG ATTGGTTTAC 60  
TGCTTTACCA CTGAGCTGAA ATGCCGTGTT TTCCATTTAT TAAATCACA CATGGCTCCT 120  
GTTTTNTCA CTCAGCACTT TTTCTCCATA TTCTCAAGA CGATTGTGAG TATGGTACGT 180  
AACAGGAATT ACATCTGGTA AGTTGTATAG TTTTGTGTAG GAACTCTATA TTCATAGCAT 240  
ATTTGTGGAA ATGATACCTA TGGAGGTTTC TCACACTGGT GTGTCATTAT ACATTAATTG 300  
TACAATATGC ATN 313

SEQ ID NO:7684

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08934

## SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCAGTAAT GGCAAGAGCC TTTNATTCTC GAATGTTTAA AGCCTAGGAG TTCTACAAAA 60  
TTGGNTTCTT TCTACAAGAN TCCCAAAATG GAATGCCTAA AGAGGTNTNN 110

5 SEQ ID NO:7685  
SEQUENCE LENGTH:132  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08935

10 SEQUENCE DESCRIPTION:  
GATCCCAAAA ACCGGGCAGC CCAGGAAGGA ACTGGGGAAG GTGGTCATTC AGGGGAAGAA 60  
CCAGGATGCA GGGCTGGCTC AGGGTCTGCG CAAGATGTTT GGCTGATTAA AAGTTAAACC 120  
TTAAAAGAGA AA 132

15 SEQ ID NO:7686  
SEQUENCE LENGTH:85  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08936

20 SEQUENCE DESCRIPTION:  
GATCCCATGC CTGAAATNTG GAAGCATATG TACAAAAATC ATTTTACGT TTTATTTTAA 60  
ATAAATCATT GTGTTTGACC GTAAA 85

25 SEQ ID NO:7687  
SEQUENCE LENGTH:333  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08937

30 SEQUENCE DESCRIPTION:  
GATCCTAGTC ATGACTATAC ATTGTGACAT GGTCATTACA TATGGATTAG ACCAACTGGA 60  
GAATTGCCAG ACTTGTGGTA CCGATTATAT CATCTCAGTC TTGAATTTAC TCACGCTGAT 120  
35 TGTGAACAG ATAAATACGA AACTGCCATC ATCATTTGTA GAAAAACTGT TTATACCATC 180  
ATCTAACTA CTATTCTTGC GTTATCATAA AGAAAAAGAG GTTGTGCTG TAGCCCATGC 240  
TGTTTATCAA GCAATGCTCA GCTTGANGAA TATTCCTGTT TTGGAGACTG CCTATAAGTT 300  
AATATTGGGN GANATGACTT GTGCCCTAAA CAN 333

40 SEQ ID NO:7688  
SEQUENCE LENGTH:333  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08938

45 SEQUENCE DESCRIPTION:  
GATCTGATTC GCTCCATCAA TGACCCGGAG CATCCACTGA CGCTAGAGGA GTTGAACGTA 60  
GTAGAGCAGG TGCGGGTTCA GGTTAGCGAC CCCGAGAGTA CAGTGGCTGT GGCTTTCACA 120  
CCAACCATTC CGCACTGCAG CATGGCCACC CTTATTGGTC TGTCCATCAA GGTCAAGCTT 180  
50 CTGCGCTCCC TTCCTCAGCG TTTCAAGATG GACGTGCACA TTA CTCCGGG GACCCATGCC 240

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TCAGAGCATG CAGTGAACAA GCAACTTGCA GATAAGGAGC GGGTGGCAGC TGCCCTGGAG 300  
AACACCCACC TCTTGGAGGT TGTGAATCAG NTN 333

5 SEQ ID NO:7689  
SEQUENCE LENGTH:110  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS08939  
SEQUENCE DESCRIPTION:  
GATCCATGAA CCCTTTTAT AAGCTGTGTG TGTCTCTGT ATTATTGTTA TTAACATTTT 60  
TTTAGNATTT GCCTGTAAGT TATTAAAGAC TGATAACTGT AGCTCTTAAA 110

15 SEQ ID NO:7690  
SEQUENCE LENGTH:186  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
20 CLONE:HUMGS08940  
SEQUENCE DESCRIPTION:  
GATCCAGCCA AACGAATTTT TGGCAAAATG GCACTGAATC ATCCATATTT TAATGATTTG 60  
GACAATCAGA TTAAGAAGAT GTAGCTTCTT GACAAAAAGT TTCCATATGT NATGTCAACA 120  
GATAGTTGTN TTTTNTTGT TAACTCTTGT CTATNTCTCT CTTATATATA TCCCNCNTTT 180  
25 ATCAAA 186

SEQ ID NO:7691  
SEQUENCE LENGTH:231  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS08941  
SEQUENCE DESCRIPTION:  
GATCATGTGA CCAATTGTGC ATTCAAGTTT CAGAATTCTT TGCTATATGA TTTGGATTAA 60  
35 TTCTATATAA TTTTGGACTT TAAATATTA AGGTAAAAA ATACCTGTAT CTAATAATTGA 120  
TTCTGTAAAC TGTTGTCTTA AAATAAAGG TATTAAAGTA TAANNTTAAA ATTNGCAATT 180  
TTTTTAAAN NNTTGCAATT TTGATTCTCA TGGGGGAAAT TGGAGATAAT N 231

40 SEQ ID NO:7692  
SEQUENCE LENGTH:277  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08942  
45 SEQUENCE DESCRIPTION:  
GATCACAAAT TAATAACAAG TAAAACTTTA CTTTTGACAA TTTTGCCACT TATTTTGTA 60  
TTTGTAAGCA CACGTTTGAA GATATATTTA TGCCATTAAT ATTTAAGGC ATGTTTAAA 120  
ATTTACTGTT TTCTGAAAAA TAAATGNNN CTGGTTTGAT TGCTGGAGAT TTATTCCAGT 180  
TTTNTCAAA TGTATTTTNA TNCTGTATGG TACATTTTNG NGGATTNCCT GATTAATGTC 240  
50 ATCTTAGCAT TATATTCTGG TTATCTATAA TNNANN 277

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EP 0 679 716 A1

SEQ ID NO:7693

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08943

SEQUENCE DESCRIPTION:

GATCTGGGCA AAGCAAATTG AAAACCTTCT GGAAAGGATT CACCATTTTA GATGCCATTA 60  
 AAAACATTCG TGATTCATGG GAGGAGGTCA AATTGTCAAC ATTAACAGGA GTTTGGAAGA 120  
 AGTTGATTCC CNNCCTCATT GATGACTATN AGGGGTTCAG GACTTCAGTG GAGGAAGTAA 180  
 GTGCAGATGT GGTGGAAATA GCAAAAGAAC TAGAATTAGA AGTAGAGCCT GAAGATGTAA 240  
 CTGANTTGCT GCAATCTCAT GNTAAANCTT TAACAGNTGA GGAGTTGTTT CTTATGGNTG 300  
 CGCAAAGAAA TN 312

SEQ ID NO:7694

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08944

SEQUENCE DESCRIPTION:

GATCTTTACT GTTCAGAATT TAGGAAAGTT CTCTGGCTGT TGCATCCAAG TAAAATTAAA 60  
 ATAAAATTGG TTGCANNTTT AAA 83

SEQ ID NO:7695

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08945

SEQUENCE DESCRIPTION:

GATCCCTTCC TCTGTCTCTC TAACTCCCA GCCATGAATT TTGGCCCCAG GGAGAGGAAT 60  
 AGGCAGTATA GGAGGGATGT CAGGGAATC ACATCTGTGG TTGAATCTCA GAAACAATGG 120  
 AAAGGCAGTT GTCTTTGGAT ATGGTGAAAT TGTGGTAGAG CACCCATGGT GGGGGTCTGG 180  
 CAGGAGCTCT GCGGCTTCGG TAGCAGCAGT ATGAGGAGAG CTGGGCCACA TGCTTATGGG 240  
 TTAGGAGAAG GTAATTTCCA GTN 263

SEQ ID NO:7696

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08946

SEQUENCE DESCRIPTION:

GATCATGGCT GAAAAAGCAG CAAATGCAGC AGGAAAAAAG TTCCGAAAGA AGAAGAAATT 60  
 TCGCAATTAA GATTTACCA GCAAACTGCA ACATTTTACA TTGCTCCTTT ATTACTTAT 120  
 TAAAGACGTT TGGAAAACTA AA 142

SEQ ID NO:7697

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08947

SEQUENCE DESCRIPTION:

GATCAAGATT GAGAAGACTA GATACATAAC AACCAACTGC AATGTTTGGT CCTTCATTGA 60  
ATGGTTGAAC AAACCAGCTG TGAAAGACAT TTTGGGACAT ACAGACATGG ACTGAGAATT 120  
AGACATAAGA AAATTATTTT GTTAACTGTT ATCATGGTTA ACAAACGGT CATATAATNT 180  
GATTATGTAG AGAAGTTAAA 200

SEQ ID NO:7698

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08948

SEQUENCE DESCRIPTION:

GATCTGCCTG CCTCAGCCTC CCAAAGTGCT GGGNTTACAC GCGTGANCAC CACACCCAGC 60  
CTCCATCTTT AAACTTTAA ATGTGAAATT TCTATCATGT ACCGTTAGCC TAACAAGATT 120  
TTNTTCTCTA TTTCTGACTG GTGCCTTTCC CCTTTTtagg AGCAACGAAA GCTACTCTCT 180  
TAGTTATGTT CTTGTGATGT GACAAAATGT CAAGAAGATA GGAGAAGAGA ATATTTTATT 240  
TCGTTGATGC TTTTGTTCCT AAGTGTGACC CTAAACTTAA GCTTTGTAGG AGTTGACATT 300  
CTTTCATGTC CTTTCCCTT ACTCATGCCG AAACATATCAA CTGGGNCATG N 351

SEQ ID NO:7699

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08949

SEQUENCE DESCRIPTION:

GATCTGTTTC TGGGGCCTCT GCGGGTGGCG GCCTGGGGCG GCGCGACGGC TGGTGCGCAG 60  
GTACANTGAT GCTGAAGTAC TATGAGCCTT CGGAACCTGT GGAGAGACTA CAANGTTTGT 120  
GNNNTATGG TCCCTTTAGT TGGGCTCATA CATTTGGGGT GGTACAGAAT CAAAAGCAGC 180  
CCTGTTTCC AAATACCTAA AAACGACGAC ATTCCTGAGC AAGATAGTCT GGGACTTTCA 240  
AATCTTCAGA AGAGCCAAAT CCAGGGGAAG TAGCAGGCTT GCAATCTTCA GGTAAAGAAG 300  
CAGCTTTGAA TCTGAGCTTC ATATCGAAAG AAGAGATTGA AAAATACCNN 350

SEQ ID NO:7700

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08950

SEQUENCE DESCRIPTION:

GATCCCGCCA GAAATGAATA GACACCGCAA GAAACAAAGC TCGAGTGAAA GCTTGTTACA 60  
TAATGATTGG ACTCACAATT ATCGCCTGCT TTGCTGTGAT AGTGTGAGCC AAAAGGGCTG 120

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5 TAGAACGACA TGAATCCTTA ACAAGTTGGN NCTTGGCAAA GAAAGCTAAG NGGCGTGAAG 180  
 AAGCTGCATT GGCTGCACAG GCTAAAGCTA AATGNTATTC TAAGTGACAA AGTGTTCCACC 240  
 TGAATACCAT CCCTGTCATC AGCAACAGTN GAAGATGGGA AAAATNGAAT ATTTACCAAA 300  
 ATNTCTGCCA TGGTTTTATT TTGGTAACCN GATGCACAAT GTCTTTTTTT N 351

10 SEQ ID NO:7701  
 SEQUENCE LENGTH:85  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08951  
 SEQUENCE DESCRIPTION:  
 15 GATCATATGT GAAGATGTCA ATTAAGCTTG CATTAAGCCA CCTGCTTTGT AAGTGGATTG 60  
 ATTAATAAAT AACTTATATT TCAAA 85

20 SEQ ID NO:7702  
 SEQUENCE LENGTH:89  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08952  
 SEQUENCE DESCRIPTION:  
 25 GATCCCAGGG GCTTATCTCT TCAAGTGTGG AGAGGGCAGG GTCCACGCCT CTGCTGTAGC 60  
 TTATGAAATN AACTAATTGA AAATTCAAA 89

30 SEQ ID NO:7703  
 SEQUENCE LENGTH:375  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08953  
 SEQUENCE DESCRIPTION:  
 35 GATCCAGTGG CAATTGTAAA ACTAGCTATT TATGGCATGC TGCCAAAAAA CCTTCACAGA 60  
 AGAACATTTN ATGGAAGAGT TGCATCTTTT TCCAGATGAG TATATTCCNN CNGATATTCT 120  
 TAAGAATTTA GTAGAGGAGC TTCTCAACC ACGAAAAATA CCTAACGTC TAGATGAGTA 180  
 CACACANGAA GAANTAGACG CCTTCCCAAG ATTTGTGGAC TCCACCTGGA AGATTATCGG 240  
 CTATAAGAGA ATAAGATTTG CAGATAATTA ACAGTTGANG TGATTGAGAC TTTCTNCTTG 300  
 40 ATGAGTTTCT CTAACCTNCA GGGTGGTGT AACCACACTGC TACAGTTCAG CACCTGTTTT 360  
 TTTGTGCCG NTTTN 375

45 SEQ ID NO:7704  
 SEQUENCE LENGTH:276  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS08954  
 SEQUENCE DESCRIPTION:  
 50 GATCACATCC TACTTCCTCA ATGAAGGGTC CCAAGCCCGT CCCCCTTCTT CCCACCGATA 60  
 TTTCTNGAA CGCGGCCTGG AGTCAGCAAC CAGCCTCTAG CAGCTGCCTC TACGCGCTCT 120

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EP 0 679 716 A1

ACCTGCTTCC CCAACCCAGA CATTAAAATT GTTTAAGGAG AACCACACGT AGGGGATGTA 180  
CTTTTGGGAC AGAAGCAAGG TGGGAGTGTG CTCTGCAGCC GNGTCCAGCT ACTTCCTTTT 240  
GGAACCTTTA AATAGAATGG GTGTTGGTTG ATTAATA 276

SEQ ID NO:7705  
SEQUENCE LENGTH:220  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08955

SEQUENCE DESCRIPTION:  
GATCCACTGC CATTCTAATT GCTTTAACAA GTCATTACCA CACTACTGTT ACATCTTAAT 60  
TATGCATACA GACAGGTAGA CTGTGTTTAC ATATGTGAAC TAACTAGTTG TCAAAGCAAA 120  
TGCAGATTGT ATTCTGCAAG TAAAGTCTTT TTCTCTCTGA AATTTCTAGG GATGTTCTTT 180  
AAGTGAAATT CATATTAATA CTGAAGATT TNGTTACAAA 220

SEQ ID NO:7706  
SEQUENCE LENGTH:252  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08956

SEQUENCE DESCRIPTION:  
GATCCAAAGT AACTNAAACA GGAGCCCACA AGACGGTCTG CCAGATTGTN AGCGAAACCT 60  
GCTCCACCAA AACCTGAACC CAAACCAAGA AAAACATCTG CTAAGAAAGA ACCTGGAGCA 120  
AAGATTAGCA GAGGTGCTAA AGGGAAGAAG GAGGAAAAGC AGGAAGCTGG AAAGGAAGGT 180  
ACTGCACCAT CTGNAATGAG TGAAACTAAA GCTGAAGAGG CACAGAAAAC TTGNTTCTNG 240  
TNGATTAACG AN 252

SEQ ID NO:7707  
SEQUENCE LENGTH:166  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08957

SEQUENCE DESCRIPTION:  
GATCTCCTGA CCTCAGGTGA TTCACCCACC TCAGCTTCCC AAAGTGCCGG GNTTACAAGC 60  
TTGAGCTACC GCGCCAGCC AACACATCAC TTTATCTTG CAGCTCCCGA GATTCTCTTT 120  
TCTGTGACTN TTAATAATTGT GCTNACATAT GTGTTTGATA TAAATN 166

SEQ ID NO:7708  
SEQUENCE LENGTH:52  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08958

SEQUENCE DESCRIPTION:  
GATCAAAATA TTCTGGAAAA AAATAATAAA AAATAATTG TATACATTGA AA 52

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SEQ ID NO:7709

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08959

SEQUENCE DESCRIPTION:

GATCATACTN GTGATTATAA AAGNTCCTAG GAGGCTAGAA GAGCCAACCA ACAGAGAAGG 60  
GAAAGCAGTC TGTTCGTAAC ATAGGGACAT AAGTTCATTC ATGCCAAGTA TCTTTCCAGC 120  
ATGTTTCTCC CATTTAGAAT ATCTAGCATN TAAGGCCTTT CAATATTAAT ATAAGCCCAA 180  
TATCAGCTCT TTCTCTNTGT ATTTTCATCTC TTTCTACTCT CCNATTTGTA TTTGGTGTTC 240  
CTNTTGAAAG TGTCGTATCT GGGAGATGAC CTGCCTTATC CTGTNCTATA ACAGTTTNTG 300  
NTTGCTGCTG TGTCTTTN 318

SEQ ID NO:7710

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08960

SEQUENCE DESCRIPTION:

GATCCAAGAA ATTACTGAAA TGGACAAGAA ATGTCATTAG TTAAGGCCA TGTTATCTTG 60  
AGCACACATA CAGTTAATTT GATAAAGAAG AGTATGCCTC TCAGCATTGT GAGATATATT 120  
TCAGACTAAT TTGATGTTCT TTAATGTTCC CTTATTTTGT AAACACGTTT TAAATGTGAA 180  
ATTAATGTCC TTCACAAAAT GTCTTTTGAA AGCACTGTTA CAGTTGTATA AAGATGATGT 240  
AAA 243

SEQ ID NO:7711

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08961

SEQUENCE DESCRIPTION:

GATCTTGGCT TCTGAGGGCT CATTTGTAGA GTGGTGAGAA TAATATCTAA CTTGCTAATC 60  
TTTCAGAGAC ATTCTGAGAG ACATATGCAA AAGAACTTG TAAATAAAAA GCACTGTACA 120  
AA 122

SEQ ID NO:7712

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08962

SEQUENCE DESCRIPTION:

GATCCTTTAT TAAGCTTCTG ATTCATAAAA AAACCTATAA GAGACATTTG GGGGGATATT 60  
TGGGGAAATA GGAAGATGGA ATGGGTAGTA GATAATGTGG TATATTTNAT TTTNCTAGAA 120  
GTGATAATTG AGTTACGTAG GATAATGTTT TAATTCTTAG GAGATGCATG CAGAAGTTTT 180  
TTTTTTAAGT TTTGAAAAGN CATGATGTTG NCAGCATATT TNCAAATAAN TATGTCCAAA 240

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SEQ ID NO:7713

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08963

SEQUENCE DESCRIPTION:

GATCTGTGTC CAAAAGTGAA CTTNAGTCAG GAATGAATCA ATTTTCAGCAT AAACAAGCAC 60  
AAAANTTTAG TCTGCTGGCT GACTGGAAGC AAAAAAGTCA AGATGGNNNN 110

SEQ ID NO:7714

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08964

SEQUENCE DESCRIPTION:

GATCTCAAAA CAATTGTTGC AGCAGGCTCC TGGCAGTCTC AAGCAGTTCA TCTTCTTGGT 60  
GTACTGGTTT CCTATTGTGA TTTTATCATG GAAAATCAAT TGGCTNNNNN N 111

SEQ ID NO:7715

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08965

SEQUENCE DESCRIPTION:

GATCCTATAG GCAGAGAGTT TTCCTTCTG ACTTTTCCC TTTGCTTTCG TGTGACCACA 60  
TGTTTTCTGT ACCAGTCACT GGGGAAAGAA GTGAGTTTAT CTCGTTTGTT TTAAGGTTT 120  
TGCTTGTCTA TTTAGCATTC CTTTTGGGT CTCAAGATT ATGGAACAAT AAATGTCATT 180  
TAATGCTGTG TGCTTATTTT GAATTCCTCA TCAGGTTTTA GAAGCGGGT AAAAATACTT 240  
AGATGCTTAT CAGACTTGAA ATTATACTGA GTGGCATTGA ACGTGAGTTT GTCCCAGTGA 300  
ACCAGGCTN 309

SEQ ID NO:7716

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08966

SEQUENCE DESCRIPTION:

GATCCATGAA GCCAGAGCCT GGCTCTGGGT GACAGCAGGA AACGGCTGGG GAAAAGNACA 60  
GCAGGGCGTC CAGCTGAGCC TGCCATTCCA GCCTGTTTCG GGGAAACAGC TCCCAATCCT 120  
AGACTGTGCT GCTCCGGGAG GGCTGCTGGT GGATATTTGG GCTGTTTCA CCATATAGCT 180  
GTCATGAAAA ATGCTTCCGT GAAA 204

SEQ ID NO:7717

SEQUENCE LENGTH:121

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08967

SEQUENCE DESCRIPTION:

GATCTCAGGA ATACAGTCCC ATGCAAAGAT TCTCTGGTTT TATGGCTTTT TTCCCTTTCT 60  
TTACACCATC CTCTCCATA AGCACCCATG TTTTGAATA TGAATGTATT TGTAAATAA 120  
A 121

SEQ ID NO:7718

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08968

SEQUENCE DESCRIPTION:

GATCACCTGA GGTCTGGGACT AAAAATACAA AAATNAGCTG GGCATGGTAG CCGGTNCCTG 60  
TAATCCCAGC TATTTNGGAA ACTNAGAACA AGAGACTTGC TTGACCCTGG GAGGTGAAGG 120  
TTGCAGAGAG CCGAGGTAGT GCCACTCCAC TCCAGCCTGG NCGACAGAGT GAAACTCCGT 180  
CTCAAA 186

SEQ ID NO:7719

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08969

SEQUENCE DESCRIPTION:

GATCAGCTCT CTGTTTGGGA AAATGGAGTA GATATAGTTC TAGGTACTCC GGGAAGACTA 60  
GATGACTTGG TGTCAACTGG AAAGCTGAAC TTATCTCAAG TTAGATTCCT GGTCTGGAT 120  
GAAGCTGATG GGCTTCTTTC TCAAGGTTAT TCTGATTTTA TAAATAGGAT GCACAATCAG 180  
ATTCCTCAGG TTACCTCTGA TGGAAAAGA CTCAGGTGA TTGTTTGCTC TGCCACTTTG 240  
CATTCTNTCG ATGTAAAGAA ACTNTCCGAG AAGATAATGC ATTTCCCTAC ATGGGTTGAC 300  
TTAAAAGGAG AAGGCTCTGT TTCCAGATTN CTGTACACCA TGTTGTTNAA N 351

SEQ ID NO:7720

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08970

SEQUENCE DESCRIPTION:

GATCCCAAAG AAGTAACGGG AAAAAGGAAT GTAAGGCATC TCGATAATNT TTTCATATTG 60  
ATTACATGTT GAAATANTAT TTTGTATNTA TTGAGTTAAG AAAAATATGT CATTAAATTT 120  
AATNTCACCT GTTTCTTTTA AA 142

SEQ ID NO:7721

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid



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TOPOLOGY:linear

CLONE:HUMGS08971

SEQUENCE DESCRIPTION:

5 GATCTTGTA ATCAAATTCA CAAACATCAG CTTGTTACAA ATCATTNTAT TTATACCCTT 60  
TAAAGAGTGT GGATTTAAGA TTCTTGAAAG GATGTAGNCT ATATANTTTC TCATTCCNTA 120  
TGGTGTAACN 130

SEQ ID NO:7722

10 SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08972

15 SEQUENCE DESCRIPTION:

GATCGTTAAT TAATATCTTT CCATNCGAAG AGNAAGCAGA TTTCTTCTGA GATTTCTGAA 60  
CAGTTCCTGG GTGTTTCCGG TTCTGCTTCA GTGTACTATC ACTTTGCCTT GCCTCAGTCT 120  
CTCCTTCCTC CGGGGCCACA GAAGGAGAAA GCCCAAAGCA TACCCATCCT GCCCTTTAAA 180

20 SEQ ID NO:7723

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS08973

SEQUENCE DESCRIPTION:

30 GATCACTGTC CCGNTTCAAA TTATTCTTCA GTCCATTTC CCGGCCTATT TCAGCTGTTT 60  
CTTTTACCT AACTGTTNAG TCATTCNGGT TTTCAAGCAG TGCTTNATCT CATGTCCTTG 120  
AATATAGTTG TGTACTTTAT TTTNAGGTA ATAATTAGAA CAGTTCCTT CAGAGGCTGC 180  
ATTGCGCTTC TTCTGCCACC TAAATATTAC TTCCCTTCAA ATCNGCCTTT GAATCATCNN 240  
NTTTAAAAAA AANTTANCAT GNTTTN 266

35 SEQ ID NO:7724

SEQUENCE LENGTH:33

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08974

SEQUENCE DESCRIPTION:

40 GATCAAAGGT ACCATGACCA AATAAGAAAC AAA 33

SEQ ID NO:7725

SEQUENCE LENGTH:219

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08975

SEQUENCE DESCRIPTION:

50 GATCTTCTTT TTTNTTCTGG AGCCAGACTT NCTGGGCTTN NATTGCTGCT ATGCTACTTA 60  
CTTGGAATC TTGGACAAGT TACCTAATTT CCTTGTTCTT AAGTTACTTC TGTTGTAAAA 120

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TGATGTGGCC AATAATAGTG CCTATCTCAT AACATGGTTA TTAGAATTAA ACAAGTTAAT 180  
ACTTTTAAAA TGCTTAGAAC AATTGTGGGT ACATACTAN 219

5 SEQ ID NO:7726  
SEQUENCE LENGTH:275  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

10 CLONE:HUMGS08976  
SEQUENCE DESCRIPTION:  
GATCTGTCTG GNAACAGTTT ATGGAAATAT AGATATTCAT GCATCANATA AAAGTGCTGT 60  
GACCATAGAT AAAGTGCAGG GAAGTTCTGT NACTGTATCT ACCGAAGATG GTTTGCTGAA 120  
AGCCAAGTAT CTTTATACAG AATCATCATT TCTGTCTTCT GCTGCTGGGG ATATTACATT 180  
15 AGGAAGTGTT CATGGNAATA TAACATTACA AAGCAAGANG GGTAGCATCA CAGTNGATTG 240  
GTCTTCTGGA TGTCTAAAAG CCTCAACTAA TCAGN 275

20 SEQ ID NO:7727  
SEQUENCE LENGTH:37  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

CLONE:HUMGS08977  
SEQUENCE DESCRIPTION:  
25 GATCCCAGGT TCTCATGAAC CAAATAAGTA ACTTAAA 37

SEQ ID NO:7728  
SEQUENCE LENGTH:97  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

30 CLONE:HUMGS08978  
SEQUENCE DESCRIPTION:  
GATCTGCCCA CCTNGGCCTC CCAGAGTGCT GGGATTACAG GCATGAGCCA CTGCGCCCGG 60  
35 NCTGTACTAA GTCTTTTTTT TTTAAATTC CTCNAAA 97

SEQ ID NO:7729  
SEQUENCE LENGTH:284  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear

40 CLONE:HUMGS08979  
SEQUENCE DESCRIPTION:  
GATCTATGAA CTTCTGCCCC ACATAACTTT TAAAGCAGTA TTTTATAAAC CCCATGAAGA 60  
45 GCTTGCTTTT TTGTCTTTGT AATTCCTTAG GGTCTGTGAT ATATGCCAGG AAATCTGATT 120  
GAAACTAATA TGCTTTTTAT TCTCCCATTA TTCCCTAAAT NGTTATATCA CAGGCACTTG 180  
CCTACATTGG GAAAGTAAGG ACAAATAATA CCCATTAAA GTAACNGCC TATTATTNNG 240  
ACTGTCTTTC GTAAGCACTT GCTGAACNGC TGACTTAACT CAGN 284

50 SEQ ID NO:7730

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SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08980

SEQUENCE DESCRIPTION:

GATCTCGCAA TGGGGAAGGC CCTGGTCGAC CAGAGGGAGC TGTACCTGGG CCTGCTCTAC 60  
CCCACGGAGG ACTACAAGGT ATACGGCTAC GTCACCAACT CCAAGGTGAA GTTTGTCATG 120  
GTGGTAGATT CCTCCAACAC AGCCCTTCGA GACAACGAAA TTCGCAGCAT NTTCCGGAAG 180  
CTACACA ACT CCTACACAGA CGTGATGTGC AACCCCTTCT ACAACCCGGG GGACCGTATC 240  
CAGTCCAGGG CCTTTGATAA CATGGTGACG TCGATGATTG ATACAGGTTG TGCTGAGTGA 300  
GCTGTGCTGC CAGCCATCGN AGAGGAGCCC NTNGCACGAC TTGTGGTGGG GTCCGTCGGT 360  
CTGTTTCTN TTTN 374

SEQ ID NO:7731

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08981

SEQUENCE DESCRIPTION:

GATCCGGTTG GACTCTGACA TCGGATGCCC TCAAACATAC AGAACTTCCA AACTCAAGTC 60  
CAGCCATAAG CTATTTTGCC AACATGTCAG AGTAATCTGT ATTTTGTAT GTGATTTCTA 120  
CTTTTATAGA CTGTGTTTAA AACAATAAAA CACATTTTAA TAAA 164

SEQ ID NO:7732

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08982

SEQUENCE DESCRIPTION:

GATCTTTCAT GAAAATTAAT TGTGCCCATG TCCAAGTTTG AATTAGAGAT ACACAGCACA 60  
CAATCATTTT TGTACCACT TTTGGAATAT CTAGCATTAG CCTTGATAGT TTTGTGTGGT 120  
GTGTTTTGAG TATATCTGAN CTGTTAGTTA TATTTGGTTA ATTTATTAAA NGATGTGTGT 180  
TAANCCTTAA TATTTATGCA GTGTTTAAGT ATTTGGAATA TATNGAAAT AAATTATCCA 240  
GTGTTTTAGA TAAATGGTTA TTTAATTGCN NAANGTGATT CTCTAAA 287

SEQ ID NO:7733

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08983

SEQUENCE DESCRIPTION:

GATCTGTGCC GTTCAATAGG CATCGTCTCT CAGCCTGAGG GAGGCTGGAT TCTGGGTTCC 60  
TG TAGTCACA GGGAGGAAAA GCTTCTTAA AAATGGACAT GTATGTGCGT GTNAGTGTGT 120  
GTGTAGATTT ATAGTTTTTG GTAGTGGCAG GAATAAAAAA AATCCATCCT AAA 173

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SEQ ID NO:7734

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08984

SEQUENCE DESCRIPTION:

GATCTCTATT TTGTGCCCAG ACTCTGAGCT GCTTTATGAA CACCTCAATT AAATNACTTC 60  
ATTGGAGTGA TTTGAGTAAT CTATCTATAG TGTAATATTT TCTATGAATA ATTTTCTGTA 120  
ACCTTATTTT ATAAGTTAAT ATCTAAAAAG TGTTTATTTT CAAATTGCCA AATAAAAGGT 180  
TTTATATTAG TCATTAAA 198

SEQ ID NO:7735

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08985

SEQUENCE DESCRIPTION:

GATCTAGAGA CTCATTCAAT AGCAATGTGA CCTTTTAAAT ACTTACATTA AGTAAACTG 60  
CCAGTAGATT AAATCATATA TATATATATA TATN 94

SEQ ID NO:7736

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08986

SEQUENCE DESCRIPTION:

GATCACCTGN ACTCCAGCTC AGATTGCCTC TCCTGGACAT GGCAATGAAT GAGTTTTTAA 60  
AAAACAGTGT GGATGATGAT ATGCTNTTNT GAGCAAGCAA AAGCAGAAAC GTGAAGCCGT 120  
GATACAAATT GGTGAACAAA AAATGCCCAA GGCTTCTCAT GTCTTTATTC TGAAGAGCTT 180  
TAATATATAC TCTATGTAGT TTNNTAAGCA CTGTACGTAG AAGGCCTTAG GTGTTGCATG 240  
TCTATGCTTG TGGAACTTT CCAAATGTGT GTGTCTGCAT GTNTGTTTGT ACATAGAAGT 300  
CATAGATGCA GANGTGGTTC TNCTGGTACG ATTTGATTCC TGTGGGATG TTTTAACTAA 360  
NAN 363

SEQ ID NO:7737

SEQUENCE LENGTH:262

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08987

SEQUENCE DESCRIPTION:

GATCTTCTTT GATGATGAGA GGCGBAATAT TGTAGACGTC AGCAAAGTGG GTGTTACCTG 60  
CATTCACATC CAGAAATGGAA TGAATCTTCA AACTCTAAGT CAAGGGTTAG AGACATTTGC 120  
AAAGGCCCAA ACTGGGCCCT TAAGGTCCAG CCTTGAGGAG AGCCCATTTN AGGCCTAAAC 180  
TGAAAGGAAA TCAAGAAGGC ATTTTCAGGT GCATTGTAA TTTATTAAAG TTCATCTGTG 240  
TGTGACAGAA AAAAAAAGTA AA 262

SEQ ID NO:7738

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08988

SEQUENCE DESCRIPTION:

GATCTGTGCC ACATGGAGGT TTTGGGATGG GATTTNAAAG CTACCTGCAG TGCATCTTGG 60  
 GTGTTGACAA TATCANAGAT GTTATCCCTT TCCCAAGGTT TCCTCATTCA TGCCTTTNAT 120  
 AGCTGGAAGA TTGGTTAAGG CAAAGCACCC CCCATGGCAG AGACACTGCA CATGATTGTN 180  
 CATACAGCAG AATGCATGTT TGGATTNTAG AAATGCAGAT TTCAATATGT AATTGTTGTG 240  
 CCATAAGATA TCATAGNAAA NNTATAAGTG GTTGTNCTTT TCTTAGAAAG TTGAGGGTAT 300  
 TTCACGTAAG GATGAGCTCC CGCAAGNNGA GGTACTTNTT AGCANGGGGA CTCTCAATCG 360  
 N 361

SEQ ID NO:7739

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08989

SEQUENCE DESCRIPTION:

GATCTTGATG TGGGTGATAG TTTTACTTAT GTACATCGAT ATACATCTAT TTAAAAACAT 60  
 GTACATTTAA ATTGTTGCAT TTTATGTATT TAAAATTTAT TGAGTANTCC TTCTGTATGT 120  
 ATTATTAAAG AGAATATAGC AAA 143

SEQ ID NO:7740

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08990

SEQUENCE DESCRIPTION:

GATCATAGAG TTTGGCTGGG GAGGGGGGCA GTTTTAGAGG CTTCCACTTG GTGTTCTCTCA 60  
 GAATGATATC TCTTACTCCG GGGGCCAAGG TAGGGGTTAG CTTTGTCTCT CTTTGTAGTT 120  
 TAGATTGTAT CTCTTGCCTT GTTCAAGTTC ACAAATCTTT TTGTGTATAC ACATATGTAC 180  
 ATGAAAATNA TGTTCATGCT TTTAATTATT TTACCCTTCA TTATTTTATT TTTNATAGTT 240  
 CTCATAGCTA TGTCTTTCAG TTCACATAAT TTTTTCACAG AGTGTTTAAAT CTGTCATTA 300  
 ATCCCATCCA AAGTATGTTT TCTCTCAGAA GAN 333

SEQ ID NO:7741

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08991

SEQUENCE DESCRIPTION:

GATCCTTGTA CACTGTTTAT ATGTGCAATA AAATGCATGG CCAGCTGACA GTATCGTCAG 60

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TGGACAGAAT GTATATAGTG CAAATATCCT TCCTTTTATT ATTTAACAGC CATTAAAATC 120  
TTGGATTGTG AAAAA 135

5 SEQ ID NO:7742  
SEQUENCE LENGTH:333  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS08992

SEQUENCE DESCRIPTION:  
GATCCCAGTT CACAATTATT CACCGGGTAT TTAGTTATTC ANAGGCTGCT CTGCTGAGAA 60  
GNTGAACAAA TTTCTTGTC AAAACAATGT ATTTCAAACG TGCCGCTCGG GCCTTTCCCG 120  
TATTGCTCAC TGGTGCTGGG AAGACAACAC TTCTGAACTA TATTTTGACA GAGCAACATA 180  
15 GTAAAAGAGT AGCGNNNNCT TTAATGAAT TTGGGGAAGG AAGTGCCTG GAGAAATCCT 240  
TAGCTGTCAG CCAAGGTGGA GAGCTCTATG AAGAGTGGCT GGAACCTAGA AACGGTTGCC 300  
TCTGCTGTTC AGTGAAGTGA GGAATGTGTT TTN 333

20 SEQ ID NO:7743  
SEQUENCE LENGTH:219  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08993

25 SEQUENCE DESCRIPTION:  
GATCCCAACT GTATAACATT CTGAAAAAGG CACAACATG GAGACAATAA AAAGAACAGA 60  
GTTTTGGATG AAGGGAGGGA TGAACAGGCA GAATACAAAC AAATTTTAGG GCAGTGAAAC 120  
TATTATTATG ATACTTTATG GATATAGAAT ATTATGCATT TTTCAAAACA CATAGAATAT 180  
30 ACAACATGAA GAATGAATGC TAATGTAAAC TGGATTTTN 219

SEQ ID NO:7744  
SEQUENCE LENGTH:59  
SEQUENCE TYPE:nucleic acid  
35 TOPOLOGY:linear  
CLONE:HUMGS08994

SEQUENCE DESCRIPTION:  
GATCTTGGGC CACACATGAA AATACACTAA CACTAATGAC AGCTGATGAG ATGCTTAAA 59

40 SEQ ID NO:7745  
SEQUENCE LENGTH:353  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
45 CLONE:HUMGS08995

SEQUENCE DESCRIPTION:  
GATCAGAGTG ATGCTGGAAC TCAGTGTGCA TAAATTTCA GTCAGTGAAT ATCACTGAAC 60  
GTCATATACT ACTTGGTATG TGACTTTGGT TTGTGTTAAG AAAGCTTGTA TATAATATTT 120  
TTNGCCATAG TAAGTGAGAA ATTGTCCTTA ATCATGCCTG TTTGATGGTA CTAGGAAAGA 180  
50 AAGGGGTAGA GATTAATTCT TGCACAGTAT AAGCAACAGT GCAACAACT ATGCCATTTN 240

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EP 0 679 716 A1

CCTTTTNCCT CTTACTTGAA GGCAGAATCG CAAAACGTTT GANATGGCTT TCCTAAACTA 300  
CTCTACTCTG GTGNGAGCTC ATTTACCACA NGAAGCCTTA TAACACCGTT TNN 353

5 SEQ ID NO:7746  
SEQUENCE LENGTH:327  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08996

10 SEQUENCE DESCRIPTION:  
GATCAGGTGA TTGCCTTTCT CAGCTGTCAG TTCTCTAATT TCAGGCTTGG TAGCTTGTAG 60  
GAACTGAAAT TGCAATTAAA ACCTTTATAA ACTCAAATAA AATCATGAAT TACAGAAAAA 120  
GTCCATTCTT CCAAACTTG ATGTTACCAC ACTTACAAGT TAAAAATATG AAGTCGACTG 180  
15 TTTAAAGGAT TCTGCATATA TTCTAGTGTG CACATTCAGA AACATTTTTC TTGGAAAAAG 240  
TACCCAACAT TTTTATAAC TGCACATATT AATTTATTGC CAGAATAAAT TGCATTGCAT 300  
GCTAAATTAA NGTCAGATAN TTCNAAA 327

20 SEQ ID NO:7747  
SEQUENCE LENGTH:153  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08997

25 SEQUENCE DESCRIPTION:  
GATCATGTAA ACTTGCTGTT TTNGTTTTTN CCTGCCGGGT GTTGTATGTG TGGTGACTTG 60  
CGGATTTATG TTTCAGTGA CTGGAACTT TCCATTTTAT TCAAGAAATC TGTTTCATGTT 120  
AAAAGCCTTG ATTAAAGAGG AAGTTTTTAT AAA 153

30 SEQ ID NO:7748  
SEQUENCE LENGTH:41  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08998

35 SEQUENCE DESCRIPTION:  
GATCTTAATT TTGTTTTTGG TTTAAATAG TGTTTCCTTT N 41

40 SEQ ID NO:7749  
SEQUENCE LENGTH:299  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS08999

45 SEQUENCE DESCRIPTION:  
GATCTATCTA AATGCCGATT TGAGTTCGCG AACTATGTA CTGCGTTTTT AATTCTTGTA 60  
TTNANACTAT TTAATCCTTT CTACTTGTCG CTAAATATAA TTGTTTTAGT CTTATGGCAT 120  
GATGATAGCA TATGTGTTCA GGTATATAGC TGTTGTGTTT AAAANTTGAA AAAAGTGGA 180  
50 ANCATCTTTG TNCATTTAAG TCTGTATTAT AATAAGCAA ANGNTTGNT GTATGNTGT 240  
TTNATATAAC ATGACAGGCA CTAGGACGTC TGCCTTTTTN NGGCAGTNCC GTTAAGGGN 299

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SEQ ID NO:7750  
 SEQUENCE LENGTH:169  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS09000  
 SEQUENCE DESCRIPTION:  
 GATCAATTAG ACATTTTGAA AATAATTAA AGTGTTTTCC TTAATGTTCT CTGAAAACAA 60  
 GTTTCCTTTG TAGTTTAAAC CAAAAAAGTG CCCTTTTTGT CACTGGATTG TCCTAGCATT 120  
 CATGATTTTT TTTTCATACA ATGAATTAA ATTGCTAAAA TCATGGAAA 169

SEQ ID NO:7751  
 SEQUENCE LENGTH:53  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS09001  
 SEQUENCE DESCRIPTION:  
 GATCATTTAA TGAATCCTCA AGGACTAATG AAATAAATGC TAGACTGCTG AAA 53

SEQ ID NO:7752  
 SEQUENCE LENGTH:252  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS09002  
 SEQUENCE DESCRIPTION:  
 GATCCTGAAA ATAAACTAA CACTCCAGTA TTTTGTCATT GTTTTTCGCA ATTGAGCTAT 60  
 CTGAAAAC TG TATTCCTAA GTAATGTTCA AAAATGATAA GTAATCTGGA TACCTTTTTC 120  
 TTATACTTTC TCCTAGGAAA ACTTTAAAC TTTAAAAAGG CAAACCTACC AATAGGAATA 180  
 ACANATTAAA TGTCAAGAGA GTATATCCAA TATTAGGATA TAANTGTATG TGTCTCAAGT 240  
 TTAACCTAC AN 252

SEQ ID NO:7753  
 SEQUENCE LENGTH:237  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS09003  
 SEQUENCE DESCRIPTION:  
 GATCTACAAA AAATTCCTGG AGCCATATAT ATACCCTCTG GTNTCCCAT TCGCTAGTCG 60  
 TATATNGCCT NAGAAAGCAA TACAAGAATC CAATAATACA AACAAAGGCA NAGTAACTT 120  
 TAAGGGNGCA GACATGAATG GCTTACCAAC AAAAGGACCA NCAGAAATCT GTGATAAAAA 180  
 GAAAGACTAA AGAAATTTTC CTAAAGGACC CCATCATTTA AAAANTGGNC CNGGNNN 237

SEQ ID NO:7754  
 SEQUENCE LENGTH:264  
 SEQUENCE TYPE:nucleic acid



TOPOLOGY:linear

CLONE:HUMGS09004

SEQUENCE DESCRIPTION:

5 GATCTTCCCA AACCCAGAGA AAGACATCAA TTTCCAAGAA CAAGAAGGTT ATCAAACACC 60  
 AGGCAGATTT AACCCAGAGG ATACTACCTC AAGGCATTTA ATAATCAAAC NNCCAAAAGT 120  
 CAAGAATAAG GAAATAATCC TAAAAGCAGC AAGAGAAAAG AAACAANTAA TATACANTGG 180  
 AGTTCCACTA TATCTGGCAG CAGACTCTTC ATTGGAAACC TTATAGGCCA GGNGNGAGTG 240  
 10 GCATGACACA TTTAANGTAC TGGN 264

SEQ ID NO:7755

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS09005

SEQUENCE DESCRIPTION:

GATCCAGAGC TGTTGCCTGT GACAGCGGTT TCTNTGGATG TCAAAGGCAG CTGCCTGGTT 60  
 20 GCCCAGCTTG CTTCTCGACT GGTGGCCCTT ATGGGTGGGT GTGCGATGGA AATNTGTTCC 120  
 TGCCGGAGTC TGAGGCACCA GGGTGTGCTC AAAGGCTGGC CCTGGTGGTG GACTGGCACC 180  
 TGTGCAGAGT GCCGTGTGCT TGTGGTGC GC CATCTGAAGC AAGAGTCCAG CGTTCTGCCG 240  
 TGTCTGTCCC CCACCATGCC CCCTACAGGC GGTACTGATG GCGCTN 286

25 SEQ ID NO:7756

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS09006

SEQUENCE DESCRIPTION:

GATCCTTTTT CCTTCAGCAG CATTTCTTAC TGGCTGTGGC TGGAATCTGC CTTTAATCAC 60  
 AGCTGTCACC ATTCTCACGT GATTCTTGTG AGACTCTTTT TGGTTATAAT TACTATTTAA 120  
 TATTTAGACT ATTTTACTGA GCAGACTTTA TAAATGAGAT ATCTACAAGG CACTTAAAGT 180  
 35 GTTACAGATG TTTTACCTTA AGANTTATTT AAGTNGTGTT GGGTTAAGAC AGTTTTTCAGT 240  
 GTACCGTAAA TGTTGTGTTT TCAGAAAAAG ACAAACGAT GGTGCTGACT GGTTTTCTGT 300  
 ATATNGCACA ACAGTCCTCA AATACACTGG ATGTATGGAA CCTNTTCCTT NCATCCAGGC 360  
 AGCATTTTTN TTNCNCTCTN CN 382

40 SEQ ID NO:7757

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS09007

SEQUENCE DESCRIPTION:

GATCATCTTT GAGTAGCACT GTTTTGGGGC CCTCGGTCTC TCTGAAGACC CTAGCAGAAC 60  
 TGATACCTAC CTGTATCTCT TGTCTCTCC TATTTGAGTT TCACTTCCAG AGAACTTGTT 120  
 CTTACGAAAG AATGTGTAC TAGTAAGGAC ATCTCTAGCA TTTCTCTAGC CTTCTTTTTC 180  
 50 TGCTGCTCAA AAATAATCGT TACAAAGCTT AGGTTTAAGC TGTATATGAA ATATTTATGC 240

55

GACTCTCAAA CTTTAAAGGA GTTGCTCCTT TGTTCCAAAA TTAAATGTGT TAGATAAA 298

SEQ ID NO:7758

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09008

SEQUENCE DESCRIPTION:

GATCATGGTC TTCAAAGATG TAAATACAAG AGAACCAAAG TTATTCCGGG CAGTTCCAGA 60  
 TTCAGAACGT GTTATTCCTC CCAGAACGAC AACGCCATAT TTCCTTTGAG GCCTTCGCCC 120  
 ATCCTGCTGA CCCATTTTNN TGCCCTCTTC TTACCCCAAT TTTNTTGTAT TACCCTCTAC 180  
 AATATACTTT TNATTGAGCA CTTTGCTGCT GAAATGCTGC CTCTTGCCCT TTTTTTTTNA 240  
 AATTTTAAAT TATCTAAATT TATGGTTTGT GGTGGTGTCT ATNGCAAAGT TN 292

SEQ ID NO:7759

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09009

SEQUENCE DESCRIPTION:

GATCTGTAA TGAAAAGTGC TGGAATACCT CAACCAAGAA AAGGCAGAAA AGGGAAGGGA 60  
 GCATATTGCT AAGAGAGCAA TGGAAAATAT GTAAGCTGCT TTCATTAATT ACCCTACTTT 120  
 CATTCTCCC ACCCAAGCA AATCCCAACA TTTCTCTTCA GTGTGTTGAC TTCTATCCTG 180  
 TTAACACTGT AATATCTTTA AATGATGTAC AGGCAGATGA AACCAGGTCA CTGGGGAGTC 240  
 TGCTTCATTT CCTCTGAGCT GTTATCTTGT GTATGGATAT GTGTAAATGT NGGTGACTCC 300  
 TTGATAN 307

SEQ ID NO:7760

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09010

SEQUENCE DESCRIPTION:

GATCTCTGAA CATGAAAACC AAGGTGGCTA TTTTCAGGTT GCTTTCAGCT CCAAGTAGAA 60  
 ATAACCAGAA TTGGCTTACA TTAAAGAAAC TGCATCTAGA AATAAGTCCT AAGATACTAT 120  
 TTCTATGGCT CAAAATAAAA AGGAACCCAG ATTTCTTTCC CTAAG 165

SEQ ID NO:7761

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09011

SEQUENCE DESCRIPTION:

GATCGATGAC GCAGGTCCTT CCAGTGAAAT GAATGGTCTC AAAAAATGGA GAGGATGTGC 60  
 TGGGGATTGA GAAGGCAGGG TAGCCAGAAA GAAGCACAAA TTACCCCCAC CATAAGCTTC 120

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ACAGAATTGC TGACGCTAAC GGCCATGGGT GAGATTTTTC CAATAAGTGT CAGCCTGATG 180  
ACAGATACCA CAGACAGTTG CAAAAATGTC CAAGTTTCTC CTGAAGTTT CTGGCAGGGC 240  
AGTGGGCTCC ATCCTTAGGA GTGAATCAGC TTTGGTGAGT ATCGTGATTG AACAGAGCCT 300  
TAACACCAGG GCCCCCTTAA CTCCGCACTC CTTN 334

SEQ ID NO:7762

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09012

SEQUENCE DESCRIPTION:

GATCGCTTTG ATTTTAAAGT TCATTGGAAC TACCAACTTG TTTCTAAAGA GCTATCTTAA 60  
GACCAATATC TCTTTGTTTT TAAACAAAAG ATATTATTN GTGTATGAAT CTAAATCAAG 120  
CCCATCTGTC ATTATGTTAC TGTCTTTTTT AATCATGTGG TTTTGTATAT TAATAATTGT 180  
NGACTTTCTT AGATTCACCT CCATATGTGA ATGTAAGCNC TTAATATGT CTCTTTGTAA 240  
TGTGTAN 247

SEQ ID NO:7763

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09013

SEQUENCE DESCRIPTION:

GATCCTTCCT GAGCGTTTCC TGGCAGTTTT AAAACGAAAA ATCAGTGTTA AGTTTGATGC 60  
AGTTATTGGA TATAAAATGA AAGCGCAATA AGCACCTAGT TTTCTGAAAA CTGATTACCT 120  
AGGTTTAGGT TGATGTCATC TAATAGTGCC AGAATTTTAA TGTTTGANCT TCTGTTTTTT 180  
CTAATTATCC CCATTCTTTC AATATCATTT TTGAGGCTTT GGCAGTCTTC ATTTACTACC 240  
ACTTGTTCTT TAGCCAAAAG CTGATTACAT ATGATATAAA CAGAGAAATA CCTTTAGAGG 300  
TGACTTTAAG GN 312

SEQ ID NO:7764

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09014

SEQUENCE DESCRIPTION:

GATCTGCCTG TCCGGGCTGG GACAGAGACT CCCCAAGNAC CCCATTCTGC CTCCTTCTGG 60  
GGAAATAAAT AAGTGTCTGT TTCAGCAGCT AAA 93

SEQ ID NO:7765

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09015

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTGGCTA AGCATCTTCC TCATGCTTTC AGTAAATTGG AAAACCCACG GAGGTAAAT 60  
ATTACCTTTT TTTTAAAA CTTAAANCA TNCTGTTTAT TTTTNNATTA CATTNCCCA 120  
TATGNGNGGA ATN 133

SEQ ID NO:7766  
SEQUENCE LENGTH:300  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09016

SEQUENCE DESCRIPTION:  
GATCGTNAAA ACCCCAAATG GACTTATTTT AAGTCACTTG CCAAATGGCC CAACTGCTCA 60  
TTTTAAAATN AGCAGNGTTC GTCTTCGTAA AGAAATTAAG AGAAGAGGCA AGGACCCAC 120  
AGANACATA CCTGAANTAA TTCTGAATAA TTTTACANCA CGGCTGGGTC ATTCANTTGG 180  
NCGTATGTTT GCATCTCTCT TTCCTCATAA TCCTCAATTN NTCGGNAGGC AGGTTGCCAC 240  
ATTCCACAAT CAACGGGATT ACATATTCTT CAGATTTTAC AGATACATAT TCAGGTGTGN 300

SEQ ID NO:7767  
SEQUENCE LENGTH:105  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09017  
SEQUENCE DESCRIPTION:  
GATCAAAGTA GCCACAACAT TCTCTTAAGC CAAAGNCCAA TCCAGAACAA NGCCCTAACT 60  
CTCTTCAATT CTATGAAGAC TAAAAAAGTA AGGAAGCTNC AGANN 105

SEQ ID NO:7768  
SEQUENCE LENGTH:216  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09018  
SEQUENCE DESCRIPTION:  
GATCGTCAAA CCATTCATCC TTTTAAAGGT TTATTTGAAG ATGCTGTAA AGTACAGAAT 60  
TTTGTGTACA GGTAGATTTT TCCGTCCCTC ATTAATAGTG CCTTCTTAAT TAATACAGNC 120  
TGGTGTAGC TATAACAAGG CNCCAGTAAG GCCAAAGAAT CCCAAGTTCT TTGTGGAAAA 180  
ANAAAAAANN NCTTTTGGGG NCAGNTTTC CCTTCN 216

SEQ ID NO:7769  
SEQUENCE LENGTH:75  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09019  
SEQUENCE DESCRIPTION:  
GATCCTCCCG TGTGTGGTTG GAAAACTTTT GTTTTTTGGG GTTTTTTTTT TCTGAATAAA 60  
AAAGATNCTA CTAAT 75

SEQ ID NO:7770

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09020

SEQUENCE DESCRIPTION:

GATCTGTGTC TTAATTGTTC AGTTAGAGTG AGAAGTTGAC CTATGATTCTN TTTTAAATT 60  
 TTATATTTGG AACAAAGCTG CAAGTTATGG TAANGTACTG TACTGNGNGA NGTATTATGA 120  
 TATTTAATGC ATCTNTGGCT TAACACTTGT GAGAGTTACC AGCTTGAAAA TGATGGTGTGTT 180  
 GACTACCTCT TGANTCACAT CTATCAACCA CTGGCACCTA CCACCAAGCT GGCTTCAATT 240  
 AGTATGTGTT GCTTTTGGT ATTAACANCT AACCGTACTA GAGACCAAAG TGAACCTGA 300  
 TTTTAAATAT GTNTTAAATA ATGGTGGTTT TATCTAGTGG N 341

SEQ ID NO:7771

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09021

SEQUENCE DESCRIPTION:

GATCCAAGCC TGGAGTTTGC AGAAGATACT GTCCTAATAA GCAGGCATTT CTAAACCAAG 60  
 TATCTAAGCC TAAGCACAGC TTGTCCTGGG TGAAATGTCT GCCACAAAAG ATAGTTTCTC 120  
 CTAGCTCAGA CTTAACCATT TATAAAGGTT GGTAATAATAC TGGCAGTGAC AACAAATTGA 180  
 CTTTTTAATT TTTTATTTG CATTATTCCA ATAAATGAAA ATCTGTCAGA GTTCTAAA 238

SEQ ID NO:7772

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09022

SEQUENCE DESCRIPTION:

GATCTGCCCC CACTGTCCTG TGAGGACAGC TGAGGCCAAG NAGTGAAAAA CCTATTACTA 60  
 CTAAGAGAAG GGGTGCAGAG TGTTTACCTG GTGCTCTCAA CAGGACTTAA CATCAACAGG 120  
 AAA 123

SEQ ID NO:7773

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09023

SEQUENCE DESCRIPTION:

GATCCAGGTA GAATTTTNAACCAATCAAA TGAAAAAAC AAACAAACAA AAAAGGAAAT 60  
 GTCATGTGAG GTTAAACCAG TTTGCATTCC CCTAATGTGG AAAAAGTAAG AGGACTACTC 120  
 AGCACTGTTT GANGATTGCN TCTTCTACAG CTTCTGAGAA TTGTNTTATT TCACTTGCCA 180  
 AGTGAAGGAC CCCCTCCCCA ACATGCCCA GCCCACCCT AAGCATGGTC CCTTGTCACC 240  
 AGGCAACCAG GAAACTGCTA CTTGTGGNCC TCACCAGAGA CCAGGAGGGT TTGGTTAGCT 300

# EP 0 679 716 A1

CACAGGACTT CCCCCACCCC AGANGNTTAG CATCCCATAC TAGACTCNTA CTCAACTTNN 360  
N 361

5 SEQ ID NO:7774  
SEQUENCE LENGTH:54  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
10 CLONE:HUMGS09024  
SEQUENCE DESCRIPTION:  
GATCAAGCGA ACTAATTTTA GGTGAAATC CGAATAAAAG AACTTTACTG GAAA 54

15 SEQ ID NO:7775  
SEQUENCE LENGTH:188  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09025  
20 SEQUENCE DESCRIPTION:  
GATCTGTATA ATGTACATTC AATATAGAAA GCTTTATATA TTAAAAAGNG TATAGAACAT 60  
TTNACAATTA CACTCATCTT TAACATAACA TCTTGACATC CATTTTNAAA TTTTTTGCA 120  
CAAGCTCCTT TNCATTCAAT TTGGTAAAGC CAGTTATACA TACTANTGTG TACTGTGAGC 180  
TTCAGAN 188

25 SEQ ID NO:7776  
SEQUENCE LENGTH:221  
SEQUENCE TYPE:nucleic acid  
30 TOPOLOGY:linear  
CLONE:HUMGS09026  
SEQUENCE DESCRIPTION:  
GATCACCTGN AGGTCAGGAA GTTTGAAAAC CAGCCTGGCC AACATGGCAA AACCCGTGTCT 60  
CTACTAAAAC AAAAATNAGC CAGCATGATG GCAGGCGCCT GTAGTCCNNN CTATTCAGGA 120  
35 GGCTGAGGCA GGAGAATCGC TTGAACTGGG AGAGGGGCAG AGGTTGCAGT GAGCTGAGAC 180  
TGCATTCCAG CCTGGGCGAC ACAGCAAGAG TCTGTCTCAA A 221

40 SEQ ID NO:7777  
SEQUENCE LENGTH:200  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09027  
SEQUENCE DESCRIPTION:  
45 GATCGTAGGA ATTGAAGGAG TGTCCCGCCT TGTGGCTGAN AACTGGACAG TGGCAGGGGC 60  
TGGAGATGGG TGTNTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGCGCG CGCGNCAGTA 120  
CAAGACCGAG ATTGAGGNAA ANCATGTCTT CTGGGTGTNA CCATGTTTCC TCTCAATAAA 180  
GTNCCCCTGT GACTCAAAA 200

50 SEQ ID NO:7778

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EP 0 679 716 A1

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09028

SEQUENCE DESCRIPTION:

GATCCTGGTC CCCTCCCTGC TGGACCTGCC ACCCAGAGCT TCCTGNCTAG TCCCACTGGG 60  
 CTGGCCCACC AGGCCTCTGA CCCAGGCTGC TCTNCGGCCC CTTCTCCTC CTNTTCCTGC 120  
 TCCAACTTCT GTCCACCTGG GGACAGTCTG TGCCTGTAGC CTNATGACCC CAACCCAGCC 180  
 CCAGGCATGG CTAACCCTG ACTGNTTGCC TCATATTTAA GCTGCTGNTN TGGCCAAGTG 240  
 NCTAATTTTA ACCCAGACCT NAATAAAGAC ACNTNTTGT ACCAAA 286

SEQ ID NO:7779

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09029

SEQUENCE DESCRIPTION:

GATCTGATTT TTCATAAAAA ACATTTGTGA ACCTTCGGCA TAAATGGGTT AAGGTGCCAT 60  
 CCTGAAACT GCAATGCAGA TATGTTCAAG TAACCTTAT TTNTTAATTA AAAATAAATC 120  
 TTTCAAA 127

SEQ ID NO:7780

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09030

SEQUENCE DESCRIPTION:

GATCTGANTT TTCATAAAAA ACATAAANTG ACCTTCGGCA TAAATAGGTT AAGAAGCCAT 60  
 CCCANAACT NCAATGCAGA TATGTTCAAG TAACCTTTAT TTTTN 105

SEQ ID NO:7781

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09031

SEQUENCE DESCRIPTION:

GATCGGCGCC GTTACAGACG TGGCTACTAT GGAAGGCGCC GTGGCCCTCC CCGGAATNCT 60  
 GGTGAGATTG GAGAGATGAA GGATGGAGTC CCAGAGGGAG CACAANTNNN GGGACCGGTT 120  
 CATCGAAATC CAACTACCG CCCAAGGTAC CGTAGCAGGG GACCTCCTCG CCCACGACCT 180  
 GCCCCAGCAG TTGGAGAGGC TGAAGATAAA GAAAATCAGC AAGCCACCAG TGGTCCAAAC 240  
 CAGCCGTCTG TTCGCCGTGG ATACCGGCGT CCCTACAATT ACCGGCGTCG NCCGNTTCCT 300  
 CCTAACGGTN CTTACANGT N 321

SEQ ID NO:7782

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09032

SEQUENCE DESCRIPTION:

GATCCACTGA GTTAGTTTCA TTGGGGCGGG GGAAAGAACT GGAATTAAAC TTGTTTAATC 60  
CTTAAA 66

SEQ ID NO:7783

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09033

SEQUENCE DESCRIPTION:

GATCCTCCCA GCTGTCGGCC GCGGACCCGG GCCGCGTGTG AGCGGCTTTT GCACCTCCTA 60  
TCCCCAGGGT CCGCCGAGAG CCACGATTTT TTTACAGAAA ATNAGCAATA AAGAGATTTT 120  
GTACTGTCAA A 131

SEQ ID NO:7784

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09034

SEQUENCE DESCRIPTION:

GATCACAAAT GCATTTTTC A TCTTTACAA TATGAAATNT ATTTATAACT TTAGTTCCAA 60  
AATGGACTCT GTAATGCATT TGCCCATATT TTTAGTCGTA ATGGATGTGA TTATATTNA 120  
TTGAATTAAA AATCTAACAG AAA 143

SEQ ID NO:7785

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09035

SEQUENCE DESCRIPTION:

GATCTTAACT TTAATAAGGC AAAACAAAAG CTTGAGCTG TTGCGTGTGT AAGTCTGTTG 60  
TGTGGATGTN CGTGTNTGGT CCCCAGCCCC AGACTGGATT GGAAAAGTGC ATGGTGGGGG 120  
CCTCGGGGCT GTCCCCACGC TGTCCTTTG CCACAAGTCT GTGGGGCAAG AGGCTGCAAT 180  
ATTCCGTCCT GGGTGTCTGG GCTGCTAACC TGGCCTGCTC AGGCTTCCCA CCCTGTGCGG 240  
GGCACANCCC CAGGAAGGGA CCCTGGACAC GGCTCCACG TCCAGGNTTA AGGTGGATGC 300  
ANTTTCNGNA ACCTCCANTC TTCTGTGTAG CANCTTTAAC CNAGN 345

SEQ ID NO:7786

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09036



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## SEQUENCE DESCRIPTION:

GATCAGCTCT CTGTGAAAAT GGACCAATCA TCAGGATGTG GGTGGGGCCA GATTAGGGAA 60  
 TAGAAGCAGG CTGTCTGAGC CAACAGTGTG ANCATGCTTG GGTCCCCTTN CATGCTGTGG 120  
 AAACTTTGTT CTTTCGCTCT TCACANTAAA TTTTGCTGCT GCTCAAA 167

SEQ ID NO:7787

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09037

## SEQUENCE DESCRIPTION:

GATCCTGGAC AAAGCTTGGC TGCCGGCTTC ATTTATTCCT GCTGATGGCT GAGAAGCATC 60  
 TGTTTTCCAT CCCACTTGCC TGTCCCAAGT TTTGTTCCAT TTTNAAAAA TTTGTTGTAA 120  
 ACTGCATGTT TTATAAAATA AAAATAAAAT ATCGTTTGTA ATTTATCTCA AA 172

SEQ ID NO:7788

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09038

## SEQUENCE DESCRIPTION:

GATCCGCCCA CCTTNGGCCT CCCAACACAA TTTATATTTT TGANGGTCCT TTTATGTGTA 60  
 TTGTGCCATA TGCTTCTNAC ATCAGCCCCA ATAAATGCTT TAGGCGTTTT ATATTATCTA 120  
 CCACTATTAC ATGCTCTCCA TCTCCAGACT ACCCATTTCT GCCATTGCCC TCATAGGGGC 180  
 CCATTCTGAT AATTCTGGAT ATGTAGAAAA ATAAATCCTG TTTATGTGTT TAAATAAATA 240  
 GATGTATACT ATAAA 255

SEQ ID NO:7789

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09039

## SEQUENCE DESCRIPTION:

GATCCCTGAC AGCAAAAAGT TTCTTTTCTG AGGCTGCCAT ACTGCCACTG TCCAGGTGGA 60  
 GACTGAGCAA AGGAAGTCCT GGGCTGTGCC AGCTCCAGA GCTTCGGAAG AAAGAGCAGC 120  
 AGCTCTCTCC CTGGGAACCA TCAGAGAATT CTGTTGATGT GTTCTGTGTC TGTCTGTCAC 180  
 CTGGTCACGA GCTTCTACCA CCTTTGCAAT TGTCATTAT CTTTCACTCC CTGAATAAAG 240  
 TATCTATGCA TATAAA 256

SEQ ID NO:7790

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09040

## SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTCCAC CTTTCGGGCC ATGTTGCCCC CGTGAGCCAA TCCCTCACCT TCTGAGTACA 60  
GAGTGTGGAC TCTGGTGCCT CCAGAGGGGC TCAGGTCACA TAAACTTTG TATATCAACG 120  
AAA 123

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SEQ ID NO:7791  
SEQUENCE LENGTH:310  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09041  
SEQUENCE DESCRIPTION:

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GATCTAGCTT CAGAGGAAGT CTACACCCCA TTCCCTTCTG CTTACAATGT ACCCATGATA 60  
TGTGTTTAGC NNNNGAATAC TGTAACAGGA CATCACATGG AAAAATCAAA GCAGCTGGCT 120  
CACTGTATTT AACTGAAAAG AATGCCTACA GATTGGATAT TTAATAGGGA AAATTAAGGC 180  
ACTTTAATAA CANACTTCAT TATGTGAAGT TGTGGAATAT TNNCATAACAN TATACCTTGT 240  
ATATTANTGC CATAGTTTTT NGAAACACTA ATTTAAACAA CANATTTNAG GGGTGTGGC 300  
ATATCCCAGN 310

20

SEQ ID NO:7792  
SEQUENCE LENGTH:61  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09042  
SEQUENCE DESCRIPTION:

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GATCCGAAGG CTGCGGGCAG CGTNTNATCC CGTGGTTTAA TAAAGCTGCC GCGCGCTCAA 60  
A 61

30

SEQ ID NO:7793  
SEQUENCE LENGTH:310  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09043  
SEQUENCE DESCRIPTION:

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GATCTTGGTC TTATTTGCAC AGTTTTTGCG TCTTGTTTGC TTCTTGCATC TGATTAACATA 60  
GAATATTTCT NTTTCCCCCT TTTAATTTGT GATGTCACTT GACCCCATTT ATGTGTAGGA 120  
GCACTACNCC ATTGGTTTCC AATACTGCAC ACATAAGATA CATACTTGTG TGCAGAAAAGT 180  
ATCTTCCTCC AGGCTTGTAA TACCCTTCAC ATGGAAGATT AATGAGGGAA ATCTTTATAT 240  
TCTGTATAAA ANCAAANGCA AATTTATATA CTAAAATCAT TTGTCTAAAA NTTTAAGTNG 300  
TTTTCAAATN 310

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SEQ ID NO:7794  
SEQUENCE LENGTH:165  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09044  
SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

GATCAGTAGA AAATGGACAT CAAGTTTGAA CAGATAAATC ATGGACAGCC TTATTGTGAT 60  
TGAAATGCTT GTAGGTTCTG TGCCAAATTT CCACCACTGT GTACTTTGTT GCTATTTAAA 120  
ACTGTATCAA CTCTAACGGA AGAATAAATT ATTTGTGATT TAAA 165

SEQ ID NO:7795  
SEQUENCE LENGTH:149  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09045

SEQUENCE DESCRIPTION:

GATCCGAGAG TNAAGGAAGT TCCCTGTNTT CCCCCTCCTT TTCCACCACT NTCGCCTCTG 60  
GCCTTCTCTG GCCACTCCTG GGAGGGACTG CCTCACCACC CCTGTCCCGC TGCCAGAAAT 120  
ACACCCACAA TAAAAACCTG AAAACCAAA 149

SEQ ID NO:7796  
SEQUENCE LENGTH:98  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09046

SEQUENCE DESCRIPTION:

GATCCAAACT AACTGCCAA GCACTACACA GCTGGACCCT GNTTCACCNT AACCCGCANC 60  
TAGCAATCAA TACAGCTTCA TTATCTGAGT TGCATAAA 98

SEQ ID NO:7797  
SEQUENCE LENGTH:265  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09047

SEQUENCE DESCRIPTION:

GATCTNTAGC CTCACCCTGN TCTCCTTCCT CCTACTGGCT GCTCAGGTGC TCCTGGTGGA 60  
GGGGAAAAAA AAAGTGAAGA ATGGACTTCA CAGCAAAGTG GTCTCAGNNC AAAAGGNCAC 120  
TCTGGGCAAC ACCCAGATTA AGCAGAAAAG CAGGCCCGGG ANCAANGGCA AGTTTGTAC 180  
CAAAGACCAA GCCAACTGCA GATGGGCTGC TACTGAGCAG GAGGAGGGCA TCTTTCTCAN 240  
GGGNNGGGTG CACTCAATTG GNNNN 265

SEQ ID NO:7798  
SEQUENCE LENGTH:146  
SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09048

SEQUENCE DESCRIPTION:

GATCTTACCC GTGCNTGGNC CCCTCCCTC ANAGCCCATG GTAACGAACC CCTAGAAAGG 60  
AGAGAACGGG CGTCAGGGGT GCACAGTCCA CAGCTGAAGA GCAAGGTTN GTGGCAGCAC 120  
GGNCCGGCCC CTCACCCTCT NTNCCN 146

SEQ ID NO:7799

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09049

SEQUENCE DESCRIPTION:

GATCTCCGGA CCTCGGCTGC AGAGGCCATC GCAGCTTTTN AAAAGTNAAG TGGTTAATTC 60  
CCATTGGTGT CTTTNCCTAT AGCATTTCN TCTAACCTAT AACAAGGGG CATTACATTT 120  
ANCTTTAGAA CATGTGAATA GGAGGTTTNC TCATGACTTA CCATTCCAGC TGNATGGGAA 180  
AGCAAAGCAG AAAACAGTGC CCCAAATGGA AAANAGNTAC TCACACAGAN CAAAACAGTT 240  
CTNGGTCTTG TCCTTGGTCT TGTCAAACCT TGCCTGATGC TCTTTCTAAN GTCNAAATAT 300  
GANTGATAAG CCNGGCN 317

SEQ ID NO:7800

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09050

SEQUENCE DESCRIPTION:

GATCTGGTTA AGTTGTGTAG TAAAGCATT A GGAGGGTCAT TCTGTGACA AAAGTGCCAC 60  
TAAAACAGCC TCAGGAGAAT AAATGACTTG CTTTTCTAAA TCTCAGGTTT ATCTGGGCTC 120  
TATCATATAG ACAGGCTTCT GATAGTTTGC AACTGTAAGC AGAAACCTAC ATATAGTTAA 180  
NATCCTGGNC TTTCTTGGTA AACAGATTTT AANTTTCTGA TATAAANCAN GCCNCAGGAG 240  
AATCGGGGA TTTNAGGTTT NCNGAATAGC CTATATATGG TGCATCGGNT AGGTCNTTAT 300  
TGATTTTTTG ACCCTTTTCG GCTTTACCTN ATGGGAAGAC CCNGTTCNTT TTAAATNAT 360  
CCNGGTTTTT GN 372

SEQ ID NO:7801

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09051

SEQUENCE DESCRIPTION:

GATCAACCTC TGAATTTTAC ATCATGAATG TAATCACCAC TGGAGCTTCA CTGTTACTAA 60  
ATTATTAATT TTTTGCCTCC AGTGTTCTAT CTCTNAGGCT GAGCATTATA AGAAAATNAC 120  
CTCTGCTCCT TTTTATTGCA GAAAATTGCC AGGGGCTTAT TTCAGAACAA CTTCCACTTA 180  
CTTTCCACTG GCTCTCAAAC TCTCTAACTT ATAAGTNTTG TGAACCCCA CCCAGGCAGT 240  
ATCCATGAAA GCACAAGTGA CTAGTCCTAT GATGTACAAA GCCTGTATCT CTGTGATGAT 300  
TTCTGTGCTC TTCCTCTTT GCAATTGCTA AATAAAGCAG ATTTTATAAA TACAAA 356

SEQ ID NO:7802

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09052

# EP 0 679 716 A1

## SEQUENCE DESCRIPTION:

GATCAAGCAG ATTCCACGAA TCCTCGGCCC AGGTTTAAAT AAGGCAGGAA AGTTCCTTC 60  
 CCTGCTCACA CACAACGAAA ACATGGTGGC CAAAGTGGAT GAGGTGAAAT CCACAATCAA 120  
 GTTCCAAATG AAGAAGGTGT TATGTCTGGC TGTAGCTGTT GGTACAGTGA AGATGCCNGA 180  
 CGATGAGCTT GTGTATAACA TTCACCTGGC TGTCAACTTC TTGGTGTCAT TGCTCAAGAA 240  
 AANCTGGCAG ANTGTCCGG GGCCTTATNT TNTCAAGAGC ACCNTGGGGN AAAGCCCCCA 300  
 GNGGCCNTTT NTTAAGGGCA CCGTTTNGAN NTAAATTTT TNGTTANCC AGTTCNAAA 359

SEQ ID NO:7803

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09053

## SEQUENCE DESCRIPTION:

GATCCGGCCA GTTCATTGAA CAAACCTTTC CTTTTCTAA AGTTCAGAA GCCTTCCTGA 60  
 AGGTGAAAAG AGGACACGCA CGAGGAAAGA CTGTAATTAA TGTGTTTAA ATAAAAATGC 120  
 AGTTTAGTGA TAAA 134

SEQ ID NO:7804

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09054

## SEQUENCE DESCRIPTION:

GATCTACTGA CATTAAGCAC TTTGTACAGT ACAAATATA GTCTACATT GTTTAAACA 60  
 AA 62

SEQ ID NO:7805

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09055

## SEQUENCE DESCRIPTION:

GATCTGGATG ATGGTTATGT AGCTGCATAT ATTTGTCAAC ATTCCTCATG CTGTATGTTT 60  
 AGATTGTGA TTTTACTATA TGTAATTAA TTCCTTAATA AAATACTATT ATAAAAATAA 120

SEQ ID NO:7806

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09056

## SEQUENCE DESCRIPTION:

GATCTAATCT TCTGTGCTCT GTGTATTGGC GACGAGCAGG GTGAGAATAA GTGCGTGCCC 60  
 AACAGCAATN AGAGATACTA CGGCTACACT GGGGCTTTCC GGTGCCTGGC TGAGAATGCT 120  
 GGAGACGTTG CATTTGTGAA AGATGTCACT GTCTTGACAG AACTGATGC CCTCCTGGAA 180

GCCTGTGAAT TCCTCAGGAA GTAAAACCN

209

SEQ ID NO:7807

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09057

SEQUENCE DESCRIPTION:

GATCTTAATT TAAAAATTA AAACCTGGNG TTTTAAAT AAAACCTTT TGTCTTAA 59

SEQ ID NO:7808

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09058

SEQUENCE DESCRIPTION:

GATCAAAGTA ATTGCTTAA TGTCTTGTTG AATNAGCTGT CACCTTATAG TTTATGTATT 60  
GTGGTGGGTA CCTTAATAAT AAAAGATTT TTAATGTAA 100

SEQ ID NO:7809

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09059

SEQUENCE DESCRIPTION:

GATCTGTTTG ATGGTTACAT CAGTGTATAT TTGTCAAAT TCCTCAAAC GTATGCTTAA 60  
GGCTTTGTGC ATTGTATTGC ATGTAAATNA TACTTCAATA AAGTACCAAT AGCATAAA 118

SEQ ID NO:7810

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09060

SEQUENCE DESCRIPTION:

GATCCATAAC CTCTTTAGAG ACCGGCTCCT GGATGCAGAA TCCTATGAGG TTCTGGCCAC 60  
ACCTGTTTCT TGTCCNTCAG GGGCTGACAC CCATGTNCCA TCCCTCTAAA CCCCTGTCCC 120  
TAAACCTACC CCATCTNATG TAACTCTGGG GTTCCTTGGT CATTAGAGGG TTTNAGGTC 180  
AAA 183

SEQ ID NO:7811

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09061

SEQUENCE DESCRIPTION:

# EP 0 679 716 A1

GATCTGAATG GTTTTAATAA GTGTCTGGNA ATTCCCCTGC TTGCACTTGT NTNTCTCGCC 60  
CACCACCACG TAAGACGTGC CTGCTTCCCC TTCTGCCATG ATTGTAAGTT TCCTGAGGCG 120  
TCCCCAGCCA TGCAGAACTG TGAGTCAATG AAACCTCTTT TTTTATAAA TTAAA 175

SEQ ID NO:7812  
SEQUENCE LENGTH:329  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09062  
SEQUENCE DESCRIPTION:

GATCCCCCAT TCCCCACCCT GGGAGATGAG GGGGTCCCCA TGTGCTTTTC CAGTTCTTCT 60  
GGAATTGGGG GACCNCCGCC AAAGACTGAG CCCCCTGTNT CCTCCATCAT TTGGTTTCCT 120  
CTTGGCTTTG GGGATACTTC TAAATTTTGG GAGCTCCTCC ATCTCCAATG GCTGGGATTT 180  
GTGGCAGGGA TTCCACTCAG AACCTCTCTG GAATTTGTGC CTGATGTGCC TTCCACTGGA 240  
TTTTGGGGTT CCCAGCACCC CATGTGGATT TTGGGGGGTC CCTTTTGTGT CTCCCCCGCC 300  
ATTCAAGGAC TCCTNTCTTT TTTCAANN 329

SEQ ID NO:7813  
SEQUENCE LENGTH:326  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09063  
SEQUENCE DESCRIPTION:

GATCTGCCAG CCCTACATCC GGCCGGGGCC CAGGGAGGGG AGCAAGGAGA AGGCAGGTGC 60  
GCGCANAAGC GGGCCCTGGA GGAAGAGGAG GGTGGCACGG AGGTCCTGTC CAAGAACAAG 120  
CAAAAGAAGC AGCTGAGGAA CCCCCACAAG ACCTTCGACC CCTCTTTGAA GCCAAAATAT 180  
GCAAAGTNTG ACCAGTGTGG AAACCCAAAG GGCAACAGAT GTNTGTTGAG CCTGTGCCGN 240  
GGCTGCTGCA NGANGCGNGC CTTCAAAGNG ACTGCAGACT GNCCAGGTNA CGGTTTGCTT 300  
TTTAAACCA ATTTNGGAGA AGTTTN 326

SEQ ID NO:7814  
SEQUENCE LENGTH:20  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09064  
SEQUENCE DESCRIPTION:  
GATCGGAATG NAAATCTAAA 20

SEQ ID NO:7815  
SEQUENCE LENGTH:248  
SEQUENCE TYPE:nucleic acid  
TOPOLOGY:linear  
CLONE:HUMGS09065  
SEQUENCE DESCRIPTION:

GATCAATGTT GAAAGTGTG TTATATGGCA AGTNTTTAAC ACATTCACAG TGTTTGTGTTG 60

EP 0 679 716 A1

5      ATTCAACTG TGAATTGTCT TACAGTTTTT TCAAACCTAG TTGTTTCTAT GGACACCTGC 120  
       TCTGAATTGT ACATTGACTN CATTACTAAA GAACAAAAAT GTTCATTTTT GTCCCAGTAA 180  
       ATTGAGACTG CTTGTACACT TTCAGAAAAA TATGTGAATT TATAAAGNTT TTGTAGATAC 240  
       TTGTCAAA 248

10      SEQ ID NO:7816  
       SEQUENCE LENGTH:87  
       SEQUENCE TYPE:nucleic acid  
       TOPOLOGY:linear  
       CLONE:HUMGS09066  
       SEQUENCE DESCRIPTION:  
       GATCCCCGGA TTTNACACTC CTTCTGTTTT GTTGCCGTTT ATTTTGTAC TCAAATCTCT 60  
       ACATGGAGAT AAATNATTTA AACCAAA 87

20      SEQ ID NO:7817  
       SEQUENCE LENGTH:267  
       SEQUENCE TYPE:nucleic acid  
       TOPOLOGY:linear  
       CLONE:HUMGS09067  
       SEQUENCE DESCRIPTION:  
       GATCCACCTG NCCCTGACCT CCGACAGTGC TGGGATTACA GGCATAGCCA CCGTGCCTGA 60  
       CCAGGGCTCT TTTAGCAAGG AAAACGTGAG GAATGAATGG CTGTTGGTGT GCAACAAATC 120  
       ATACTTGCTA CATGTTGTGA ACCTGAAAGT ATTTGTTAGT CTGTATGAAG AATGTACCCC 180  
       AGAGATGCAC CCTGTATCTG CCTTATGTCT CTTACAATGG AGGTTCTCTC CTGTTATATT 240  
       GCTGAATAAA CTATGTGAAC TGCTAAA 267

30      SEQ ID NO:7818  
       SEQUENCE LENGTH:22  
       SEQUENCE TYPE:nucleic acid  
       TOPOLOGY:linear  
       CLONE:HUMGS09068  
       SEQUENCE DESCRIPTION:  
       GATCTTCAAG CAAGAAAATA AA 22

40      SEQ ID NO:7819  
       SEQUENCE LENGTH:90  
       SEQUENCE TYPE:nucleic acid  
       TOPOLOGY:linear  
       CLONE:HUMGS09069  
       SEQUENCE DESCRIPTION:  
       GATCATAGCT GAAAAATTAAT GATACTGTCA ATTTGAGATA GCAGAAGTTT CACACATCAA 60  
       AGTAAAAGAT TTGCATATCA TTATACTAAA 90

50      SEQ ID NO:7820  
       SEQUENCE LENGTH:25

55



EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS09070  
 SEQUENCE DESCRIPTION:  
 GATCATTAAA AAATTAATAA AGAAA 25

SEQ ID NO:7821  
 SEQUENCE LENGTH:33  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS09071  
 SEQUENCE DESCRIPTION:  
 GATCCCAATG AAACGAATTC TGTCTCCCTG AAA 33

SEQ ID NO:7822  
 SEQUENCE LENGTH:23  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS09072  
 SEQUENCE DESCRIPTION:  
 GATCTTCAAG CAAGTTAANT AAA 23

SEQ ID NO:7823  
 SEQUENCE LENGTH:75  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS09073  
 SEQUENCE DESCRIPTION:  
 GATCTTCATT TAGCTCCTTT ACTGGGATTT ATTGGATGCT NGTAAAAAAA TAAAATTTAC 60  
 ACTGTNTATG CGAAA 75

SEQ ID NO:7824  
 SEQUENCE LENGTH:284  
 SEQUENCE TYPE:nucleic acid  
 TOPOLOGY:linear  
 CLONE:HUMGS09074  
 SEQUENCE DESCRIPTION:  
 GATCAAGAAA GGGCTGTGGC TTGTATCAAA GGGTGTTTAA AAGGATTTAC TATCAGATTT 60  
 GGCCTTGTTT TCTGTGATTT TGGNNAGCGT TCAAGGAAGC CAGGCTTTGG TCTGGATTGG 120  
 ATGTTCTCAG GTCATGAATA TAATTCTCTG GGAAGTCCCA AAGTTCTCAT CTACAAAGCA 180  
 GAAGTTAATT GGAGCTGAAA ACTAATCAGT AAAGCCACAG CAGCCAGTCA TATGGGGGAG 240  
 AAGAGGGGAA TGTTTGATGG TTTTGTGGT TTAGAGGTGA GTTN 284

SEQ ID NO:7825  
 SEQUENCE LENGTH:21

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09075

SEQUENCE DESCRIPTION:

GATCCTTTGT TAACAAATAA A

21

SEQ ID NO:7826

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09076

SEQUENCE DESCRIPTION:

GATCATATTT ATTTTAACTA TTTTITTAGA AAATTATTAA TTTTAATTGT ATTTTGTAT 60

TTAAAAAGCT TCTTCACTTG TTTTCCCTAA NNNTTCANAT TGCTGCCCAA AAGTATGACT 120

GTGGAGGAAA AAAAANTACT TNAAAANTCC ACACITTTN 159

SEQ ID NO:7827

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09077

SEQUENCE DESCRIPTION:

GATCTGTGCA GGGTATTAAC GTGTCAGGGC TGAGTGTCTC GGGATTCTC TAGAGGCTGG 60

CAAGAACCAG TTGTTTTGTC TTGCGGGTCT GTCAGGGTTG GAAAGTCCAA GCCGTAGACC 120

CAGTTTCCTT TCTNAGCTGA TGTCTTTGGC CAGAACACCG TGGGCTGTTA CTTNCNTTNA 180

GTTGGAAGCG GTTTGCATTT ACGCCTGTAA ATGTATTCAN TCTTAANTTA TGTAAGGTNT 240

TTNTTGACG CAATTCTCGG TTCTTTGANG NGATGGCAAC AAATTTTGGG NTTCTACTGT 300

TATGTTGGGG NNCATTNGGG CCCANGNN 328

SEQ ID NO:7828

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09078

SEQUENCE DESCRIPTION:

GATCTCCTGA CCTCGTCATC CGCCCGTNTC GGCCTCCCAT AGTGCTGGGN TTACAGGCAT 60

GAGCCACCAC GCCCGGCTGT TTTATTTCTT ATAAGTGTAC AGGANNNN 108

SEQ ID NO:7829

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09079

SEQUENCE DESCRIPTION:

GATCATGAAG CCATCAGCTC CTCTGGGGCC AGCTANAGGA CAACAGAACT NTCACCAAAG 60

GACCAGACAC AGTGAGCACC ATGGGACAGT NTCGGTCAGC CAACGCAGAG GATGCTCAGG 120  
AATTCANTGA TGTGGNGAGG GCCATTGAGA CCCTCATCAA GAACTTTCAC CAGTACTCCG 180  
TGGAGGGTGG GNAGGNGACG CTGACCCCTT CTAAGCTACG GGACCNGGGT CACCCAGCAG 240  
CTGCCCCATN TTNATGCCGA GCAACTTNTN GNCTGGN 277

SEQ ID NO:7830

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09080

SEQUENCE DESCRIPTION:

GATCAGACCA AACAGTGCTG TTTCCCGGGG AGGAAACACT TTTTAATTA CCCTTTTGCA 60  
GGCTCCCACC TTTAATCTGT TTTATACCTT GCTTATTAAG TGAGCGACTT AAAATNATTG 120  
AAA 123

SEQ ID NO:7831

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09081

SEQUENCE DESCRIPTION:

GATCCAGAAA TGGAGACTGG ACCTTCCAGA CCCTGGTGAA TGCTGGAAAC AGTTCCTCGG 60  
AGTGGAGAGG TTTACACCTG CCAAGTGGAG CACCCAAGCC TGACGAGCCC TCTNACAGTG 120  
GAATGGAGAG CACGGTCTGA ATCTNCACAG AGCAAGATGC TGAGTGGAGT CGGGGGCTTC 180  
GTGCTGGGCC TGCTCTTCCT TGGGGCCGGG CTGTTCATCT ACTTCAGGAA TCAGAAAGGA 240  
CACTCTGGAC TTCAGCCAAC AGGATTCCTG AGCTGAAGTG AAGATGNCCA CATTCAAGGA 300  
AGAACCTTCT GCCCCAGCTT TGCAGGATGA ANCACTTN 338

SEQ ID NO:7832

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09082

SEQUENCE DESCRIPTION:

GATCTAATCT CAAATACAGT GCTTAGTAAG GGAACCTTTG TGCCTTTGGG GATTTGGGGA 60  
TTAAAACGAA TCTTTTAAAT ATATTTCCAA ATATTTAAAT ATAAAAGGAT ATTTCTCTG 120  
ATGTAAAAG TGAGTATGGG GGTGGCACAT TATATGGAAA GTNCCATGTT TGCTTAANTG 180  
CTATGTAAAA TAACTGGCA TATTANTGA CTTTGANTGT GAAANTCATA TGCCCTTNGA 240  
NTATGGNTGC CTTAGCTCAT TTGACANCTG GNAGANTACT TGTNTATCTN GTTTNAGACA 300  
CATTGANTN 309

SEQ ID NO:7833

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS09083

SEQUENCE DESCRIPTION:

GATCCAAAGT GGCAGGAGGT CTGTGTTGTC ATGGNGAACT GGAGTTTCTC TTGTAAGAGT 60  
TCCCTCATCT GAAATCATGT ATCTNTCTCA CAAATACAAG CATAAGTAGA AGATTGTTG 120  
AAGACATAGA ACCCTTATAA AGAATTATTA ACCTTTATAA NCATTTAANG TCTTGTNAGC 180  
ACCTGGGAAT TAGTATAATN CCANTGTAA TTTTTNNAT TTACATTTTG TNN 233

SEQ ID NO:7834

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09084

SEQUENCE DESCRIPTION:

GATCGGAATT TNACAGAATT GGGACTGTGG AACCNNGGGT CACTTGAATT TCCTATATT 60  
TGATGGCCA AATCAGGAAC CAGACAGTCT CCATAGTCN 99

SEQ ID NO:7835

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09085

SEQUENCE DESCRIPTION:

GATCAGCCGA TGACAGAGAT TGTAAGCCGT GTGTCGAAGC GAAACTGGNG CCGCCACGTG 60  
CGGGCNCTGG TGCTTGACCT GTGCTGTAAC GACGAGAGCG GCGAGGATGT CGNGGGGCNA 120  
NAAAANCNGT ACACCATCCG CTGACCCCGT CTGCTCCTCT AGGCTGGCCC CTGTCCACC 180  
CCTCTCCACA CCCCTTCCAG CCCAGGGTTC CCATTTGGCT TCTGGCAGTG GCCCAACTAG 240  
CCAAGTCTGG TGTTCCCTCA TNATCCCNCT TACCTGAACC CNTNTTGN 288

SEQ ID NO:7836

SEQUENCE LENGTH:32

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09086

SEQUENCE DESCRIPTION:

GATCTAAATA AAATGGACNG TTCTACCTTA AA 32

SEQ ID NO:7837

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09087

SEQUENCE DESCRIPTION:

GATCTGAAAC AGATGAAAGT TATAATAGTT TACATACCTT ACCTTAAAGT ATGGTTTTTA 60  
AATACTTAAG ATGTGATATG ACATATAGTG TGTATATATA TCTNATNCTA NNGGAAAAAG 120  
GGACATTAAA AAAGCTTATG TTAAGATA-AA 152

5  
10  
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45  
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SEQ ID NO:7838  
SEQUENCE LENGTH:108  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
GATCGTTTCTT CATGGGGGTA AGAAAAGCTG GTCTGGAGTT GCTGAATGTT GCATTAATTG 60  
TCCTGTTTGC TTGTAGTTGA ATAAAAATAG AAACCTGAAT GAAGGAAA 108

SEQ ID NO:7839  
SEQUENCE LENGTH:30  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
TGAAAATTTA TTACTACAGT GTTTTCACCA 30

SEQ ID NO:7840  
SEQUENCE LENGTH:20  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
TAATACGACT CACTATAGGG 20

SEQ ID NO:7841  
SEQUENCE LENGTH:25  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CTTCTTTCTG TAGCCAGGTA ACTCT 25

SEQ ID NO:7842  
SEQUENCE LENGTH:25  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
TTTTCGGCGC TCCATTTAT TCCTT 25

SEQ ID NO:7843  
SEQUENCE LENGTH:35  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CACGAATTCA CTATCGATTC TGGAACCTTC AGAGG- NH2 35

SEQ ID NO:7844  
 SEQUENCE LENGTH:37  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 SEQUENCE DESCRIPTION:  
 CTCGCTCGCC CATCCTTATA CAGGCTCAGT TTTGTCT 37

SEQ ID NO:7845  
 SEQUENCE LENGTH:37  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 SEQUENCE DESCRIPTION:  
 CTCGCTCGCC CATGTATAGG GACAGCATTT CTGAGAG 37

SEQ ID NO:7846  
 SEQUENCE LENGTH:38  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 SEQUENCE DESCRIPTION:  
 CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

SEQ ID NO:7847  
 SEQUENCE LENGTH:22  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 SEQUENCE DESCRIPTION:  
 CCAGGGTTTT CCCAGTCACG AC 22

SEQ ID NO:7848  
 SEQUENCE LENGTH:22  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 SEQUENCE DESCRIPTION:  
 TCACACAGGA AACAGCTATG AC 22

## 50 Claims

1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

2. A DNA probe consisting of a purified single-stranded DNA , a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

Fig. 1

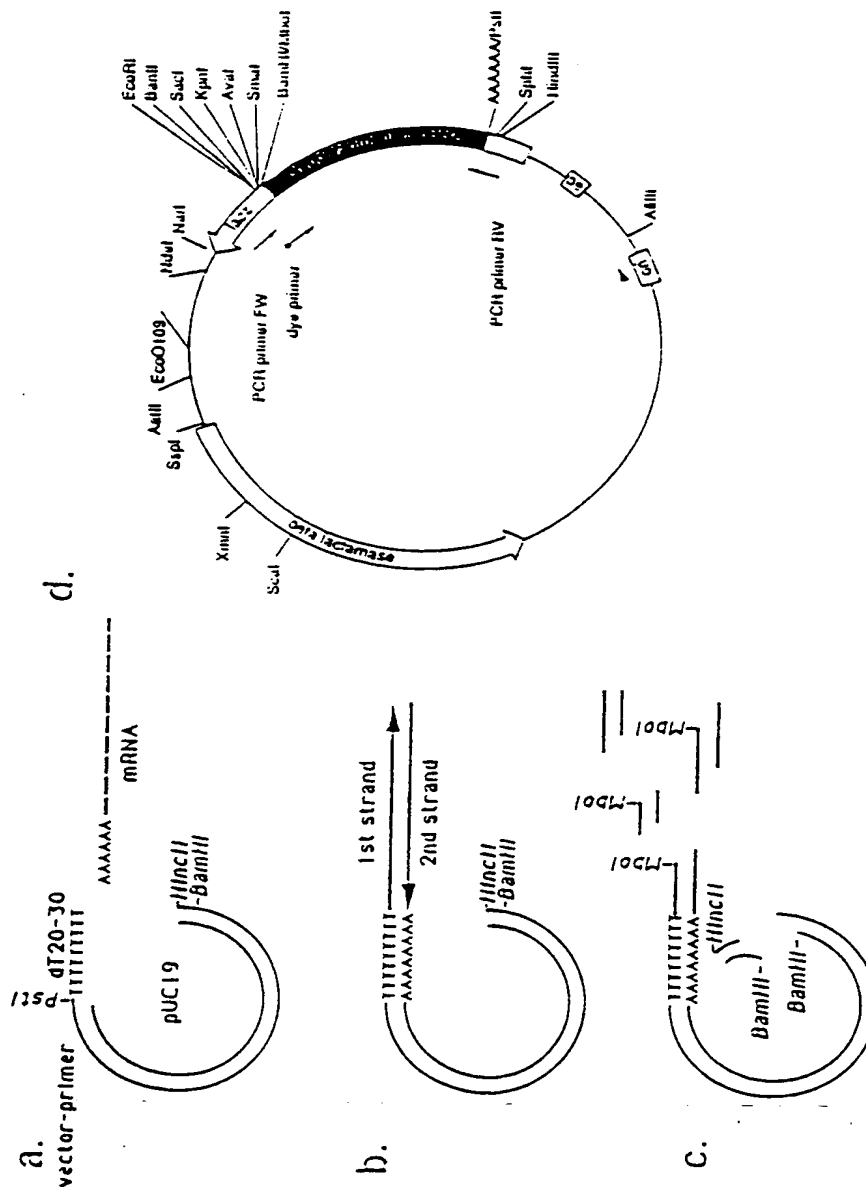




Fig. 2

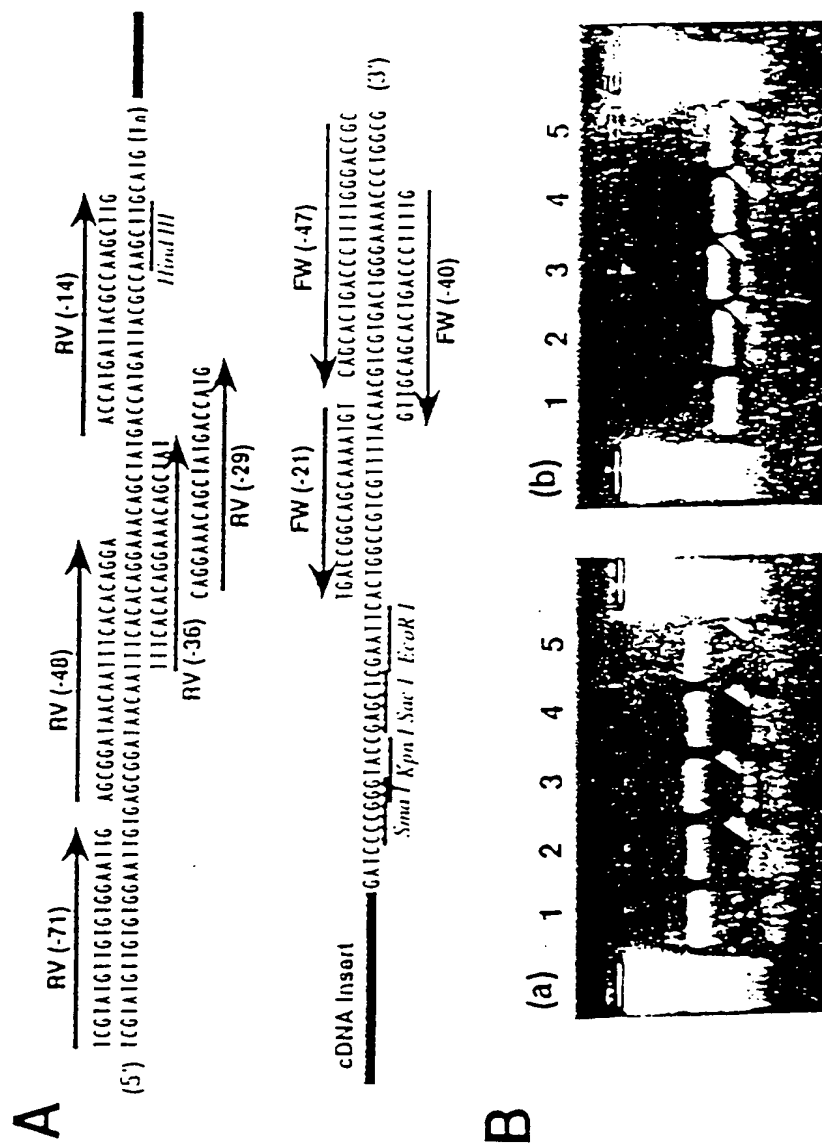


Fig. 3

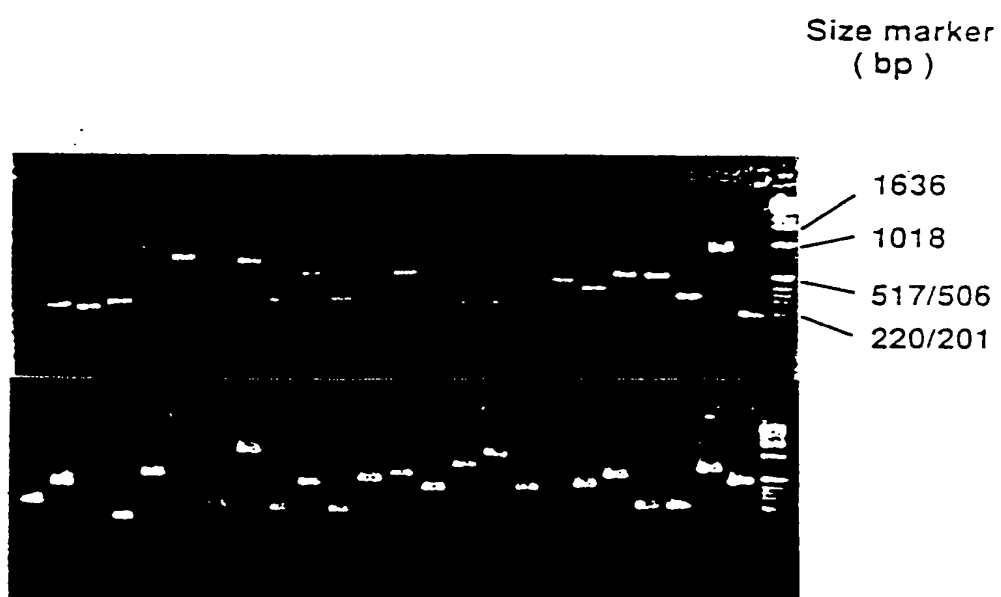


Fig. 4

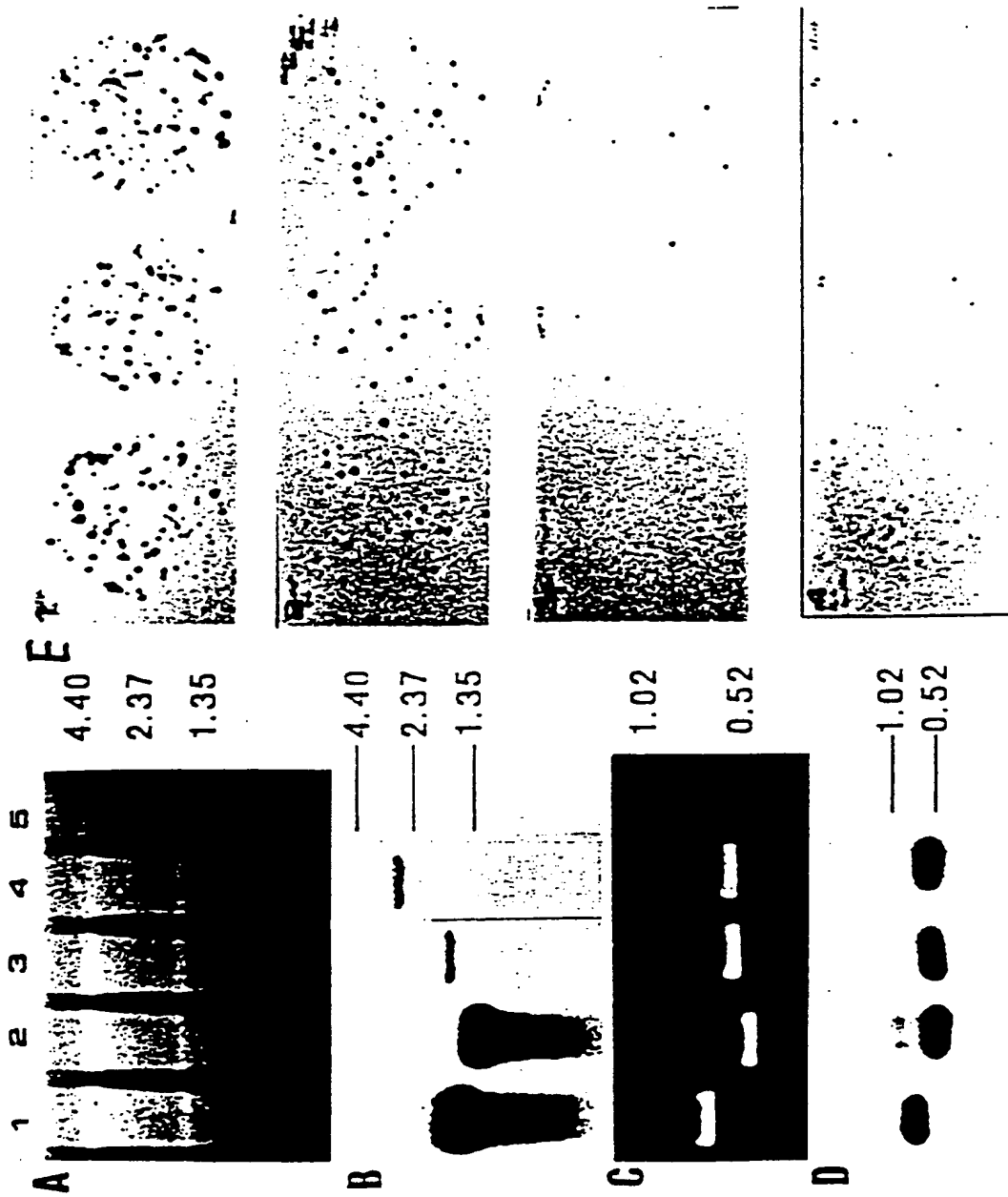


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- $\alpha$	$\alpha$ 1-antitrypsin	HnRNP core protein A1	Inter- $\alpha$ -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b) $\times 10$	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library				
Group	Clone	Gene	A in 982 (%)	B "in 8,800 (%)" C "in 26,400 (%)"
I	a15	Elongation factor - 1A $\alpha$	22 (2.2)	307 (3.5)
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)
	lb030	$\alpha$ -1-antitrypsin	8 (0.8)	119 (1.4)
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)
	c13a04	NADP(H) Menadione oxidoreductase	4 (0.4)	27 (0.3)
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)
	lb042	Human RNP core protein A1	2 (0.2)	7 (0.1)
	s155	unknown	1	5 (0.02)
	s159	unknown	1	4 (0.02)
	s639	unknown	1	3 (0.01)
II	s635	unknown	1	2 (0.01)
	s170	unknown	1	1 (0.004)
	s154	unknown	1	1 (0.004)
	s167	unknown	1	1 (0.004)
	s645	unknown	1	1 (0.004)
	s647	unknown	1	1 (0.004)
	s632	unknown	1	0 (<0.004)
				0 (<0.004)

Fig. 6

Sequences of primers													
GS	Cit	Chromosomal position	Sense		Anti-sense		AT	HO	HE	HO	CO	G	T
			Sense	Anti-sense									
91000788	pm2366	1	CAGAGCCCGAGTACACTAT	AAGTTATGTGGGGTCTAG	48	114	115	104	110	1	2		
91001026	pm2444	1	AATGGGACAGTTACACTGA	CCAGCTTCCTTGACTTGAGA	48	83	81	>200	>200	1	1		
91001075	pm0883	1	TGGACTGTGGATACCTATCT	ACAAGTACCCCTGATGGCT	48	124	124	103	107	4	4		
91001087	pm1772	1	GTACTCTCAGCCATAGCAC	ACCATCTCAGCCACACACT	50	104	104	180	>200	6	6		
91001094	pm0347	1	GCCCTTAACACGAGGAAGT	TAAITCCCACCTCCGTAAC	51	114	116	>200	200	1	1		
91001116	pm1771	1	GGGTTTCAATAGGGGTAGACC	GCCCAATCTGTCAAACTG	49	95	95	78	107	1	1		
91001191	pm0609	1	TTCGTGATGTAACTTTG	GGCTGAACATTCACCTTTG	47	97	97	200	200	1	1		
91001200	pm1351	1	TTAAGAAGACCCCTATGGAGACC	AATAATCTGGTGTAGTCACTAC	47	97	98	200	200	1	1		
91001346	pm0982	1	TCAGGTCTGCTGGAGGATG	AATCAGACACACAGTATTTG	53	120	122	>200	>200	1	1		
91001446	pm1518	1	AAGGTGTACAGGATATTTGCAGA	TGCATAGCCCAATCTCAT	47	130	125	>200	>200	1	1		
91001464	pm1439	1	CCAAAGACTCCGTTGAACA	TTGGGAGAGCCATAGACAG	51	100	100	>200	200	1	1		
91001468	pm0427	1	TACTCAGTGGMAAGATAAAC	CAGTGGAGCACATTTCTTA	40	98	98	200	200	2	2		
91001521	pm2785	1	CCCAATCAATTTGTTAAATG	TTTGAATCAGACATGAAGTT	43	102,175	100	>200	>200	1	1		
91001554	pm2291	1	CCAGAGAGTTCAGGGATG	GGTACAAGTGTCCAAAGCT	46	57	57	78	155	1	1		
91001572	pm2006	1	CCACATGGTCTTAGCACAG	AACTTATTCGAGCTCTT	44	58	59	>200	>200	4	4		
91001620	pm1350	2	CATGATACTCTCGGTGGTA	AAACAGTAGTTCGAGCAT	46	84	109	200	200	1	1		
91001636	pm1730	2	AGCTGAAATGTGGCATGCT	CCCGTATTCGTACATGCT	48	119	119	93	115	1	1		
91001681	pm0931	2	AAGCAATACAAATACCAA	TTCAATATGTTAACCACTA	40	90	90	200	200	1	1		
91001690	pm0925	2	TAACTACACAGTGAATAG	TAACTAATATGACGGTAA	45	88	88	200	200	1	1		
91001713	pm2010	2	CCAGATGGAAAGGGAAGTCT	CTGGAATATGGAGATCAACAG	47	125	125	150	>200	1	1		
91001752	pm0935	2	TGAGATTGTCTCTAATA	GGAAATATCGCTTCAGTTG	43	103	103	200	200	1	1		
91001768	pm2093	2	AGTCTCTCTGGCTCTCAT	TATCGTACGTCCTTTATTG	52	137	137	>200	200	1	1		
91001771	pm2435	2	TTTGTACCTACGTAGAGTACT	ATCCGTGCCACACATAGTA	45	105	108	200	200	1	2		
91001785	pm1671	2	TTATTAGGAGTCAATATCTGTG	AGTCCCATCTCCACATG	45	67	65	>200	>200	1	2		
91001826	pm1245	2	TGCTTCCCGTCTCTAAGT	ATGTACAATTGGGTATGTAGG	45	75	75	170	190	1	1		
91001835	pm1246	2	ATCTACTGTTGTGAAAGTG	ACTGATTTGGTCCCATCTG	44	68	67	200	200	1	1		
91001875	pm0449	3	CGAACATTCACCTCTCATA	ATGATTTATTTAGGCAGGAA	43	68	69	200	200	3	6		
91001901	pm1758	3	TCTGGCTCTTTGGTGTGGA	GGCCCACTGAGTACAAATGTC	51	115	115	200	200	1	1		
91001918	pm2434	3	AAGAAAGCACACTGCCATA	ATGTATAGACAAATCCAAAG	42	90	90	200	200	1	1		
91001919	pm0668	3	GTAGTCTCTGCCCTTAGC	AAGGATTTGATTTCTACAT	43	77	77	200	200	1	1		
91001977	pm1729	3	GGTCTGTTTATTTGACAT	AACAAGAGGATGGTTCAGA	43	75	75	155	>200	1	1		
91001306	pm1822	3	GATCTGTGTGTAGTTCAGTC	CTGCAAAATACAGGGAATCAT	46	83	83	160	140	1	1		
91001418	pm2209	3	ACCCAGTCCCAATCCAGT	ACACTCCCGCCCTTACT	55	105	105	113	>200	1	1		
91001466	pm2455	3	ATCTAGCTGGCTGTAGTAT	TTAAGAGATGAATTTATGGT	42	130	130	190	>200	1	1		
91002271	pm1252	4	GTCTTTGCTATCTGTGTA	AAGCAATTTATTCAGCTTAA	43	90	90	95	>200	1	3		

Fig. 7

91000148	pm2256	4	GGCCAAAGTTTCTCTAGTAT	GTCAGTTTATTCAGAGCA	42	62	62	62	69	1	2
91001052	pm1151	4	GTCCCAATGCACTGTGTAT	GTCAATATTCATCATCAA	43	80	80	-	-	1	1
91001215	pm0988	4	AGAAATTAAGTAGAGT	TAGATCAAGTTGCTGTG	43	100	100	130	-	1	1
91001298	pm2367	4	ATCAAGTTTAATTCITCA	CATCCATCACATACAGTC	43	116	116	>200	180	1	1
91000993	pm0901	5	TCTGTGAAGAGCAGCACA	TCTAAGGAAGAACAGCATC	49	101	102	113	200	1	1
91000998	pm1809	5	AAGCATGCCCTATCCACAG	CTAAGAGCTTGAACCCITCAT	45	87	87	>200	>200	1	1
91001065	pm0319	5	TCACCAGATAATTACAGT	GAGACATAGCAGGTAGAT	44	120	120	-	-	1	1
91001101	pm2364	5	TTACCTTACCGTGTCTTAC	AGACAATATCCCAAAAGC	47	89	89	100	>200	1	1
91001461	pm1160	5	ATTTGTAGTGGTTTACTA	AGAAATGGATGCTTTATTC	43	101	99	>200	>200	1	1
91000053	pm2720	6	AATGTCATAGTCTGCTTCA	TGCATCCTCAATGCTCTCT	41	78	78	72	>200	2	3
91001326	pm1154	6	CATTGAGACAGCAGCAACAG	CCTGCCCTCTCTCCAGTCA	53	102	104	145	200	1	1
91001434	pm1216	6	TAGGCAAAACAGGAGAGAG	AAGGAGCTGGTGTCAGGTC	48	65	65	110	>200	1	1
91001457	pm1785	6	TATATGCAATATCCAAAGTCTG	TCTAATAATCTGGTCCCTTATCT	46	90	>200	>200	>200	1	1
91001523	pm0285	6	TTGTAACTGTGTGCTGAGT	TTTAAATGTCATGGTAAT	42	86	70	>200	100	1	1
91001525	pm0378	6	GCACCTAAGCCGCCAAAGT	TTTATATCAGTCCCAAGGC	49	138	130	>200	>200	1	1
91001562	pm2619	6	TCTGCAATGACAGGACCAC	TTTGAGATTTAATGAGTCATTC	43	62	62	>200	45	1	1
91000624	pm0991	7	GACCTGAAGTGTGAATGAGT	AACCTAGCTTATGGGATTT	45	119	119	>200	-	1	2
91001145	pm0281	7	AGCCAAACTCGGGTGCATCT	CCAGGGACAGGTGAGTCAT	56	159	159	115	>200	4	4
91001469	pm0219	7	AATCATTTGGGAGACTGTA	AAGACAATTTATCCAGACA	45	88	89	130	-	1	1
91001579	pm1102	7	TCAGGCAGTCTGTCAGATA	TTTCCAGGTAACTGTTTA	44	77	76	170	-	1	1
91001726	pm0956	8	AACAGTATTCGGTTCAGACTAG	TCCATTAAAGCCAGCTCTCAG	47	81	81	105	70	1	1
91001248	pm2527	9	TGCTATTCATGGTGTCTAC	AAACCCAGAACACACTAAG	48	99	59	110	180	1	1
91001248	pm2708	9	TGTATTCGATTTGGATTCIC	CAACCCAGAACACACTAAG	44	95	95	-	85	1	1
91000260	pm0995	97	TTGCCATCAAAACACATACA	CTTGTGAGTTTGGTTTCTG	43	55	55	-	-	1	1
91001055	pm0959	97	TTAAGATACCCCTCATTTG	CACATGCTTATTTGGACACT	44	74	74	72	73	1	1
91001157	pm0547	10	AAGTATTTGCAAGATGTA	AAGAAACACTGCCCTGTGG	45	138	139	>200	>200	2	3
91001268	pm2245	10	TGTGAATGCTATCTCTCT	GCAATCGTTTCCATATCAGT	47	100	100	200	>200	1	1
91000278	pm2664	11	ATCAAAACAAACATCCAGA	ACTATATATCTGCCAAGT	42	117	121	134	95	2	2
91001159	pm0880	11	GAATAGCTTGGAGATTTCAC	GGAGATCATACCTTCAGCA	46	100	100	84	95	1	1
91001315	pm0445	11	AAAGTGACCTTGTGGACAGTGG	TCGAGCCAAATACATGCTGACT	50	153	153	>200	160	1	2
91001352	pm2943	11	AGGGTGAAGGGTATTTTACG	CACATCATGGTTGAGAGCTA	47	83	85	-	-	2	2
91001469	pm0559	11	AAGCCTCTAGTAAGGCATTG	TTATTAAACCAATCCAGTA	37	47	47	125	53	1	1
91001570	pm2810	11	CTGTAAAGGTTTGTGGAAATTATGT	TTCATTTTCTACCAGATTATTT	42	75	82	145	>200	3	3
91000279	pm0266	12	AGTGTGGAAGACCTTGAG	GTTCATTTGAACGGTGTAGC	48	130	130	103	>200	1	2
91001163	pm2756	12	TCTCCCTATCACACCACT	AATGATTCGTAGGATAGCA	49	88	88	>200	120	1	2
91001193	pm1193	12	CACAGCATAAAGAATCATA	ACCCATTTAGTTTCTCAG	46	100	100	-	-	1	1
91001235	pm2790	12	CATCATGGTACAGTCAGAAG	CAGTTTGTCAAAATGTAATG	44	83	82	93	87	1	1
91001274	pm1355	12	AGATGTCAGTATCTCTCTATGG	GAGAACAGCAGTAAAGCAACAC	47	87	87	>200	>200	1	1
91001308	pm0368	12	CCAAAGTCTAGGGTTACAG	TTCAATAGACCTTGGGTTTAC	47	95	165	>200	>200	1	1
91000159	pm2645	13	CTAAGATTAAATGCGATTCC	AGTTAGTGTATGCGCAGAGTA	46	104	104	>200	-	1	2

Fig. 8

91001044	pml1659	13	TTGTAGCGCTATCAGAGTCA	AGACAGACTATGCCATCTA	44	109,200	109	>200	100	1
91001290	pml1731	13	GGTCTTCCTGCTGCTGGT	GCAGTAATCATGGCTATCTCC	50	122	122	>200	180	1
91001362	pml0118	13	ACTGAAATGGAACATAGTCT	TACATTACATGACATGTGA	40	61	61	95	103	1
91001366	pml0364	13	TGCTTAGCTTTCCTCCTCTA	GAGCATTCGTGTTCTCTA	45	67	67	-	-	1
91001389	pml2301	13	CATGACCTGCTCAGACAA	GCCTTACTTAAATGCTGACC	51	100	100	100, >200	-	1
91001492	pml0541	13	AAATGAATGTAATAGCACT	ATTAGTTACAGGAGAAAT	41	72	72	-	74	1
91001367	pml0441	14	GGTTTAAGTTTGTATTTGGG	CATCCAGCTTACATTCTT	41	77	77	>200	180	3
91001584	pml2307	14	CGTTCCCAACTCTGAAATC	AATGCTCATTTATCTCAAG	42	55	55	>200	>200	4
91001576	pml2019	14	ATCACATTACCTTTAGTGG	ACGAATACCTTATTTGGAGT	39	69	69	-	-	1
91001339	pml2220	15	TCCCATCCTCAGTTGAAAT	TGAGACAAAGGAACCAAGT	47	70	70	80	150	1
91000980	pml0985	16	TTGGAATGGAAGCCTTGCTA	ACITATGCTGCCTGAATGG	48	79	79	66	70	2
91001242	pml1127	16	CCCTTGTTTTACATGTCCA	TATTAATCTCCCATTCAT	44	105	105	103	102	2
91001516	pml2543	16	ACAGTGTAAATCAAGGTGG	TCGACACTCAGGTGCAAT	45	70	70	>200	-	1
91001566	pml0913	16	TTTGTGCGGACTATGTAAT	TCACITTTAATGGGAACCA	41	53	53	>200	>200	1
91000806	pml0913	17	CTCTCAATGTTCTCTACAAG	TAGAGGGAATCTGTGGTT	47	77	77	140	>200	2
91001015	pml2369	17	ATATCACCCTCCCATCCAT	TCAATACGTCCTCTCAAGC	50	80	80	>200	>200	1
91001156	pml202	17	CAGAAATTAAGTCCAGCAAT	TCGTATCTGCATCTTTAAGT	45	103	100	>200	>200	2
91001173	pml2117	17	AAATCTGTGGTTATTTCC	GTGATCTACTGTACATGCG	41	118	118	145	200	1
91001301	pml1878	17	TAAATTTGGAAATCTTTGGA	ACACATTTGGTTTGTCTTAC	47	100	100	95	97	1
91001316	pml0511	17	TGTGACAGCAGCAGCTTCAT	TCGTACATTTAATCCACC	45	128	129	-	1	1
91001356	pml0538	17	CATCTCACAGACAGGAAC	ACCTAAGACTCCAGAGAAC	48	90	90	69	>200	1
91001495	pml2212	17	TGACTCGATAAGGAGTTGT	GAACATACCAGTTTATTTCT	46	90	90	180	>200	1
91001522	pml0642	17	GTCTCAGCAGATTTCAAGT	ACTTCTCTCTGAGGACACA	45	68	68	160	-	1
91001078	pml1815	19	TGTGTTCTCCAGCTTTGTAG	GTTCATTTGCCCTTGGTACAG	49	65	65	>200	>200	1
91001417	pml289	19	GGATCAGACCAACAGTCTCG	GCAAGGTATTAACAGATTA	46	50	50	-	-	1
91001467	pml1688	19	GAAGCCACCCTGCACCTCA	GGAGAGTATTTGGGAACGGT	54	93	93	>200	>200	2
91001069	pml1879	20	GCCATGCTTGTAAAGTGTGT	TTAAGAGCCATTAGCTAGGATA	48	140	140	-	-	1
91001068	pml1146	20	GCCCTTAGGATTCAGTCTC	ACCACCCAGGTCTTTCAGG	52	66	66	180	>200	1
9100112	pml0112	20	TGCTGATGACTTCTACAG	TCCCTATCATGGCTGCTGT	49	59	59	59, 115	59	1
91001128	pml0332	20	CTGCTCGGTAGTCTGACTC	CAATGGTCTAAGAGGACAT	49	135	135	153	160	1
91001132	pml0647	20	TCGAAATGATGATGGAACA	ATCCTAGTCCCAACCCAGTA	48	109	109	-	-	1
91001158	pml1774	20	GGAGCCACATGGATTGATG	AAATGTACCCCTGGCACCTC	52	124	124	>200	>200	1
91001210	pml1235	20	AGCCATCTGGTTATGTCTTA	GGAGCAGAAATGAACTTCAC	44	90	90	>200	>200	1
91001377	pml1701	20	TCCATGGTTAGAAAGCCAG	CCACATCTCCAAACAGGGAGT	54	142	142	>200	74	1
91001395	pml2101	21	GTGAGCTCAATGCTACACAG	TTTATAGTGCACACACAGAGT	45	130	130	180	>200	1
91001427	pml0648	21	CTTCTGCTAATAAGTAGAG	ACAATGGTTTCACTAAATGA	39	58	58	145	>200	1
91000378	pml0912	22	GGTGTAGTGTAAACATTAG	AGTTCACCCCATCTCCGTGC	46	124	124	>200	>200	1
91001444	pml0911	22	GGTCTTGTCTCCCATCTGT	AGAAAGCCCAAGTAGTCC	48	65, 80	65	100	125	1
91001473	pml2231	22	TGAGCTGGCACTACCTGTGAGAG	AAGCAGGTGAGTTGGGTTTCT	50	94	94	67	135	2
91001479	pml2328	22	TACAGCCCTCCCAAGCTAAAC	TTTATCTGCATCCACTACAA	46	65	65	190	>200	1



Fig. 9

91000999	pm1759	X	CTGCCATAGTTACCTGGATT	TACCCACCACIATTTAGCA	47	103	103	-	-	1	1
91001149	pm2180	X	GGAGGGAGATAGATATGT	AAAAATCCAGAGACIGA	46	70	70	135	150	1	1
91001161	pm0508	X	TTCTATAAGTTGACCCAGTT	GGAGGATTGAGATACACAT	40	85	85	>200	71	1	1
91001406	pm1294	X	TAATGCCAGTGAATGTTGCGTAA	GTAAAGGTTTATCCTTGCATCAGA	47	82	82	>200	80	2	3
91001160	pm2289		ATCCCTGCGAATACATCTG	GGGAGAGACATCACATGAC	46	70	70	68	130	1	1
91001436	pm0113	1,10	GATCCGATGGAGTGTAAT	AATACAGCTAACCCACA	44	69	69	170	-	1	1
91001404	pm2272	1,2,12,13,Y	TTGGAATGACATCTCTAT	TTTATGTAAACAGCACT	43	130	130	150	132	2	2
91000303	pm0314	1,2,3,5,8,12,14,17,X	TATCAGCTGAATATGTCAC	TTACGATCCAGCCCAACCA	45	93	93	110	-	1	3
91000140	pm1461	1,2,6,X	TCCMATGAAGAGGTGTIA	AGTTGACAGCCAGGTGAATG	43	96	96	100	100	1	3
91001354	pm1561	1,3,4,5,8,16	GTCTGCAAGCCAGATTCA	TTTATTTGTTGCTCCAAGT	43	110	110	170	150	1	1
91000336	pm2795	2,20,21,22	GACCTGTGACATCTGGACT	TTATATGGTTTACACTCG	43	61	61	-	-	2	6
91001077	pm0943	2,4,5,10,12,15,17,20,22,Y	GCCTGTGTTATTCACCACTC	ATCTCCCTTTGCTCCAGTIA	46	82	82	>200	82	1	1
91001192	pm1853	2,5,14,C	TCTGAGGACATTCAGACAG	CAGTCAMAGCCACACGGTAT	49	95	95	93	160	1	1
91000213	pm1778	2,8,12	TGCATTAAGGGAAAGACCA	CCGTGTAGGTGATGAATG	49	78	80	>200	>200	1	2
91000919	pm0885	2,9,13,17,X	GTCAATTGTATGCAATTCC	ACATTTTATTTTTCACGG	37	45	45	-	-	1	2
91001109	pm0457	20,X	CATGTACTCAGAGGCCTTC	GCACCTACAAATCCCAACT	50	133	133	>200	150	2	2
91000071	pm2651	3,10,15	CAGGACTCAGAGGCACTTC	GATTTAACCCATAGGAGC	50	101	101	101	88	3	3
91001426	pm2632	3,4,M	TTAGGAAATATGGTTAGACAG	ATAGTATGGGTGACACAGTA	43	80	80	>200	120	1	1
91001391	pm1133	3,6	TGGATTGCTTACCTGTT	ACACCTCAGGAGATGTTAC	47	93	93	95	>200	1	1
91000077	pm2750	3,8	GCATACAGCCAAATCAGA	CTCTTACACCAACAGCAG	50	96	96	>200	>200	2	10
91000605	pm0626	3,9,10,15	GGATTCTATTGCTGTCAT	GTTATGTACGGCATTTAC	44	105	100	>200	>200	2	4
91001212	pm1234	4,6	GCATTAACAGCAAAACATA	CTGTCCATGGCATAAACC	44	110	110	105	107	1	1
91001312	pm0606	6,20	AGATGCTACATTAGGGATA	TTTATAGACATACAGAGGAT	43	81	81	102	-	1	1
91001441	pm1253	7,18	CCAGACTACAGGCTGATGCC	CCCTTACCCAGCACTCTT	55	75,130	75	>200	>200	1	1
91001357	pm0115	9,11	ACCAATGTCATGCTTCTAAATA	CCCATATAGTGAAGAGTATCTC	48	125,155	127	125	>200	1	1
91001261	pm0428	9,M	AAGAAATGTTTACTGGATT	TTATCTGACITGGAGGAAAT	42	107	107	-	-	1	1
91001456	pm2120	10,15,22	ACTACCCCTGAGATATTAGTT	TTCAITTTATTTGATTAGTTGA	46	100	100	170	-	1	1
91000290	pm2303	10,15,22	ATACCACTCCGCTGTACAG	GAGGAGGCTCTACTGGCTCT	50	72	74	72	>200	3	20
91000314	pm2643	11,M	GCACCAAGAGCAGTTCCAG	TTGGGATGAGAAATAACT	46	83	83	81	-	1	7
91002773	pm2773	12,19	GATCTCAGTCTCGCTTTAT	TACATACAGATGCCAACAGT	44	80	80	79	68	1	1
91001487	pm2725	12,M	ATCTGTGTGCTGCTTCC	GTCTCTCTCTGATGGCTGA	46	62	60	135	180	1	1
91000376	pm2780	13,16	AACCTGTTTACCCGATCTT	AGGTTATTTGTCACCAGAA	48	87	87	>200	>200	1	1
91001435	pm1683	14,16	TGTTGGTTCACCATGAGAC	AGAACACATCAAGATGTC	46	90	90	>200	90	1	1
91001393	pm1746	17,20,C	TATATCCAGCAAGCAGTAC	CTAGTTATATCTTGGCTCTG	44	81	81	>200	200	1	1
91000056	pm0964	17,22,Y	TTATGCCAGCAAGCAAC	TCTTCTCTCTACCTCTCTC	49	120	120	>200	170	4	11
91001369	pm2217	17,C	ACTTAAGATGCTTTGACG	TGCCTCTGGTCTGTATAATA	43	95	95	>200	95	1	1
91001440	pm1213	16,C	CCCAGTTAAGATTTATGT	AGTGACGATGGAGGATGTA	44	92	92	-	92	1	1
91001217	pm1118	19,20	TGCAGATGATTTTCAGAG	CGTAGGTCATCTCTTTCAGC	46	75	72	160	65	1	1
91001009	pm2824	19,22	ATCCCTCTCTCTATTCACAC	GCCTGTTTAACTACACTCAG	46	110	110	130	170	2	2
91001172	pm0987	19,22	GCCTGCATCTGTGTTGACTT	AACCTCTGGGAAACAAATCAT	48	91	89	160	86	1	1

Fig. 10

91001057	pm12049	C	AGGACACAAACACGCTAT	TTTCTGATTATGACATGAC	45	75	75	101	75	1	1
91000173	pm11753	M	ATCTCTTTAGCCATCTG	GTTAAAGTGTGATGCCATT	42	64,100	64	64	>200	1	1
91001096	pm2236	M	GTAGAGCTGATGACTACC	ACAGACAGGAATATACATA	42	100,96	110	110	112	1	1
91001166	pm0506	M	GTCCACAGTCCAGCCTAAC	GCCACATATTAGATCCATC	46	74	74	74	>200	1	1
91001151	pm2354	M	TGCTTTGTGGACTCTGCCT	TTTAAAGTCAATAATACATGTT	44	110	110	110	106	1	1
91000029	pm2492	M1C	GCTAGAAAGAGGGCACTCA	CTTAACTCGATAGCCAGGTC	46	75	75	75	75	1	1
91000753	pm2786	M1C	CACAAACAGCAACTTCAG	ATGGTTATTTATCAGATTG	41	83	83	82	83	2	3
91000785	pm1704	M1C	TCCACCAGAGAGGACACT	AATCATAGGAATAGGTC	48	75,130	75	75	75	1	23
91000302	pm2318	M1C	TGAGAGAGGACAAATCAC	GAACAGGTTATGCCATTCG	48	50	50	58	58	1	1
91000543	pm1689	M1C	CATGAGCTACGGAAACAGG	AGGAGTCCGTGGCTCTGAG	51	81	84	84	84	4	18
91000675	pm1442	M1C	AAAGCATCTTGAGAGGAACA	GGAGGACTCGCTTGGCTCTTA	49	110,200	110	110	110	1	9
91000732	pm1452	M1C	GCAGCAGATACCTTTACACC	TGGTTCTTTCAGTCTCTTC	51	102	105	102	102	3	13
91000995	pm0268	M1C	GAAGCTCTTGAGGAAAGT	CAGACCCCATCTTTATACC	47	79	79	79	79	3	4
91001016	pm2703	M1C	ACGATATTATAGTAGTG	TCMAACTTTAATATATGCT	40	93	93	91	92	1	1
91001053	pm1144	M1C	AGATGAGTGTGGTTCAGAGA	CCATCCGTGATCCAGT	52	135	140	135	135	1	1
91001127	pm1290	M1C	ACTGGTGATGGAAAGTTACA	CCACACAGTACGACCGTCT	47	55	55	55	55	1	1
91001167	pm1626	M1C	GAGAGCCCTTGCATCTTTA	CTTCCCTTGGTCTTTCTGT	49	100	100	100	100	1	1
91001216	pm2109	M1C	TAGTCAGAGATTCAGTAAT	ACGTATTTTGTATATCTT	42	110	110	110	110	1	2
91001253	pm1240	M1C	ACTGGTTCATCAAGACTG	AGTGAATAAACTCTCCACTCC	48	120	120	120	120	1	1
91001281	pm1131	M1C	ACTTAAACCCACACAGCAT	ACACACAGCATCAATAGAA	47	97	97	97	97	1	1
91001375	pm0952	M1C	AGAGGAGTTTCCCTGCTCA	ATCATGGCAGATGGCAAGGA	51	89	89	89	150	1	1
91001356	pm2216	M1C	ATGCGATGAGCTATATCT	CGTCTCTTTATTTGACAT	45	100	108	108	108	1	1
91001411	pm0958	M1C	ATGGGTTATCAGGGGTTTC	GAGACAAAGGCACCTCTTA	47	80	77	80	80	1	1
91001460	pm2626	M1C	ACATTGAATGGGATGAGGT	GGACATTTCTAGCCACAGC	51	75,55	75	75	75	1	2
91001482	pm1210	M1C	TTGTTGACATTCCTTTTAGAA	CAGTCCCTCTGCTAGAGACA	46	85	85	85	85	1	2
91001450	pm0109	M1C	CCCCACAGACATCATCTT	TCTTAGTAGGTGCTCTGGTG	51	90	90	98	98	1	1
91000168	pm2042	No product	CACCCAGTTAGGTTGAAAGT	GAATAATCCTGTCTATCTA	45	87	87	-	-	1	1
91000450	pm0304	No product	CTTGGGATATTTTCTCAT	CCCTCGGGTACTTTCTATG	43	60	60	62	-	1	2
91000983	pm1673	No product	AGCCAGCCTCTTGTATGTG	CTGGATTGTATTTTCATTAG	44	87	87	-	112	1	1
91001254	pm1673	No product	TGTTGATGAAATATCTGA	TTATGATGAAAGACAACACT	43	98	98	163	>200	1	1
91001265	pm2908	No product	CAGTAGTGTGTTTGAATG	TTATGATGAAAGTGGTGT	41	63	63	-	150	3	3
91001373	pm0361	No product	TACAGCCGCTCTAAAGTC	TTTGAGCATCAAGGAATCT	46	82	82	-	>200	1	1
91001556	pm0849	No product	TACATCTCAGACTCATCG	TTTTCAAAACCTTTATCTT	40	86	86	>200	100	1	1
91001574	pm1284	No product	ATCAGAGCTCAGTCTCTGTAG	ATTTCCTCTTGCATGGTC	44	57	57	67	67	2	2
91001622	pm1606	No product	GATCTGAGCCCTTAAGTGA	TTTGCAGTTCAGCTTATTC	45	54	54	-	-	1	1
91001640	pm0852	No product	GATCTCTGTCTTTTCAAC	TTTAAACAAAGACACCATAC	36	45	45	-	-	1	1

Fig. 11

pm 2209 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y H H C N

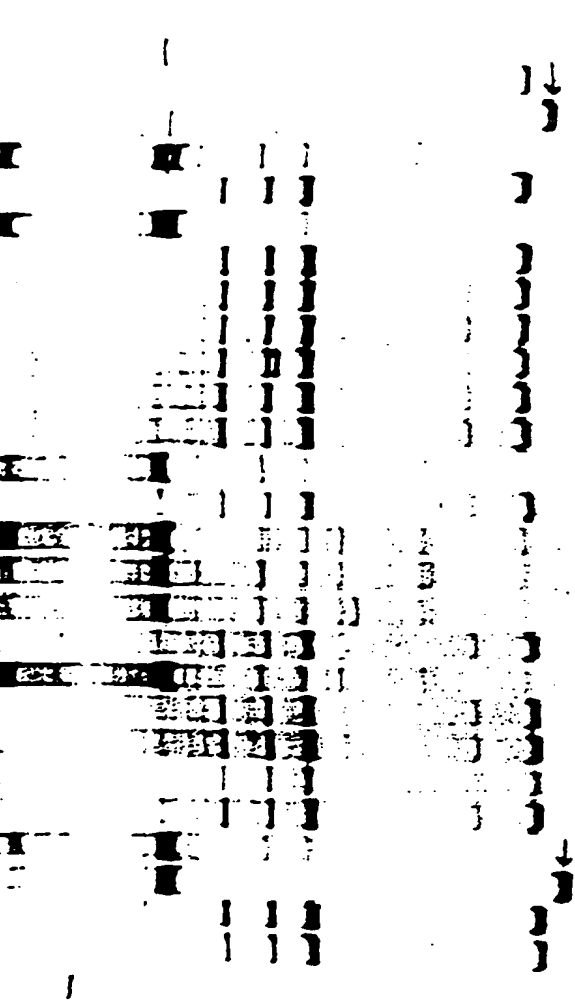


Fig. 12

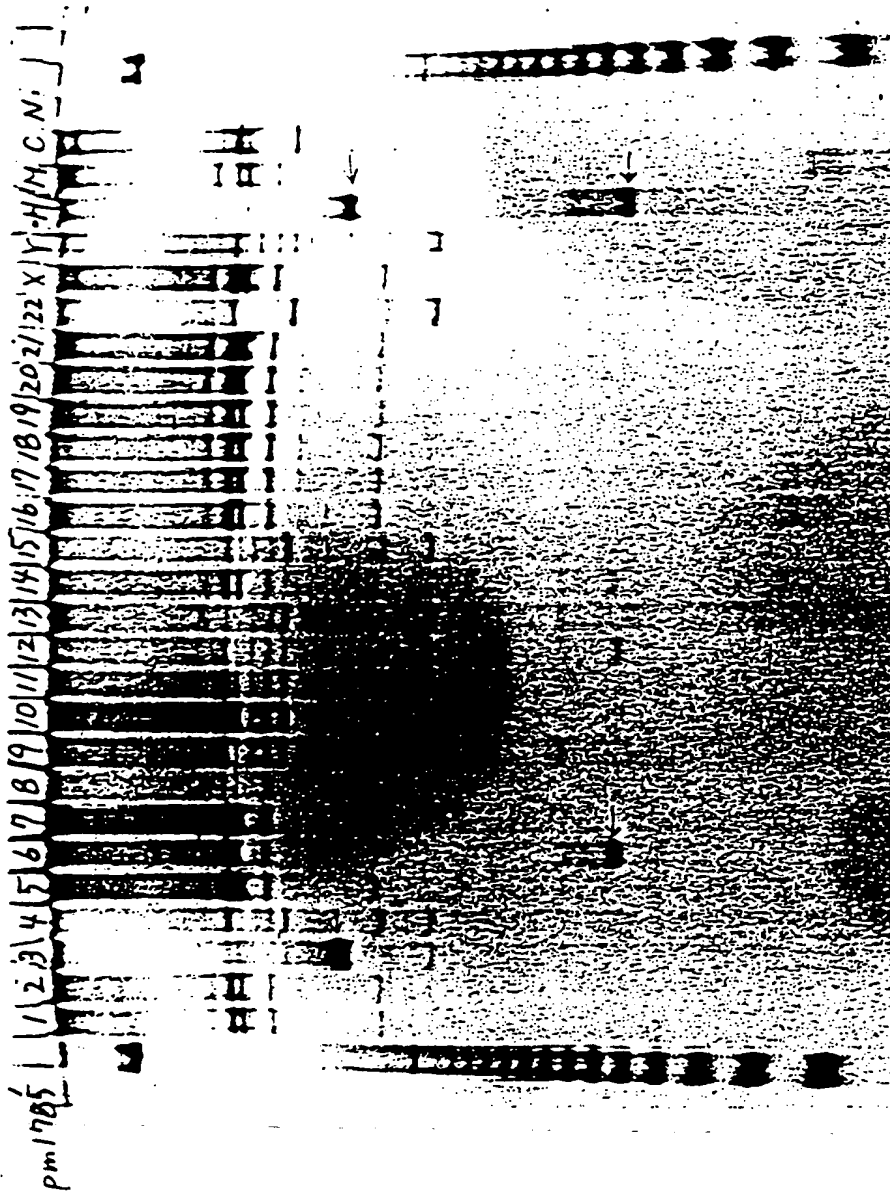


Fig. 13

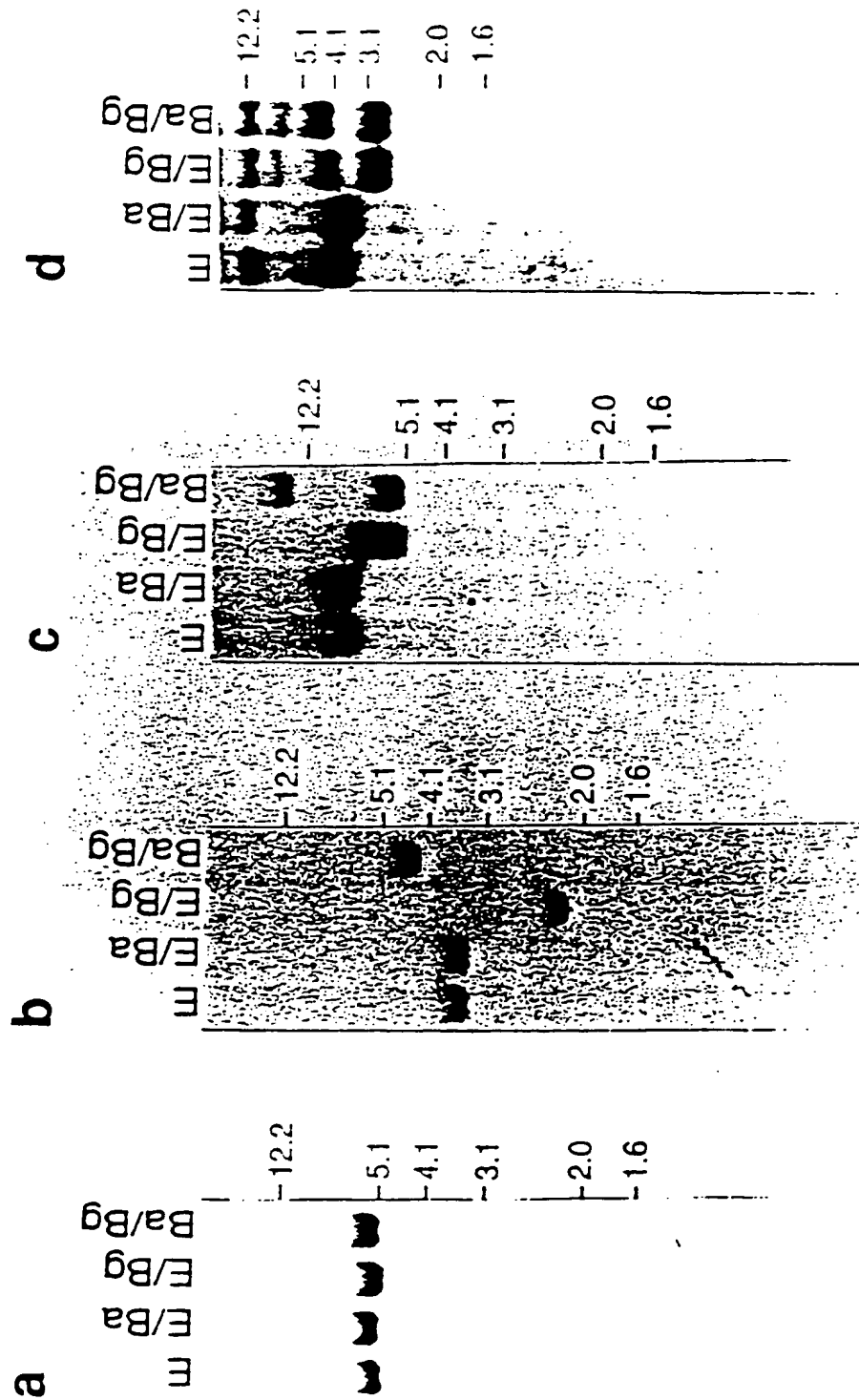


Fig. 14

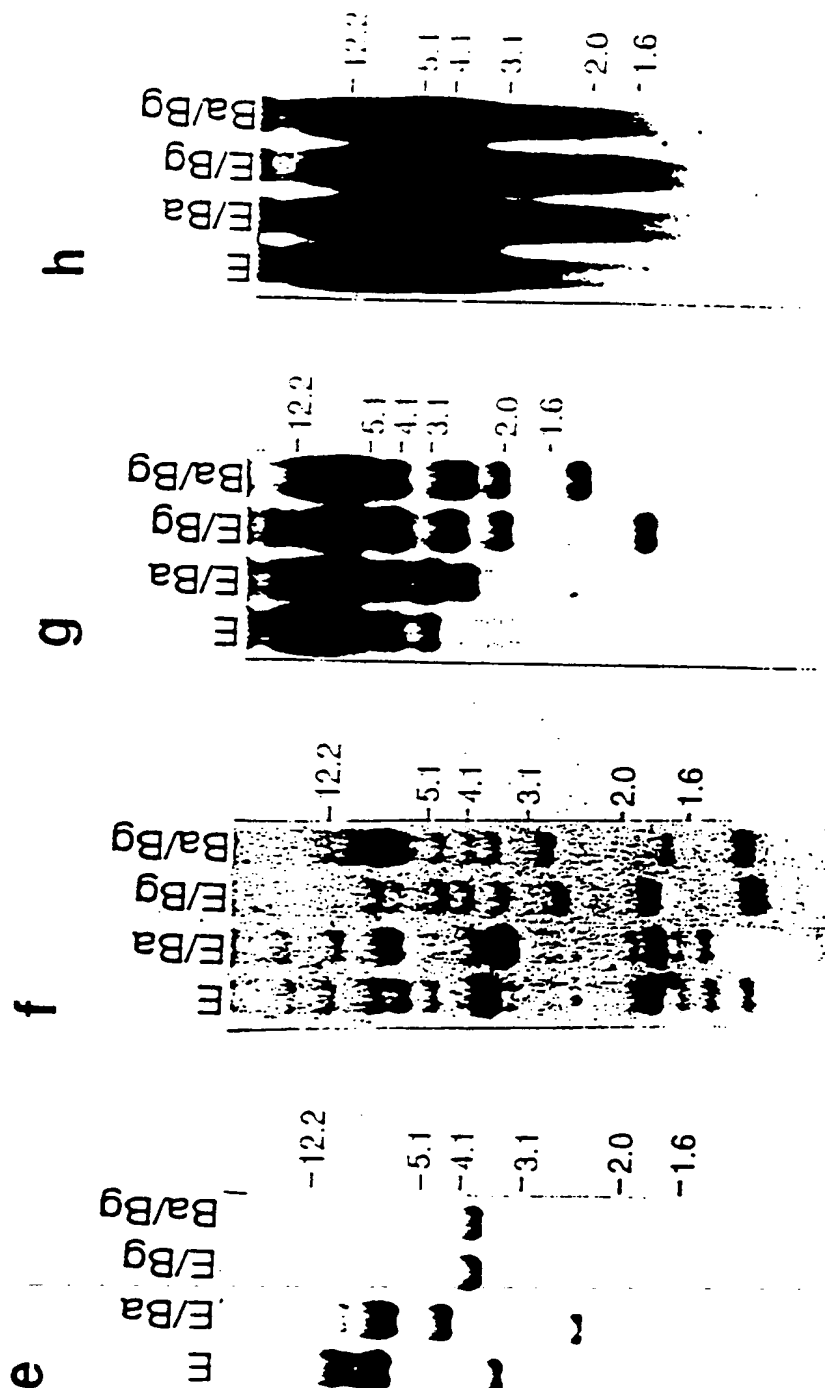


Fig. 15

## Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (3)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A *	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868 *	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418 *	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

Fig. 16

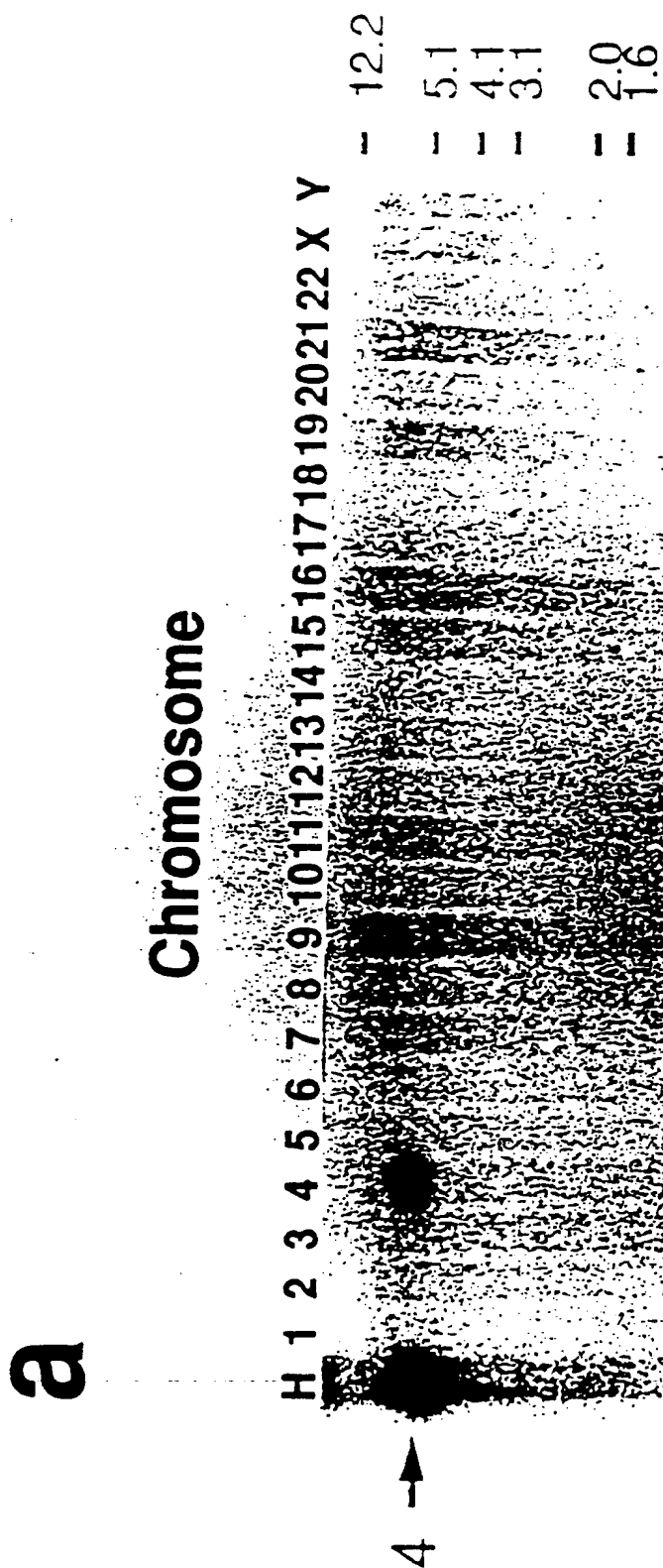




Fig. 17

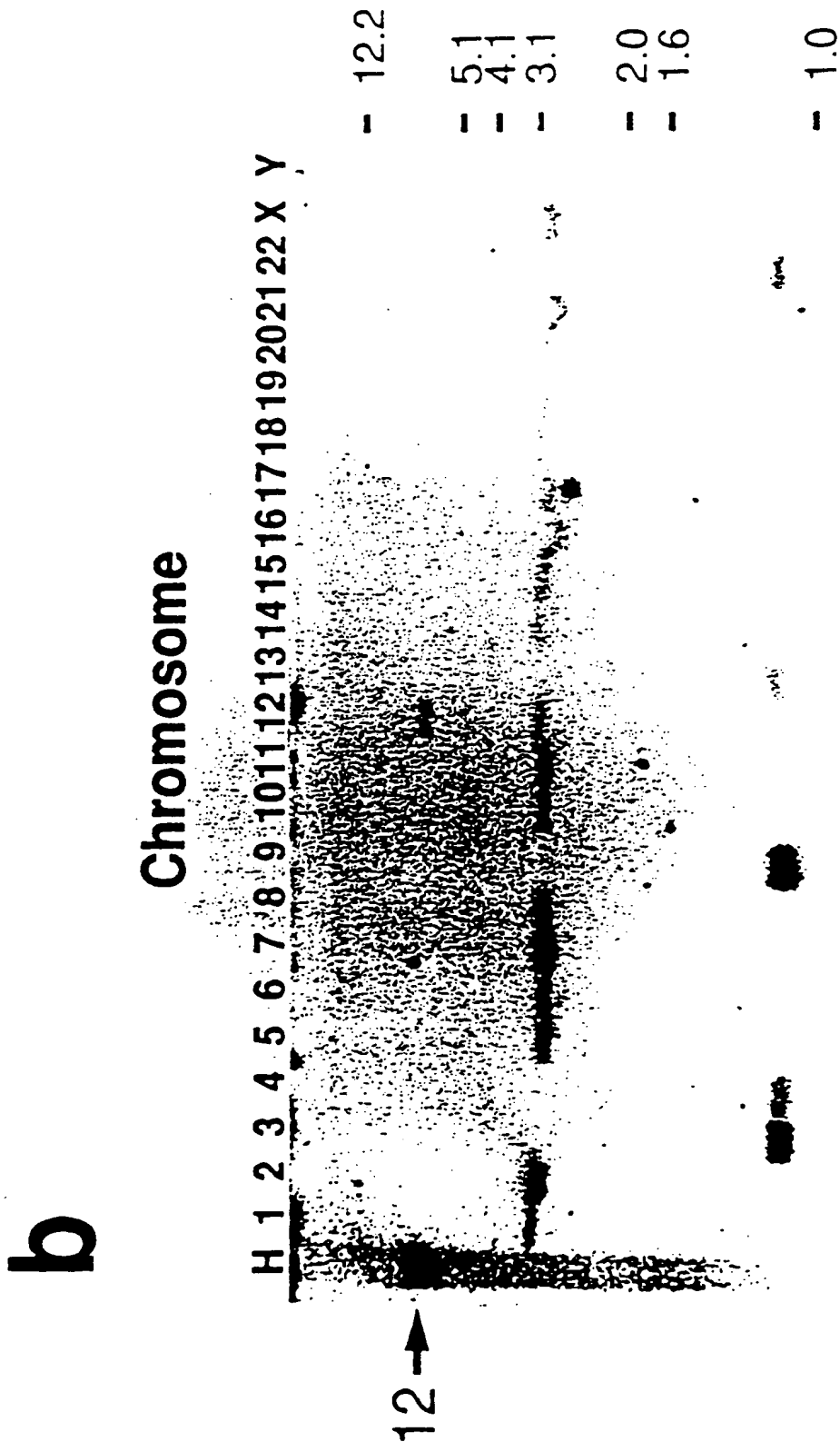


Fig. 18

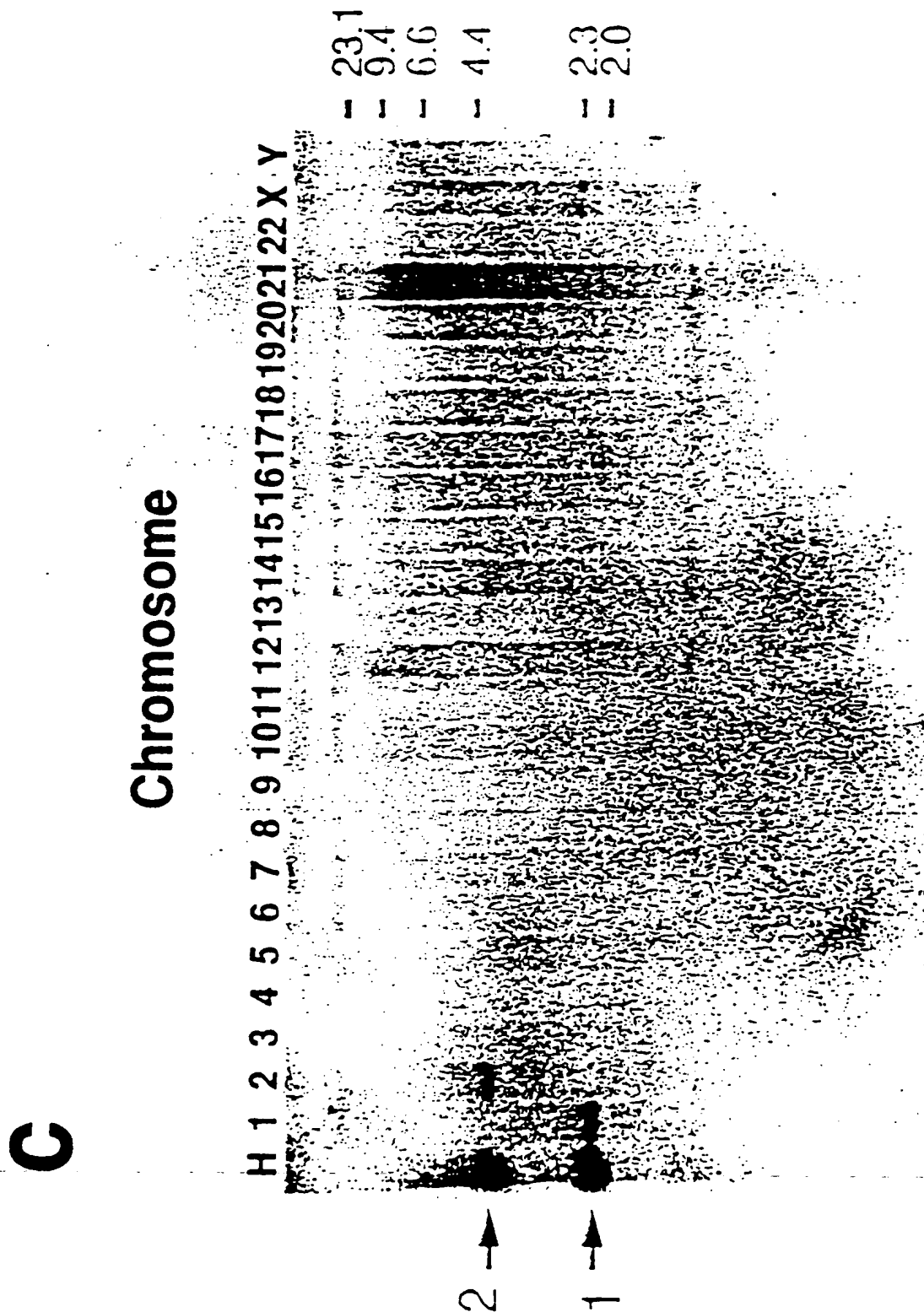


Fig. 19

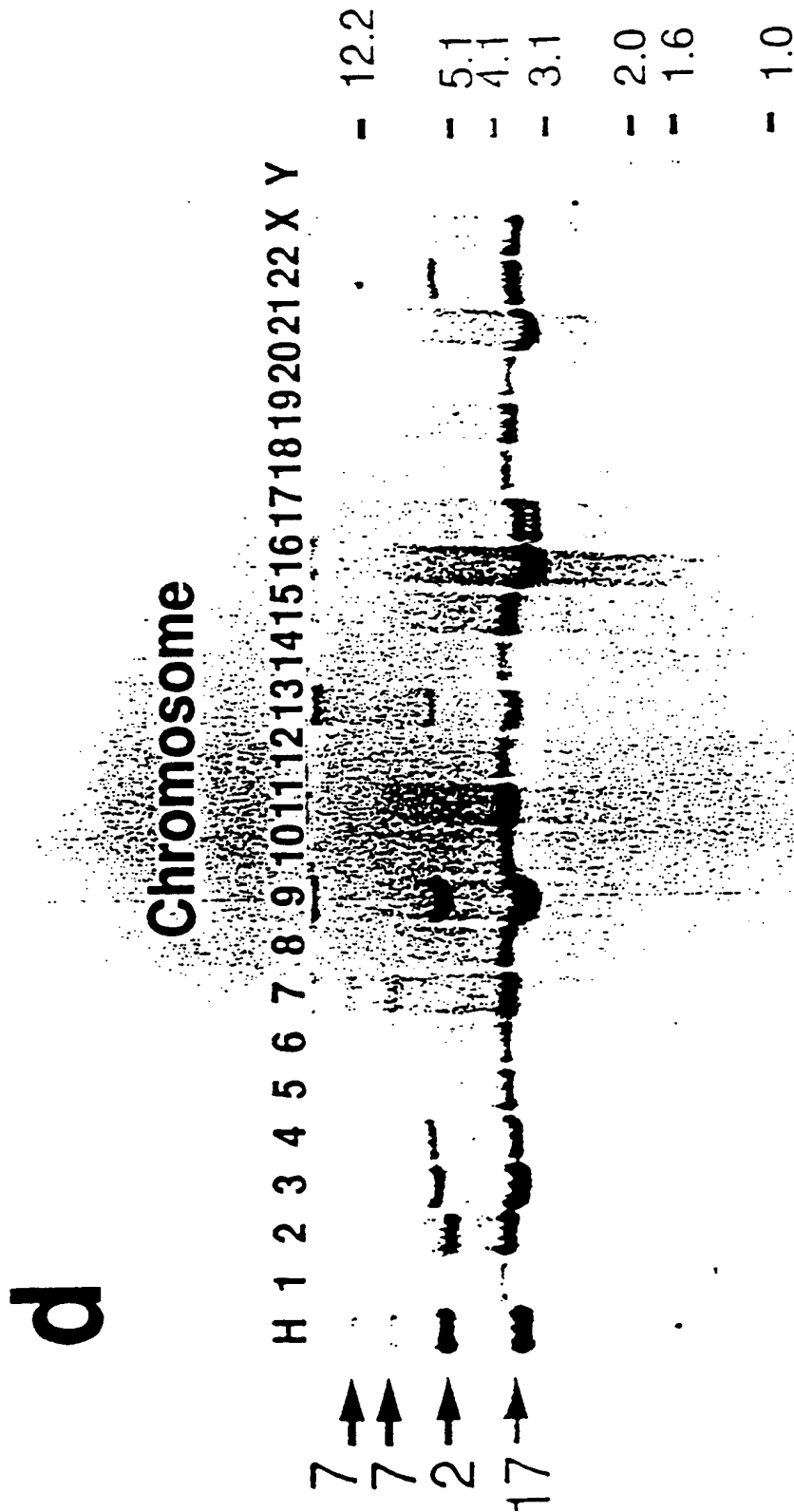


Fig. 20

e

# Chromosome

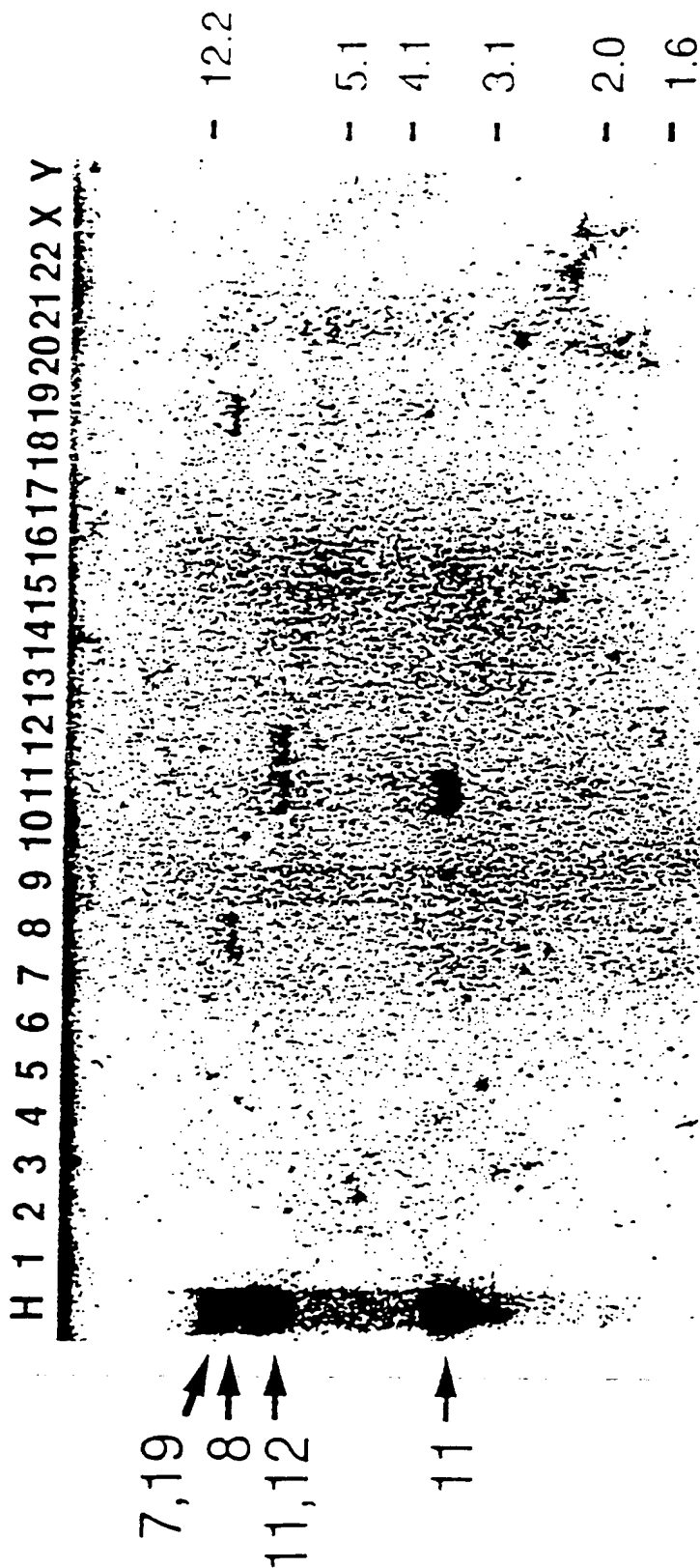


Fig. 21

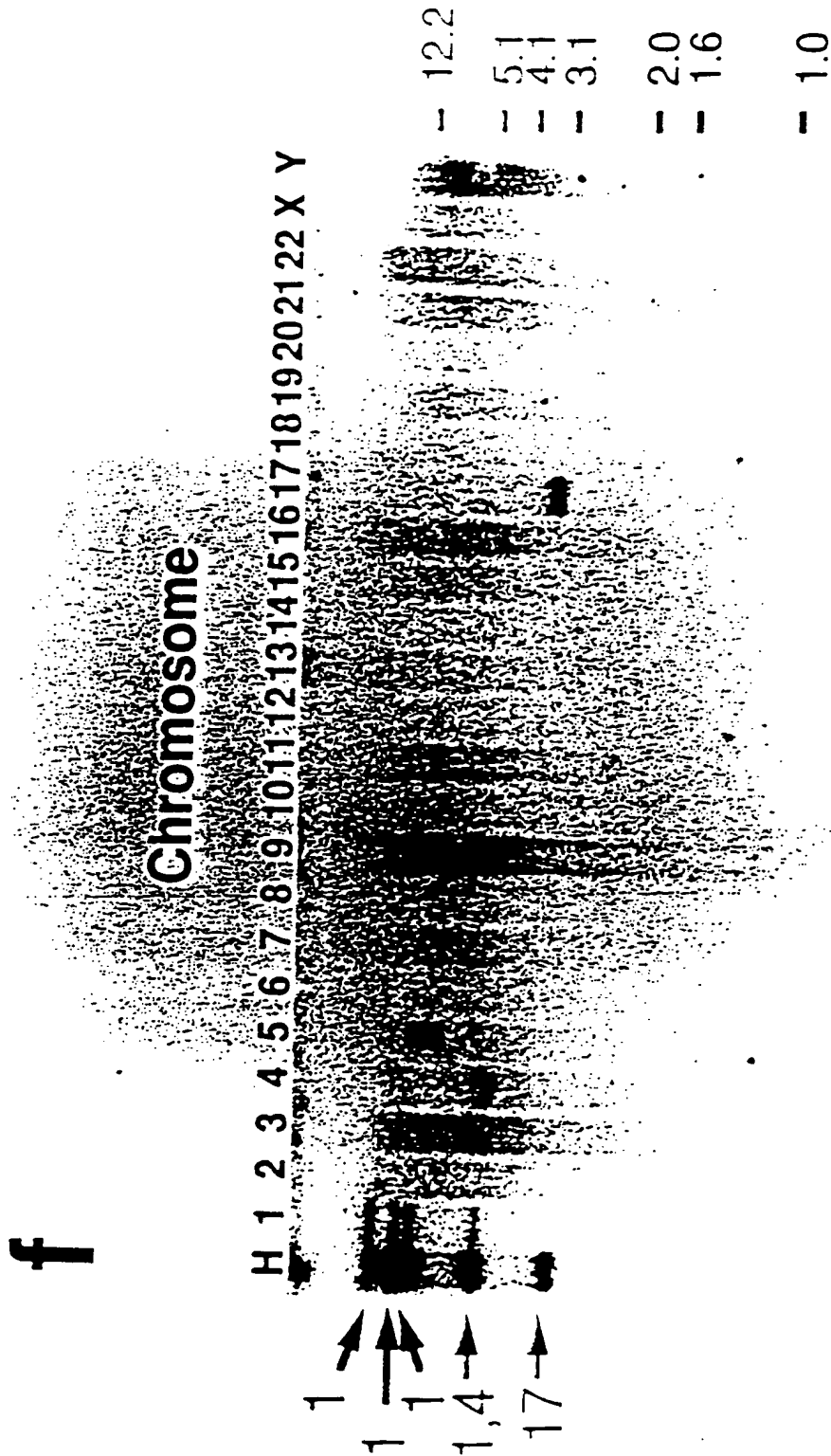


Fig. 22

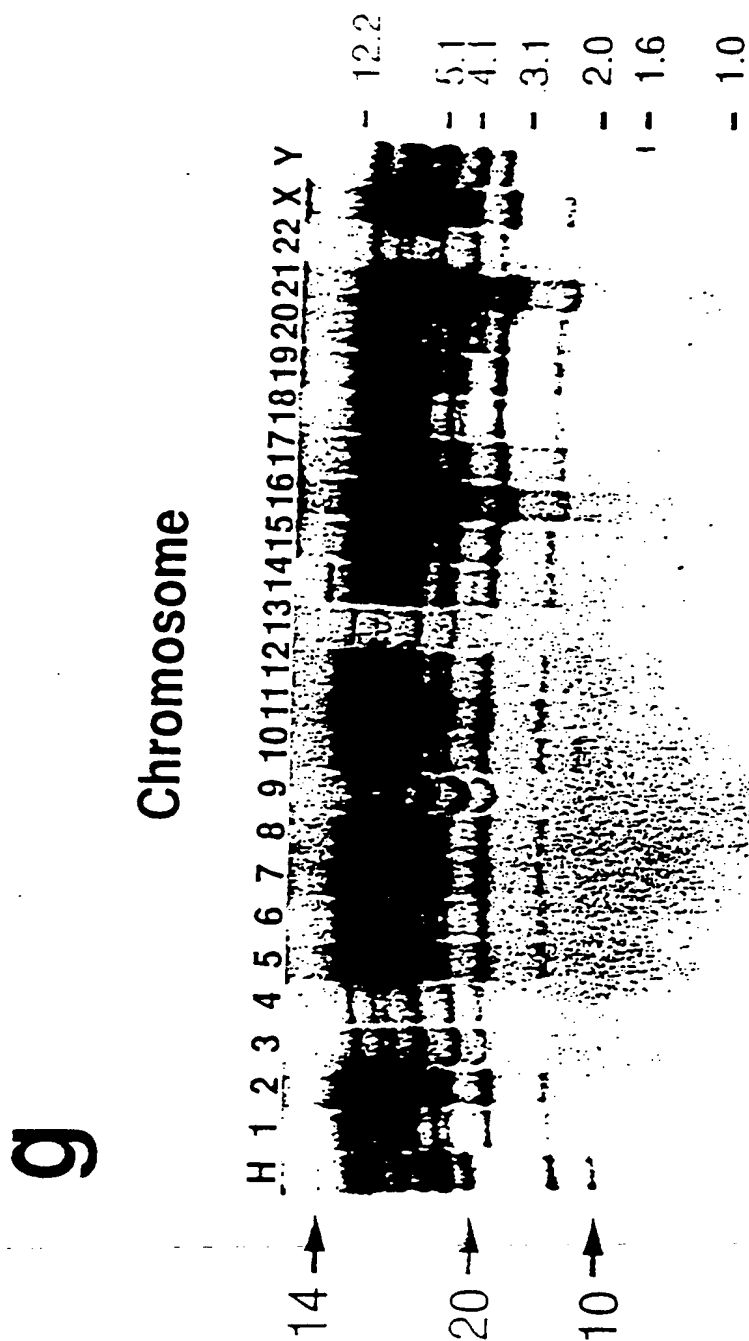


Fig. 23

## Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes				Chromosomes assigned			Background		
Clone	Sequence length	$\Xi$	$\Xi/\Xi_1$	$\Xi/\Xi_2$	$\Xi_1/\Xi_2$		Mouse	Chinese hamster	
Single band group:									
c12c11	GS000075	432	1	1	1	1	9	0	0
c12c06	GS000062	540	1	1	1	1	6.15	0	0
c12c01	GS000290	212	1	1	1	1	2	1	1
c13c05	GS000117	359	1	1	1	1	11-	0	0
c13c07	GS000120	355	1	1	1	1	2	0	0
c13f10	GS000206	267	1	1	1	1	14	0	0
c13h01	GS000279	135	1	1	1	1	12-	0	0
c13h02	GS000222	167	1	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	1	3	0	0
d0h07	GS000164	313	1	1	1	1	11	1	1
d1b10	GS000343	153	1	1	1	1	20	0	0
hm01a12	GS000223	246	1	1	1	1	27	0	0
hm01c09	GS000423	157	0	1	1	1	1	0	0
hm01c12	junk	394	1	1	1	1	17	0	0
hm01f05	GS000066	454	1	1	1	1	19.22	0	0
hm01f10	GS000299	173	0	1	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	1	6	0	0
hm01h07	GS000115	363	1	1	1	1	12	0	0
hm02a02	GS000130	344	1	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	0	10	0	0
hm02c01	GS000203	271	1	1	1	1	16	0	0
hm02c01	GS000015	590	1	1	1	1	20	0	0
hm02c02	GS000342	156	0	1	1	1	14	0	0
hm02c05	GS000401	223	1	1	0	0	n.d.	0	0
hm02g02	GS000191	278	1	1	1	1	17	0	0
hm05a05	GS000251	219	1	1	1	1	6	2	0
hm05a10	junk	392	1	1	1	1	1	1	1
hm05c10	GS000009	606	1	1	1	1	1	0	0
kmd01	junk	169	1	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	1	5	0	0
s110	GS000057	471	1	1	1	1	8	0	0
s11d11	GS000307	#175	0	0	0	1	7	0	0
s11h01	GS000269	204	1	1	1	1	3	0	0
s147	GS000060	461	1	1	1	0	2	0	0
s14c06	junk	639	1	1	1	1	1	0	0
s14g02	GS000152	322	1	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	1	4	1	1
s150	GS000143	330	1	1	1	1	17	0	0
s156	GS000002	306	1	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	1	14	0	0
s179	GS000275	196	1	1	1	1	n.d.	0	0
s246	GS000234	241	1	1	1	1	9	0	0
s247	GS000347	153	1	1	1	1	1	0	0
s270	junk	135	1	1	1	1	19	0	0

Fig. 24

Numbers of bands detected with human whole chromosomes				Chromosomes assigned		Background			
Clone	Sequence length	$\Xi$	$\Xi/\Xi_1$	$\Xi/\Xi_2$	$\Xi_1/\Xi_2$	Mouse	Chinese hamster		
s306	GS000256	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000323	165	1	1	1	1	4	3	2
s331	GS000295	207	1	1	0	1	6,15	1	1
s334	GS000165	312	1	1	1	1	1	0	0
s337	GS000276	195	1	1	1	1	17	0	0
s339	GS000295	130	1	1	1	1	n.d.	0	1
s443	GS000330	251	1	1	1	1	n.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	587	1	1	1	1	2	0	0
s633	GS000166	311	1	1	1	1	22	2	1
s550	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000025	537	1	1	1	1	3,7	0	0
tw1-19	GS000213	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	3	1	1
tw1-43	GS000093	173	1	1	1	1	14	0	0
tw1-96	GS000133	339	1	1	1	1	11	0	0
Two band group :									
e12f12	GS000195	277	1	2	2	2	1,	1	1
e13d02	GS000042	503	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,13	3	5
hm01a07	GS000207	269	2	2	2	2	7,	0	0
hm01d05	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000131	292	2	2	2	2	1,2	0	0
hm02a03	GS000435	302	2	2	2	2	3,	1	1
hm02c04	GS000221	253	2	2	2	2	3,	0	0
hm02c05	GS000146	332	2	2	2	2	17,19,22	0	0
hm05f07	GS000043	503	1	1	2	1	3,	0	0
s11d06	GS000268	205	2	2	2	2	11,12	0	0
s11g12	GS000337	255	2	2	2	2	6,	0	0
s124	GS000033	404	2	2	2	2	9,	1	1
s144	GS000132	342	1	2	2	2	1,7	0	0
s14f03	GS000239	243	1	2	2	2	2,	3	2
s15c02	junk	439	2	2	1	2	6,	0	0
s16b09	junk	420	1	1	1	2	10,14	0	0
s17c09	GS000248	223	2	2	2	2	14,	0	0
s231	junk	234	2	2	2	2	11,	0	0
s254	GS000124	353	2	2	2	2	1,	3	1
s255	GS000235	219	2	2	2	2	11,	0	0
s272	junk	195	2	2	2	2	10,16	1	1



Fig. 25

Numbers of bands detected with human whole chromosomes				Chromosomes assigned				Background	
Clone	Sequence length	E	E/B <sub>1</sub>	E/B <sub>2</sub>	3 <sub>1</sub> /B <sub>3</sub>			Mouse	Chinese hamster
s311	GS000092	333	1	1	2	2	16.	1	1
s313	junk	132	2	2	1	0	20.	0	0
s317	GS000100	339	0	0	1	2	14,14	1	1
s336	GS000134	337	2	2	2	2	12,14	0	0
s333	GS000139	233	2	2	2	1	22,X	0	0
s339	GS000233	137	2	1	1	2	17.	0	0
s394	GS000063	449	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17.	0	1
s455	junk	452	1	2	2	1	4.	0	0
s456	GS000236	132	2	2	2	2	8,10	1	2
s465	GS000201	274	1	1	2	2	6,15	0	0
s635	junk	260	1	1	1	2	9,13	0	0
s639	GS000297	203	1	2	2	2	2X	0	0
s656	GS000025 #590	2	2	0	2		6,11	0	0
twl-33	junk	352	2	2	2	2	1.	0	0
twl-39	GS000153 #321	2	2	2	2		17.	0	0
twl-70	GS000061	441	1	1	2	1	11.	0	0
twl-80	junk	453	2	2	1	2	9,17	2	2
twl-87	GS000153	316	2	2	2	2	7.	0	0
Three band group									
d0h06	GS000030	417	3	3	3	1	1.	0	0
hm05b07	junk	336	2	3	3	3	5.	0	0
hm05g02	GS000209	267	2	2	2	1	3,17,19	1	1
s129	GS000107	373	3	3	3	3	n.d.	1	1
s173	GS000357	146	1	2	2	3	2.	0	0
s17a10	GS000294	131	3	3	3	3	2,13,22	1	1
s308	GS000412	633	2	2	2	3	XX	1	1
s401	GS000224	249	2	3	3	3	6,6.	0	0
s654	GS000045	491	3	3	3	3	1,22.	0	0
twl-82	GS000208	267	3	3	3	3	13.	4	0
Four band group									
c12g07	GS000134	320	4	4	2	3	5, 14.	0	0
c13a08	GS000055	508	3	3	4	4	2,7,7,17	1	2
c13c04	GS000106 #376	4	3	3	3		n.d.	0	2
c13c09	GS000302	195	4	2	4	4	2,17.	7	2
s136	GS000160	315	4	4	4	4	4X.	2	1
s163	GS000004 #613	4	4	4	2		4,4,8,20	3	1
s479	GS000130	293	4	4	2	2	7,8,11,11,12,19	0	0
Group with 5 or more bands									
c12f08	GS000253	217	5	5	5	2	2,7,9,14.	2	0
lic01	junk	374	12	12	13	13	1,2,6.	22	20
hd10	junk	361	4	4	4	8	n.d.	12	6
hel0	junk	173	6	2	3	3	6,3,9,19,21.	3	3
hm01c05	GS000305	176	9	7	5	5	X	9	8
hm01f04	GS000246	215	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14	6

Fig. 26

Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background		
Clone	Sequence length	$\Sigma$	$\Sigma/3$	$\Sigma/3$	$\Sigma/3$		Mouse	Chinese hamster	
hm02f09	GS000273	442	3	7	7	5	3,3,6,11,13,14,15,16	0	0
hm05a02	GS000096	373	5	6	4	6	2,3,17,	3	3
hm05a04	GS000236	#239	6	6	6	7	n.d.	3	5
kmb01	junk	350	3	5	5	5	13,	14	7
s11f06	GS000316	170	6	6	6	4	1,2,2,3,4,6,13,15,	0	3
s14f01	GS000407	262	12	11	10	9	1,5,9,13,	6	3
s173	GS000094	397	5	4	6	3	1,1,1,1,4,17	0	0
s255	GS000323	167	10	12	11	14	13,	9	5
s341	junk	494	9	9	3	6	n.d.	15	3
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X,	3	5
tw1-63	junk	203	3	10	10	12	3,4,	17	11
Bands no detected:									
c13g02	GS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	GS000274	196	0	0	0	0	-	-	-
s323	GS000273	194	0	0	0	0	-	-	-
s359	GS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	GS000012	#734	0	0	0	0	-	-	-
s647	GS000103	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

## A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl<sup>6</sup> C12N15/11, C12Q1/68//G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl<sup>6</sup> C12N15/11, C12Q1/68//G01N33/566

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiations, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
X	J. Biol. Chem., Vol. 265, 1990, Wilkin, D. J. et al. "Isolation and sequence of the human farnesyl pyrophosphate synthetase cDNA:coordinate regulation of the mRNAs for farnesyl pyrophosphate synthetase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and 3-hydroxy-3-methylglutaryl coenzyme A synthetase" p. 4607-4614	1-6 (255)

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"&amp;" document member of the same patent family

Date of the actual completion of the international search

February 6, 1995 (06. 02. 95)

Date of mailing of the international search report

March 7, 1995 (07. 03. 95)

Name and mailing address of the ISA/

Japanese Patent Office

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## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Batra, S. K. et al. "Molecular cloning and sequence analysis of the human ribosomal protein S16" p. 6830-6833	1-6 (275)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
X	J. Biol. Chem., Vol. 263, 1988, Fischer, R. et al. "Multiple divergent mRNAs code for a single human calmodulin" p. 17055-17062	1-6 (386)
X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
X	J. Biol. Chem., Vol. 265, 1990, Natsumeda, Y. et al. "Two distinct cDNAs for human IMP dehydrogenase" p. 5292-5295	1-6 (454)
X	Genes Dev., Vol. 7, 1993, Patton, J. G. et al. "Cloning and characterization of PSF a novel pre-mRNA splicing factor" p. 393-406	1-6 (706)
X	Nucleic Acids Res., Vol. 16, 1988, Stanford, D. R. et al. "The complete primary structure of the human snRNP E protein" p. 10593-10605	1-6 (711)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 84, 1987, Inoue, C. et al. "Evolutionary conservation of the insulinoma gene rig and its possible function" p. 6659-6662	1-6 (723)
X	J. Immunol., Vol. 144, 1990, Jongstra-Bilen, J. et al. "Human and mouse LSP1 genes code for highly conserved phosphoproteins" p. 1104-1110	1-6 (741)
X	Biochem. J., Vol. 248, 1987, Sakai, I. et al. "The cDNA and protein sequences of human lactate dehydrogenase-B" p. 933-936	1-6 (772)

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## INTERNATIONAL SEARCH REPORT

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## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochim. Biophys. Acta., Vol. 1089, 1991, Tamura, T. et al. "Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multicatalytic proteinase complexes)" p. 95-102	1-6 (775)
X	Mol. Cell. Biol., Vol. 3, 1983, Cowan, N. J. et al. "Expression of human alpha-tubulin genes: interspecies conservation of 3' untranslated regions" p. 1738-1745	1-6 (820)
X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIB of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
X	Gene, Vol. 93, 1990 Taanman, J. W., Schrage, C., Ponne, N., Das, A., Bolhuis, P. A., de Vries, H. and Agsteribbe, E. Isolation of cDNAs encoding Subunit VIB of human cytochrome c oxidase and steady-state levels of coxVib mRNA in different tissues p. 285-291	1-6 (844)
X	J. Biol. Chem., Vol. 264, 1989, Gray, P. W. et al. "Cloning of the cDNA of a human neutrophil bactericidal protein: Structural and functional correlations" p. 9505-9509	1-6 (861)
X	Immunogenetics, Vol. 32, 1990, Angelisova, P. et al. "The human leucocyte surface antigen CD53 is a protein structurally similar to the CD37 and MRC OX-44 antigens" p. 281-285	1-6 (1158)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Koken, M. H. et al. "Structural and functional conservation of two human homologs of the yeast DNA repair gene RAD6" p. 8865-8869	1-6 (1181)
X	Oncogene, Vol. 5, 1990, Firmbach-Kraft, I. et al. "Tyk 2, prototype of a novel class of non-receptor tyrosine Kinase genes" p. 1329-1336	1-6 (1345)
X	Science, Vol. 248, 1990, Smith, C. A. et al. "A receptor for human tumor necrosis factor defines an unusual family of cellular and viral proteins" p. 1019-1023	1-6 (1431)

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

## INTERNATIONAL SEARCH REPORT

International application No.  
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## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 263, 1988, Luster, A. D. et al. "Molecular and biochemical characterization of a novel gamma-interferon-inducible protein" p. 12036-12043	1-6 (1455)
X	J. Clin. Invest., Vol. 83, 1989, Look, A. T. et al. "The human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N" p. 1299-1307	1-6 (1469)
X	J. Cell Biol., Vol. 105, 1987, Argraves, W. S. et al. "Amino Acid Sequence of the Human Fibronectin Receptor" p. 1183-1190	1-6 (1607)
X	Nucleic Acids Res., Vol. 18, 1990, Liebhaber, S. A. et al. "Characterization of a human cDNA encoding a widely expressed and highly conserved cysteine-rich protein with an unusual zinc-finger motif" p. 3871-3879	1-6 (1642)
X	J. Biol. Chem., Vol. 264, 1989, Didsbury, J. et al. "Rac, a novel ras-related family of proteins that are bolulinum toxin substrates" p. 16378-16382	1-6 (1709)
X	EMBO J., Vol. 6, 1987, Willison, K. et al. "The human homologue of the mouse t-complex gene, TCP1, is located on chromosome 6 but is not near the HLA region" p. 1967-1974	1-6 (1749)
X	J. Biol. Chem., Vol. 266, 1991, Wu, Y. et al. "Activation of globin gene expression by cDNAs from induced K562 cells: Evidence for involvement of ferritin in globin gene expression" p. 17566-17572	1-6 (1785)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ikuta, T. et al. "Three human alcohol dehydrogenase subunits: cDNA structure and molecular and evolutionary divergence" p. 634-638	1-6 (1864)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Fukumoto, H. et al. "Sequence, tissue distribution, and chromosomal localization of mRNA encoding a human glucose transporter-like protein" p. 5434-5438	1-6 (1878)

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

## INTERNATIONAL SEARCH REPORT

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## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Clin. Invest., Vol. 76, 1985, Cooke, N.E. et al. "Serum vitamin D-binding protein is a third member of the albumin and alpha fetoprotein gene family" p. 2420-2424	1-6 (1888)
X	J. Biol. Chem., Vol. 264, 1989, Huang, S.-H. et al. "Human deoxycytidine kinase: Sequence of cDNA clones and analysis of expression in cell lines with and without enzyme activity" p. 14762-14768	1-6 (1894)
X	J. Biol. Chem., Vol. 266, 1991, Huang, S.-H. et al. "Additions and corrections Human deoxytidine kinase. Sequence of cDNA clones and analysis of expression in cell lines with and without anzyme activity" p. 5353-5353	1-6 (1894)
X	Somat. Cell Mol. Genet., Vol. 11, 1985, Bell, G.I. et al. "Human alpha-2-macroglobulin gene is located on chromosome 12" p. 285-289	1-6 (1895)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 81, 1984, Yang, F. et al. "Human transferrin: cDNA characterization and chromosomal localization" p. 2752-2756	1-6 (1902)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ny, T. et al. "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor" p. 6776-6780	1-6 (1904)
X	J. Biol. Chem., Vol. 267, 1992, Bausch-Jurken, M. T. et al. "Molecular cloning of AMP deaminase isoform L: Sequence and bacterial expression of human AMPD2 cDNA" p. 22407-22413	1-6 (1908)
X	Gene, Vol. 44, 1986, Board, P. G. et al. "Molecular cloning and nucleotide sequence of human alpha-1 acid glycoprotein cDNA" p. 127-131	1-6 (1921)
X	Eur. J. Biochem., Vol. 155, 1986, Wathelet, M. et al. "Molecular cloning, full-length sequence and preliminary characterization of a 56-kDa protein induced by human interferons" p. 11-17	1-6 (2101)

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## INTERNATIONAL SEARCH REPORT

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## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids Res., Vol. 11, 1983, Chebath, J. et al. "Interferon induced 56,000 mr protein and its mRNA in human cells: molecular cloning and partial sequence of the cDNA" p. 1213-1226	1-6 (2101)
X	Biochemistry, Vol. 25, 1986, Koide, T. et al. "Amino acid sequence of human histidine-rich glycoprotein derived from the nucleotide sequence of its cDNA" p. 2220-2225	1-6 (2174)
X	Biochemistry, Vol. 22, 1983, Friezner-Degen, S. J. et al. "Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin" p. 2087-2097	1-6 (2214)
X	Biochem. J., Vol. 268, 1990, Steinkasserer, A. et al. "Heterogeneity in human serum amyloid A protein. Five different variants from one individual demonstrated by cDNA sequence analysis." p. 287-193	1-6 (2238)
X	Nucleic Acids Res., Vol. 17, 1989, Fabrizi, G. M. et al. "Sequence of a cDNA specifying subunit VIIa of human cytochrome c oxidase" p. 7107-7107	1-6 (2264)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 86, 1989, Sims, J. E. et al. "Cloning of the interleukin 1 receptor from human T cells" p. 8946-8950	1-6 (2265)
X	Eur. J. Biochem., Vol. 169, 1987, Mackinnon, C. M. et al. "Molecular cloning of cDNA for human complement component C1s. The complete amino acid sequence" p. 547-553	1-6 (2266)
X	J. Virol., Vol. 65, 1990, Tsujimoto, A. et al. "Isolation of cDNA for DNA binding proteins which specifically bind to TAX-responsive enhancer element in the LTR of HTLA-1" p. 1420-1426	1-6 (2475)
X	Immunogenetics, Vol. 37, 1993, Emi, N. et al. "Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superfamily" p. 193-198	1-6 (2556)
X	Nature, Vol. 353, 1991, Kelly, A. P. et al. "A new human HLA class II-related locus, DM" p. 571-573	1-6 (2583)

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## INTERNATIONAL SEARCH REPORT

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PCT/JP94/01916

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 265, 1990, Hla, T. et al. "An abundant transcript induced in differentiating human endothelial cells encodes a polypeptide with structural similarities to G-protein-coupled receptors" p. 9308-9313	1-6 (2600)
X	J. Biol. Chem., Vol. 267, 1992, White, R. T. et al. "Human adipsin is identical to complement factor D and expressed at high levels in adipose tissue" p. 9210-9213	1-6 (2802)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Rouault, T. A. et al. "Cloning of the cDNA encoding RNA regulatory protein-the human iron-responsive element-binding protein" p. 7958-7962	1-6 (2832)
X	Nucleic Acids Res., Vol. 17, 1989, Sawada, R. et al. "Complementary DNA sequence and deduced peptide sequence for CD59/MEM43 antigen, the human homologue of murine lymphocyte antigen Ly-6c" p. 6728-6728	1-6 (2954)
X	DNA Cell Biol., Vol. 9, 1990, Sawada, R. et al. "Isolation and expression of the full-length cDNA encoding CD59 antigen of human lymphocytes" p. 213-220	1-6 (2954)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Weller, P. A. et al. "Complete sequence of human vinculin and assignment of the gene to chromosome 10" p. 5667-5671	1-6 (2983)
X	Cell, Vol. 58, 1989, Mellentin, J. D. et al. "LYL-1, a novel gene involved by chromosomal translocation in T-cell leukemia, codes for a protein with a helix-loop-helix DNA binding motif" p. 77-83	1-6 (3023)
X	Cell, Vol. 60, 1990, Uze, G. et al. "Genetic transfer of a functional human interferon alpha receptor into mouse cells: Cloning and expression of its cDNA" p. 225-234	1-6 (3041)
X	Biochem. Biophys. Res. Commun., Vol. 179, 1991, Xiao, L. et al. "Characterization of a full length cDNA which codes for the human spermidine/spermine N-1-acetyltransferase" p. 407-415	1-6 (3053)

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## INTERNATIONAL SEARCH REPORT

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## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Casero, R. A. Jr. et al. "Isolation and characterization of a cDNA clone that codes for human spermidine/spermine N-1-acetyltransferase" p. 810-814	1-6 (3053)
X	Nucleic Acids Res., Vol. 20, 1992, Wintzerith, M. et al. "Sequence of the human RNA polymerase II largest subunit" p. 910-910	1-6 (3083)
X	J. Cell Biol., Vol. 103, 1986, Lawler, J. et al. "The Structure of Human Thrombospondin, an/ adhesive Glycoprotein with Multiple Calcium binding Sites and Homologies with Several Different Proteins" p. 1635-1648	1-6 (3266)
X	Nature, Vol. 352, 1991, Maslen, C. L. et al. "Partial sequence of a candidate gene for the marfan syndrome" p. 334-337	1-6 (3334)
X	J. Cell Biol., Vol. 111, 1990, Fishman, G. I. et al. "Molecular Characterization and Functional Expression of the Human Cardiac Gap Junction Channel" p. 589-598	1-6 (3403)
X	Cell, Vol. 40, 1985, Ebina, Y. et al. "The human insulin receptor cDNA: The structural basis for hormone-activated membrane signalling" p. 747-758	1-6 (3447)
X	Oncogene, Vol. 5, 1990, Westin, E. H. et al. "Alternative splicing of the human c-myb gene" p. 1117-1124	1-6 (3529)
X	Genomics, Vol. 4, 1989, Todd, S. et al. "cDNA sequence, interspecies comparison and gene mapping analysis of argininosuccinate lyase" p. 53-59	1-6 (3575)
X	FEBS Lett., Vol. 207, 1986, Codina, J. et al. "-Subunits of the human liver Gs/Gi signal-transducing proteins and those of bovine retinal rod cell transducin are identical" p. 187-192	1-6 (3796)
X	Nucleic Acids Res., Vol. 18, 1990, Roessler, B. J. et al. "Cloning of two distinct copies of human phosphoribosyl pyrophosphate synthetase cDNA" p. 193-193	1-6 (3828)

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biochem., Vol. 109, 1991, Sonoda, T. et. al. "Complete nucleotide sequence of human phosphoribosyl pyrophosphate synthetase subunit I (PRS I) cDNA and a comparison with human and rat PRPS gene families" p. 361-364	1-6 (3828)
X	J. Biol. Chem., Vol. 263, 1988, Wermuth, B. et al. "Human carbonyl reductase: Nucleotide sequence analysis of a cDNA and amino acid sequence of the encoded protein" p. 16185-16188	1-6 (4033)
X	Biochim. Biophys. Acta. Vol. 1048, 1990, Forrest, G. L. et al. "Induction of a human carbonyl reductase gene located on chromosome 21" p. 149-155	1-6 (4033)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Schuetz, T. J. et al. "Isolation of a cDNA for HSF2: Evidence for two heat shock factor genes in humans" p. 6911-6915	1-6 (4093)
X	Nucleic Acids Res., Vol. 13, 1985, Hallewell, R. A. et al. "Human Cu/Zn superoxide dismutase cDNA: isolation of clones synthesising high levels of active or inactive enzyme from an expression library" p. 2017-2034	1-6 (4110)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 80, 1983, Sherman, L. et al. "Nucleotide sequence and expression of human chromosome 21 - encoded superoxide dismutase mRNA" p. 5465-5469	1-6 (4110)
X	J. Biol. Chem., Vol. 268, 1993, David, V. et al. "Interaction with newly synthesized and retained proteins in the endoplasmic reticulum suggests a chaperone function for human integral membrane protein IP90 (calnexin)" p. 9585-9592	1-6 (4373)
X	J. Exp. Med., Vol. 172, 1990, Tekamp-Olson, P. et al. "Cloning and Characterization of cDNAs for Murine Macrophage Inflammatory Protein 2 and its Human Homologues" p. 911-919	1-6 (4452)

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochemistry, Vol. 30, 1991, Tomkinson, B. et al. "Characterization of cDNA for human tripeptidyl peptidase II: The N-terminal part of the enzyme is similar to subtilisin" p. 168-174	1-6 (4522)
X	J. Biol. Chem., Vol. 263, 1988, Verma, A. K. et al. "Complete primary structure of a human plasma membrane Ca <sup>2+</sup> pump" p. 14152-14159	1-6 (4673)
X	J. Biol. Chem., Vol. 267, 1992, Shechter, I. et al. "Solubilization, purification and characterization of a truncated form of rat hepatic squalene synthetase" p. 8628-8635	1-6 (4818)
X	J. Biol. Chem., Vol. 267, 1992, McKenzie, T. L. et al. "Molecular cloning, expression, and characterization of the cDNA for the rat hepatic squalene synthase" p. 21368-21374	1-6 (4818)
X	Nucleic Acids Res., Vol. 13, 1985, Furutani, Y. et al. "Cloning and characterization of the cDNAs for human and rabbit interleukin-1 precursor" p. 5869-5882	1-6 (4872)
X	Proc. Natl. Acad. Sci U.S.A., Vol. 89, 1992, Katoh, M. et al. "K-sam gene encodes secreted as well as transmembrane receptor tyrosine kinase" p. 2960-2964	1-6 (4914)
X	Differentiation, Vol. 42, 1989, Kuruc, N. et al. "Synthesis of cytokeratin 13, a component characteristic of internal stratified epithelia, is not induced in human epidermal tumors" p. 111-123	1-6 (5264)
X	J. Biol. Chem., Vol. 266, 1991, Kiefer, M. C. et al. "Identification and molecular cloning of two new 30-kDa insulin-like growth factor binding proteins isolated from adult human serum" p. 9043-9049	1-6 (5374)

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 265, 1990, Opipari, A. W. et al. "The A20 cDNA induced by tumor necrosis factor alpha-encodes a novel type of zinc finger protein" p. 14705-14708	1-6 (5427)
X	J. Biol. Chem., Vol. 265, 1990, McLean, J. W. et al. "cDNA sequence of the human integrin beta-5 subunit" p. 17126-17131	1-6 (5715)
X	Cell, Vol. 66, 1991, Ge, H. et al. "primary structure of the human splicing factor ASF reveals similarities with drosophila regulators" p. 373-382	1-6 (5860)
X	Cancer Res., Vol. 52, 1992, Kondoh, N. et al. "Differential expression of S19 ribosomal protein, laminin binding protein and HLA class I mRNAs associated with colon carcinoma progression and differentiation" p. 791-796	1-6 (6439)
X	J. Biol. Chem., Vol. 263, 1988, Collart, F. R. et al. "Cloning and sequence analysis of the human and chinese hamster inosine-5' -monophosphate dehydrogenase cDNA" p. 15769-15772	1-6 (6471)
X	J. Biol. Chem., Vol. 261, 1986, Romeo, P. -H. et al. "Molecular cloning and nucleotide sequence of a complete human uroporphyrinogen decarboxylase cDNA" p. 9825-9831	1-6 (6569)
X	J. Cell Biol., Vol. 106, 1988, Leube, R. E. et al. "Molecular characterization and expression of the stratification-related cytokeratins 4 and 15" p. 1249-1261	1-6 (6875)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Daher, K. A. et al. "Isolation and characterization of human defensin cDNA clones" p. 7327-7331	1-6 (7106)
X	J. Exp. Med., Vol. 172, 1990, Larsen, A. et al. "Expression Cloning of a Human Granulocyte Colony-stimulating Factor Receptor: a Structural Mosaic of Hematopoietin Receptor, Immunoglobulin, and Fibronectin Domains" p. 1559-1570	1-6 (7126)

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## INTERNATIONAL SEARCH REPORT

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PCT/JP94/01916

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Oncogene, Vol. 8, 1993, Schulz, A. S. et al. "The genomic structure of the human UFO receptor" p. 509-513	1-6 (7790)
A	Nature Genetics, Vol. 2, 1992, Okubo, K. et al. "Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression" p. 173-179	1-6
A	Nature Genetics, Vol. 2, 1992, Khan, A. S. et al. "Single pass sequencing and physical and genetic mapping of human brain cDNAs" p. 180-188	1-6

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